

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
19 July 2001 (19.07.2001)

PCT

(10) International Publication Number  
**WO 01/51659 A2**

- (51) International Patent Classification<sup>7</sup>: C12Q 1/68 (74) Common Representative: GENSET; Intellectual Property Dept., 24, rue Royale, F-75008 Paris (FR).
- (21) International Application Number: PCT/IB01/00116 (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (22) International Filing Date: 11 January 2001 (11.01.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data: 60/175,854 13 January 2000 (13.01.2000) US (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- (71) Applicant (*for all designated States except US*): GENSET [FR/FR]; Intellectual Property Dept., 24, rue Royale, F-75008 Paris (FR).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): CHU, Tom [US/US]; 5394 Camino Playa Norte, San Diego, CA 92124 (US). BLUMENFELD, Marta [FR/FR]; 5, rue Tagore, F-75013 Paris (FR). COHEN, Daniel [FR/FR]; 1, boulevard Richard Wallace, F-92200 Neuilly-sur-Seine (FR).

**Published:**

— without international search report and to be republished upon receipt of that report

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

WO 01/51659 A2

(54) Title: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING GENES INVOLVED IN CENTRAL NERVOUS SYSTEM DISORDERS

(57) Abstract: The invention provides polynucleotides including biallelic markers derived from genes involved in CNS disorders and from genomic regions flanking those genes. Primers hybridizing to regions flanking these biallelic markers are also provided. This invention also provides polynucleotides and methods suitable for genotyping a nucleic acid containing sample for one or more biallelic markers of the invention. Further, the invention provides methods to detect a statistical correlation between a biallelic marker allele and a phenotype and/or between a biallelic marker haplotype and a phenotype.



## **BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING GENES INVOLVED IN CENTRAL NERVOUS SYSTEM DISORDERS**

### **FIELD OF THE INVENTION**

5           The present invention is in the field of pharmacogenomics, and is primarily directed to biallelic markers that are located in or in the vicinity of genes that play a role in disorders of the brain and nervous system and to the uses of these markers. The present invention encompasses methods of establishing associations between these markers and central nervous system (CNS) disorders such as psychiatric disorders and neurodegenerative diseases as well as associations  
10       between these markers and treatment response to a variety of therapeutic agents. The present invention also provides means to determine the genetic predisposition of individuals to such diseases and means to predict responses to such drugs.

### **BACKGROUND OF THE INVENTION**

15           Advances in the technological armamentarium available to basic and clinical investigators have enabled increasingly sophisticated studies of brain and nervous system function in health and disease. Numerous hypotheses both neurobiological and pharmacological have been advanced with respect to the neurochemical and genetic mechanisms involved in central nervous system (CNS) disorders, including psychiatric disorders and neurodegenerative  
20       diseases. However, CNS disorders have complex and poorly understood etiologies, as well as symptoms that are overlapping, poorly characterized, and difficult to measure. As a result future treatment regimes and drug development efforts will be required to be more sophisticated and focused on multigenic causes, and will need new assays to segment disease populations, and provide more accurate diagnostic and prognostic information on patients suffering from CNS  
25       disorders.

#### **A. Neurological Basis of CNS Disorders**

          Neurotransmitters serve as signal transmitters throughout the body; therefore, diseases that affect neurotransmission can have serious consequences. For example, for over 30 years the leading theory to explain the biological basis of many psychiatric disorders such as depression  
30       has been the monoamine hypothesis. This hypothesis proposes that depression is partially due to a deficiency in one of the three major biogenic monoamines, namely dopamine, norepinephrine and serotonin. However, this hypothesis has been replaced by one that takes into account the overall function of the brain and no longer only considers a single neuronal system.

#### **Dopamine**

35       Dopamine is synthesized via the hydroxylation of tyrosine to dihydroxyphenylalanine (DOPA), involving the enzyme tyrosine hydroxylase (TH) and catechol O-methyl transferase (see Table 2: TH and COMT). Tyrosine hydroxylase is the rate-limiting enzyme in the synthesis

of catecholamines such as dopamine and norepinephrine. Dopamine and the enzymes involved in its biosynthesis and degradation are known to be involved in the pathophysiology of a depression, schizophrenia and Parkinson's disease. For example, it is believed tyrosine hydroxylase may be involved in the pathophysiology of psychiatric disorders and positive associations have been reported for tyrosine hydroxylase gene markers in mood disorders. However, a recent study was unable to conclude tyrosine hydroxylase variants are related with depressive symptomatology in subjects affected by mood disorder (Serretti A. et al.; *American Journal of Medical Genetics* 81(2):127-130, 1998).

Dopamine, released from the nerve terminals, is largely recaptured by a re-uptake mechanism involving dopamine transporter (DAT) (see Table 2: DAT). Following re-uptake, dopamine is metabolized by monoamine oxidases A and B (MAOA/B) (see Table 2: MAOA and MAOB). Monoamine oxidase A and B are critical enzymes in deamination of biogenic amines and may be involved in the pathophysiology of major psychoses, including mood disorder, Parkinson's disease and schizophrenia. Recently, evidence for genetic association between the MAOA gene and bipolar mood disorder was demonstrated in a Caucasian population, but not seen in a Japanese population (Sasaki T. et al.; *Biological Psychiatry* 44(9):922-924, 1998).

Receptors for dopamine regulate dopaminergic neurotransmission. A plethora of dopamine receptors exist, including the presynaptic dopamine transporter and at least five pharmacologic subtypes ( $D_1$  -which is linked to the enzyme adenylyl cyclase,  $D_2$  -not linked to adenylyl cyclase,  $D_3$ ,  $D_4$ , and  $D_5$ ). Classically, the most extensively investigated dopamine receptor is the  $D_2$  receptor, as it is stimulated by dopaminergic agonists for the treatment of Parkinson's disease and blocked by dopamine antagonist neuroleptics for the treatment of schizophrenia (see Table 2: DRD2). Recently, other dopamine receptors, particularly the  $D_4$  receptor, have become targets for new antipsychotics in the treatment of Parkinson's disease (see Table 2: DRD4). It appears the interaction of all or some of the dopamine receptors play a role in many CNS disorders. However, only a limited number of studies investigating the association of such disorders with genes of the dopaminergic pathway have been completed and often with conflicting results.

#### Norepinephrine

The noradrenergic system is known to play a large role in the determination of mood, dysfunction of contributes to the "functional" disorders of depression, mania and anxiety. It is believed depressed patients are unable to produce sufficient norepinephrine in some parts of the brain for neuronal transmission, while mania may result from excessive activity or sensitivity of this system.

The amino acid tyrosine, having been actively taken up by adrenergic neurons, is converted to DOPA by means of tyrosine hydroxylase. DOPA is then converted to dopamine and later into norepinephrine in the synaptic vesicles. Conversion of norepinephrine to

epinephrine occurs in the adrenal medulla and also in certain restricted parts of the brain. Catecholamine degradation is enzymatically controlled by MAOA/B intraneuronally, with the main norepinephrine metabolite being 3-methoxy-4-hydroxyphenylglycol.

The noradrenergic neuron is regulated by a multiplicity of receptors and for  
 5 norepinephrine, these being designated  $\alpha_1$ ,  $\alpha_2$ ,  $\beta_1$  and  $\beta_2$ . Postsynaptic norepinephrine receptors bind norepinephrine released from the presynaptic neuron and activate a molecular cascade in the postsynaptic neuron. Specifically, the activation of  $\alpha_2$  receptors causes inhibition of norepinephrine, whereas activation of  $\beta_1$  receptors leads to increased release of norepinephrine from adrenergic terminals (see Table 2: ADRB1R). Systemically, the adrenoreceptor subtypes  
 10  $\alpha_1$ ,  $\alpha_2$ ,  $\beta_1$  and  $\beta_2$  are functional in a variety of other ways ranging from vasodilatation to initiating smooth muscle relaxation. The action of norepinephrine is terminated by the norepinephrine transporter (NET), a membrane protein that serves as a reuptake pump for synaptic norepinephrine (see Table 2: NET). These receptors and transporter are the target of many therapeutic agents currently used to treat psychiatric disorders particularly depression.

#### 15 Serotonin (5-hydroxytryptamine, 5HT)

The serotonergic system is an anatomically diverse system with pathways that follow closely those of the noradrenergic system, but are quite different from those of the dopaminergic distribution. The physiological functions in which the serotonergic system is involved include sleep, appetite, nociception, diurnal rhythmicity, neuroendocrine regulation and mood. At the  
 20 level of consciousness there is also the suggestion that rational thought processes arise, using previously stored information, with the aid of the serotonergic system. Serotonergic projections innervating the hypothalamus influence the secretion of several anterior pituitary hormones. There is evidence that serotonin may serve as the final common pathway by which other neurotransmitters act in controlling secretion of many hormones.

25 Tryptophan is taken up by active transport into the neurons where it is hydroxylated by tryptophan hydroxylase to 5-hydroxytryptophan (5HTP). The latter is then decarboxylated to serotonin which, following release from the neurons, is recovered by a re-uptake mechanism. Degradation of serotonin occurs by way of MAOA/B and the majority of the metabolites are excreted in the urine.

30 Serotonin receptors come in 13 or more subtypes that can vary in their sensitivity to serotonin and in the effects they produce. An increasingly complex series of serotonin receptors is being identified. Presynaptic serotonin uptake sites and serotonin receptors designated 5HT<sub>1</sub> (and further subdivided into 5HT<sub>1a</sub>, 5HT<sub>1b</sub>, 5HT<sub>1c</sub>), 5HT<sub>2</sub>, 5HT<sub>3</sub>, 5HT<sub>4</sub>, and 5HT<sub>6</sub>, have been identified by means of pharmacological studies (see Table 2: 5HTT, 5HT1A, 5HTR2C, 5HTR6,  
 35 and 5HTR7). As a whole, communication between two neurons is complex and may be

mediated by more than one neurotransmitter; for example, the serotonergic system may co-exist with other neurotransmitter in the same synapses.

#### Gamma aminobutyric acid (GABA)

Gamma aminobutyric acid (GABA) is an important amino acid which functions as the most prevalent inhibitory neurotransmitter in the central nervous system. Gamma aminobutyric acid works in partnership with a derivative of Vitamin B-6, pyridoxine, to cross from the axons to the dendrites through the synaptic cleft, in response to an electrical signal in the neuron and inhibits message transmission. This helps control the nerve cells from firing too fast, which would overload the system.

The gamma aminobutyric acid (a) receptor (see Table 2: GABRA5 and GABRG2) appears to play a key role in modulating anxiety and could be involved in either the etiology or the pathogenesis of anxiety disorders (Crowe et al. *Am J Psychiatry* 154:8). A benzodiazepine binding site is located on this receptor, and ligands that bind to this site can either increase or decrease anxiety.

#### Growth associated protein (GAP43)

Growth associated protein (GAP43) is localized exclusively to nerve tissue and is known to play a role in synaptic transmission and membrane permeability. The expression of GAP43 is associated with mammalian peripheral nerve regeneration (Kosik et al. *Neuron* 1:127-132, 1988). A polymorphism in the 3'-untranslated region of GAP43 is found at slightly lower frequencies in Alzheimers and Parkinson's patients (Poduslo. *Hum Genet.* 92:635-636, 1993).

#### Subreceptor Activity

The activity of subreceptors has also been investigated in recent years for its role in a wide range of CNS disorders. When neurotransmitters bind to receptors on the membranes of postsynaptic neurons, they elicit a target response in the cell via a second or third messenger. Several different messenger chemicals are known including cyclic adenosine monophosphate (AMP). G proteins serve as signal transduction subunits in the cyclic AMP pathway (see Table 2: Gbeta3). G protein coupled receptors are thought to have seven membrane spanning domains and have been divided into 2 subclasses: those in which the binding site is in the extracellular domain for example receptors for glycoprotein hormones, such as thyroid stimulating hormone (TSH) and follicle stimulating hormone (FSH) and those in which the ligand binding site is likely to be in the plane of the 7 transmembrane domains for example rhodopsin and receptors for small neurotransmitters and hormones for example muscarinic acetylcholine receptor. However, orphan G-protein coupled receptor (see Table 2: HM77) does not contain N-linked glycosylation sites near the N-terminus like other members of this protein family.

There is evidence that various monoamine or monoaminergic receptors are able to alter cyclic AMP levels through the same G protein. Therefore, G proteins serve as an important cross-talk mechanism between transmitter systems in the CNS. An abnormality in a G protein or

in the responsiveness of cyclic AMP to any of the receptors may result in an alteration in monoaminergic neurotransmission. For example, guanine nucleotide binding protein olfactory type (see Table 2: GOLF) is believed to play a role in signaling involving the cAMP mediated signaling pathway as well as the norepinephrine pathway.

5    B. Endocrine Basis of CNS Disorders

Biological theories of many CNS disorders have long revolved around the main monoamine systems, namely dopamine, norepinephrine and serotonin. It is apparent, however, that these three systems do not completely explain the pathophysiology of many CNS disorders. The hypothalamic-pituitary-adrenal (HPA) axis, including the effects of corticotrophin-releasing factor and glucocorticoids, plays an important role in the pathophysiology of CNS disorders.

The hypothalamus lies at the top of the hierarchy regulating hormone secretion via the hypothalamus-pituitary-adrenal (HPA) axis. It manufactures and releases peptides that act on the pituitary, thus stimulating or inhibiting the pituitary's release of various hormones into the blood. These hormones, among them growth hormone, thyroid-stimulating hormone and  
15    adrenocorticotrophic hormone (ACTH), control the release of other hormones from target glands. In addition to functioning outside the nervous system, the hormones released in response to pituitary hormones feed back to the pituitary and hypothalamus. There they deliver inhibitory signals that serve to limit excess hormone biosynthesis.

Also included in the regulation of the HPA axis is vasopressin receptor 1A (see Table 2:  
20    AVPR1A). Vasopressin receptors are present in a number of tissues including the anterior pituitary, where they stimulate adrenocorticotrophic hormone (ACTH) release (Thibonnier et al. *Genomics* 31: 327-334, 1996).

Dysregulation of the HPA axis appears to be an important feature of many psychiatric disorders and neurodegenerative diseases. When a threat to physical or psychological well-being  
25    is detected, the hypothalamus amplifies production of corticotrophin-releasing factor (CRF), which induces the pituitary to secrete ACTH (see Table 2: CRF, CRHBP, CRFR1 and CRFR2). ACTH then instructs the adrenal glands to release cortisol. Therefore, it is believed chronic activation of the HPA axis may lay the ground for illness.

The increased HPA drive is primarily mediated by hypersecretion of corticotrophin-releasing factor. Patients with major depression show increased levels of lumbar cerebrospinal  
30    fluid (CSF) corticotrophin-releasing factor as compared to matched controls or patients with other neurologic illnesses (Plotsky, P.M., *Psych. Clin. Of North Am.*, 21(2):293-307, 1998). Dysregulation of hypothalamic corticotrophin-releasing factor neurons, whether intrinsic or extrinsic to these neurons, can result in corticotrophin-releasing factor hypersecretion leading to  
35    elevations in cortisol followed by adaptive down regulation of both pituitary and central glucocorticoid receptors and corticotrophic-releasing receptors.

The anxiolytic effects of corticotrophin-releasing factor appear to be mediated by the activation of the central noradrenergic system. A CRF-positive projection has been identified linking limbic structures to the noradrenergic locus ceruleus, stimulation of which plays an important role in emotional memory and increases tyrosine hydroxylase activity. Therefore,  
 5 primary or secondary dysfunction of corticotrophin-releasing factor would be expected to initiate a cascade of maladaptations.

Glucocorticoids and mineralocorticoids are both classes of steroid hormones that play an important role in the HPA axis; and have therefore been implicated in the pathophysiology of various psychiatric disorders and neurodegenerative diseases (see Table 2: GRL and MLR).  
 10 Glucocorticoids exert numerous effects on metabolism, reproduction, inflammation and immunity. In addition, glucocorticoids serve as the primary negative feedback mechanism that regulates the HPA axis. Mineralocorticoids maintain electrolyte balance by regulating salt and water retention in the kidneys.

Brain-derived neurotrophic factor (see Table 2: BDNF) is a member of a group of  
 15 proteins that includes neurotrophin-3/4/5 and nerve growth factor (NGF) and are believed to play a role in the etiology of a number of CNS-related disorders including schizophrenia and Parkinson's disease (Hawi et al. *Psychiatry Research* 81: 111-116, 1998 and Gasser et al. *Annals of Neurology* 36(3)387-396, 1994). BDNF plays an important role in promoting growth and maintenance during normal development and differentiation of the vertebrate system (Hanson et al. *Genomics* 13: 1331-1333, 1992). Further, it is believed BDNF has an effect on the  
 20 differentiation of dopaminergic and serotonergic neurons (Studer et al. *Euro. J. of Neuroscience* 7: 223-233, 1995).

### C. Examples of CNS Disorders

Neurotransmitter and hormonal abnormalities are implicated in disorders of movement  
 25 (e.g. Parkinson's disease, Huntington's disease, motor neuron disease, etc.), disorders of mood (e.g. unipolar depression, bipolar disorder, anxiety, etc.) and diseases involving the intellect (e.g. Alzheimer's disease, Lewy body dementia, schizophrenia, etc.). In addition, Neurotransmitter and hormonal abnormalities have been implicated in a wide range of disorders, such as coma, head injury, cerebral infarction, epilepsy, alcoholism and the mental retardation states of metabolic  
 30 origin seen particularly in childhood.

#### Schizophrenia

In developed countries schizophrenia occurs in approximately one per cent of the adult population at some point during their lives. There are an estimated 45 million people with schizophrenia in the world, with more than 33 million of them in the developing countries.  
 35 Moreover, schizophrenia accounts for a fourth of all mental health costs and takes up one in three psychiatric hospital beds. Most schizophrenia patients are never able to work. The cost of schizophrenia to society is enormous. In the United States, for example, the direct cost of

treatment of schizophrenia has been estimated to be close to 0.5% of the gross national product. Standardized mortality ratios (SMRs) for schizophrenic patients are estimated to be two to four times higher than the general population and their life expectancy overall is 20 % shorter than for the general population.

5           The most common cause of death among schizophrenic patients is suicide (in 10% of patients) which represents a 20 times higher risk than for the general population. Deaths from heart disease and from diseases of the respiratory and digestive system are also increased among schizophrenic patients.

          Schizophrenia comprises a group of psychoses with either 'positive' or 'negative'  
10   symptoms. Positive symptoms consist of hallucinations, delusions and disorders of thought; negative symptoms include emotional flattening, lack of volition and a decrease in motor activity.

          A number of biochemical abnormalities have been identified and, in consequence, several neurotransmitter-based hypotheses have been advanced over recent years; the most  
15   popular one has been "the dopamine hypothesis," one variant of which states that there is over-activity of the mesolimbic dopamine pathways at the level of the D<sub>2</sub> receptor. However, researchers have been unable to consistently find an association between various receptors of the dopaminergic system and schizophrenia.

          In addition to the hypotheses which are briefly presented here, and which attempt to  
20   draw together the neurochemical observations in schizophrenia, one should add that some abnormalities of cortical neuropeptides are well documented. These abnormalities include changes in the levels of somatostatin, substance P, cholecystokinin (CCK) and vasoactive intestinal peptide (VIP) found in association with negative symptom defect states in the temporal area of the brain (i.e. the hippocampus, amygdala and neocortex), in particular.

#### 25           Bipolar Disorder

          Bipolar disorders are relatively common, occurring in about 1.3% of the population, and  
have been reported to constitute about half of the mood disorders seen in psychiatric clinics. Bipolar disorders have been found to vary with gender depending of the type of disorder; for example, bipolar disorder I is found equally among men and women, while bipolar disorder II is  
30   reportedly more common in women. The age of onset of bipolar disorders is typically in the teenage years and diagnosis is typically made in the patient's early twenties. Bipolar disorders also occur among the elderly, generally as a result of a neurological disorder or other medical conditions. In addition to the severe effects on patients' social development, suicide completion rates among bipolar patients are reported to be about 15%.

35           Bipolar disorders are characterized by phases of excitement and depression; the excitement phases (mania) and depressive phases can alternate or occur in numerous admixtures with varying degrees of severity and duration. Because bipolar disorders can exist in different

forms and display different symptoms, the classification of bipolar disorder has been the subject of extensive studies resulting in the definition of bipolar disorder subtypes and widening of the overall concept to include patients previously thought to be suffering from different disorders. Bipolar disorders often share certain clinical signs, symptoms, treatments and neurobiological features with psychotic illnesses in general and therefore present a challenge to the psychiatrist to make an accurate diagnosis. Furthermore, because the course of bipolar disorders and various mood and psychotic disorders can differ greatly, it is critical to characterize the illness as early as possible in order to offer means to manage the illness over a long term.

Diagnosis of bipolar disorder can be very challenging. One particularly troublesome difficulty is that some patients exhibit mixed states, simultaneously manic and dysphoric or depressive, but do not fall into the DSM-IV classification because not all required criteria for mania and major depression are met daily for at least one week. Other difficulties include classification of patients in the DSM-IV groups based on duration of phase since patients often cycle between excited and depressive episodes at different rates. In particular, it is reported that the use of antidepressants may alter the course of the disease for the worse by causing "rapid-cycling". Also making diagnosis more difficult is the fact that bipolar patients, particularly at what is known as Stage III mania, share symptoms of disorganized thinking and behavior with bipolar disorder patients. Furthermore, psychiatrists must distinguish between agitated depression and mixed mania; it is common that patients with major depression exhibit agitation, resulting in bipolar-like features.

For both schizophrenia and bipolar disorder, all the known molecules used for treatment have side effects and act only against the symptoms of the disease. There is a strong need for new molecules without associated side effects or reduced side effects which are directed against targets that are involved in the causal mechanisms of schizophrenia and bipolar disorder. Therefore, tools facilitating the discovery and characterization of these targets are necessary and useful.

The aggregation of schizophrenia and bipolar disorder in families, the evidence from twin and adoption studies, and the lack of variation in incidence worldwide, indicate that schizophrenia and bipolar disorder are primarily genetic conditions, although environmental risk factors are also involved at some level as necessary, sufficient, or interactive causes. For example, schizophrenia occurs in 1% of the general population. However, if a subject has one grandparent with schizophrenia, the risk of getting the illness increases to about 3%, while one parent with Schizophrenia increases risk to about 10%. When both parents have schizophrenia, the risk rises to approximately 40%. Consequently, there is a strong need to identify genes involved in schizophrenia and bipolar disorder. The knowledge of these genes will allow researchers to understand the etiology of schizophrenia and bipolar disorder and could lead to



drugs and medications which are directed against the cause of the diseases, not just against their symptoms.

There is also a great need for new methods to detect susceptibility to schizophrenia and bipolar disorder, as well as for preventing or following up the development of the disease.

- 5 Diagnostic tools could also prove extremely useful. Indeed, early identification of subjects at risk of developing schizophrenia would enable early and/or prophylactic treatment to be administered. Moreover, accurate assessments of the eventual efficacy of a medicament as well as the patient's eventual tolerance to it may enable clinicians to enhance the benefit/risk ratio of schizophrenia and bipolar disorder treatment regimes.

10 Depression

- Depression is a serious medical illness that affects 340 million people worldwide. In contrast to the normal emotional experiences of sadness, loss, or passing mood states, clinical depression is persistent and can interfere significantly with an individual's ability to function. As a result, depression is the leading cause of disability throughout the world with an estimated cost
- 15 of \$53 billion each year in the United States alone.

- Symptoms of depression include depressed mood, diminished interest or pleasure in activities, change in appetite or weight, insomnia or hypersomnia, psycho-motor agitation or retardation, fatigue or loss of energy, feelings of worthlessness or excessive guilt, anxiety, inability to concentrate or act decisively, and recurrent thoughts of death or suicide. A diagnosis
- 20 of unipolar major depression (or major depressive disorder) is made if a person has five or more of these symptoms and impairment in usual functioning nearly every day during the same two-week period. The onset of depression generally begins in late adolescence or early adult life; however, recent evidence suggests depression may be occurring earlier in life in people born in the past thirty years.

- 25 The World Health Organization predicts that by the year 2020 depression will be the greatest burden of ill-health to people in the developing world, and that by then depression will be the second largest cause of death and disability. Beyond the almost unbearable misery it causes, the big risk in major depression is suicide. Within five years of suffering a major depression, an estimated 25% of sufferers try to kill themselves. In addition, depression is a
- 30 frequent and serious complication of heart attack, stroke, diabetes, and cancer. According to one recent study that covered a 13-year period, individuals with a history of major depression were four times as likely to suffer a heart attack compared to people without such a history.

- Depression may be a feature in up to 50% of patients with CNS disorders such as Parkinson's disease and Alzheimer's disease. The neuronal loss in the locus ceruleus, typical of
- 35 Alzheimer's disease, is greatest in those patients who have depression; such patients also have lower norepinephrine levels than do those who lack depressive features. Approximately 50% of

patients with Alzheimer's disease have less norepinephrine than normal in the majority of cortical and subcortical areas of the brain that have been examined to date.

Many neurochemical findings are coming to light implicating a biological basis for the depression, at least for certain subtypes. Abnormalities of monoamine function have been  
5 recognized in depression for many years involving norepinephrine, serotonin and dopamine. Changes in adrenoceptor density and function as well as changes in adrenoceptors associated with the pituitary-adrenal axis function strongly implicate a disorder in central noradrenergic transmission in depression. This dysfunction may be caused by changes in the activity of tyrosine hydroxylase. The effect of corticotrophin releasing factor in modulating the activity of  
10 noradrenergic neurons in the locus ceruleus may provide the link between environmental trigger factors and central noradrenergic dysfunction, along with dysfunction of the HPA axis.

Dysfunction of serotonin metabolism, as shown by decreased concentrations of the metabolite 5HIAA in cerebrospinal fluid (CSF), is linked with depression; nevertheless, it is not a feature in all patients with depression. Therefore, a subgroup entitled "serotonin depression"  
15 has been proposed. Often included among those who suffer from serotonin depression are patients who also suffer a number of neurological diseases. A reduction in the number of serotonin-containing neurons in the median raphe in Parkinson's disease, Alzheimer's disease and, possibly, the elderly, is associated with the development of depression.

Low levels of the dopamine metabolite HVA are found in the CSF in patients with  
20 depression. In addition, dopamine agonists produce a therapeutic response in depression.

Presently, antidepressants are designed to address many of the symptoms of depression by increasing neurotransmitter concentration in aminergic synapses. Distinct pharmacologic mechanisms allow the antidepressants to be separated into seven different classes. The two classical mechanisms are those of tricyclic antidepressants (TCAs) and monoamine oxidase  
25 inhibitors (MAOIs). The most widely prescribed agents are the serotonin selective reuptake inhibitors (SSRIs). Three other classes of antidepressants, like the SSRIs, increase serotonergic neurotransmission, but they also have additional actions, namely dual serotonin and norepinephrine reuptake inhibition; serotonin-2 antagonism/reuptake inhibition; and  $\alpha_2$  antagonism plus serotonin-2 and -3 antagonism. The selective norepinephrine and dopamine  
30 reuptake inhibitors define a novel class of antidepressant that has no direct actions on the serotonin system.

Recent findings suggest some re-appraisal and modifications of the monoamine hypothesis are necessary. The increased levels of monoamine transmitters at the synapses, although quickly produced in response to antidepressant therapy, are in contrast with the much  
35 slower clinical recovery of the patient from depression, which takes about two weeks to begin and may only reach maximal levels several weeks later. Moreover, should acute depletion of either norepinephrine and/or serotonin occur experimentally in a normal individual, then

depression does not, in the short-term, occur. Not in keeping with the hypothesis, too, is the cerebral resistance generated in response to the pharmacological changes induced by antidepressant compounds. These counteractive changes comprise reduction in the number of post-synaptic  $\beta$ -receptors, together with a lowered firing rate of noradrenergic neurons.

5           In addition, there are subsets of patients with differential responses to antidepressants. Thus far, biochemical predictors of treatment response have failed to identify definite parameters that could correctly identify patients more likely to respond to particular classes of antidepressants (Schatzberg, Alan F., *Journal of Clinical Psychiatry*, 59:15-18, 1998). As a result, psychiatrists often must choose a treatment based on intuition or trial and error. However, 10 probes such as biallelic markers could serve as an invaluable tool to successfully identify patients who might respond preferentially to existing and new antidepressants (Charney, Dennis S, *Journal of Clinical Psychiatry*, 59:11-14, 1998). In particular, markers from genes known to affect drug response such as transcription factors (see Table 2: SEF-1B) and drug metabolizing enzymes (see Table 2: CYP3A4) need to be investigated to determine "responders" and "non-responders" to medicaments. 15

While modulating monoamine activity as a therapeutic strategy continues to dominate research, an important new development has been the emergence of novel mechanisms of action, notably modulation of the activity of neuropeptides, namely through the neuropeptide receptor Y1, the tachykinin NK1 receptor and nicotinic receptors (see Table 2: NPY1R, TACR1 and 20 CHRNA7). Recent clinical trials showed that tachykinin NK1 receptor antagonists are effective in treating depression and chemotherapy-induced emesis. Therefore, it is well possible that such antagonists will be clinically useful for treatment of specific CNS disorders. Nicotinic receptors are known to serve as important ligand-gated ion channels active in classical, excitatory neurotransmission and perhaps more novel forms of neurochemical signaling. Their critical 25 functional roles both centrally and peripherally make them ideal targets for regulation of the nervous system. Finally, new antidepressants that may render the HPA axis more sensitive to glucocorticoid feedback are being investigated as well.

In addition to monoamine dysfunction as a possible cause of depression, researchers have reported increased activity in the HPA axis in untreated depressed patients, as evinced by 30 raised levels of cortisol in urine, blood and cerebrospinal fluid, as well as by other measures. Numerous studies have confirmed that substantial numbers of depressed patients, particularly those most severely affected, display HPA axis hyperactivity. Patients with depression frequently have symptom clusters which point strongly to involvement of the HPA system as a relay station between neurocircuitries in the brain and peripheral hormone and autonomic 35 nervous function. It has been proposed that this increased, state-dependent hyperactivity of the HPA system in depression is probably initiated and/or maintained by the combination of enhanced central production of corticotrophin-releasing factor and desensitization of the binary,

glucocorticoid receptor binding system in the hippocampus, which is the central regulator of HPA system activity.

Deeper investigation of the phenomenon has now revealed alterations at each level of the HPA axis in depressed patients. For instance, both the adrenal gland and the pituitary are enlarged, and the adrenal gland hypersecretes cortisol. But many researchers, have become persuaded that aberrations in CRF-producing neurons of the hypothalamus and elsewhere bear most of the responsibility for HPA axis hyperactivity and the emergence of depressive symptoms.

Many studies have shown corticotrophin-releasing factor concentrations in cerebrospinal fluid to be elevated in depressed patients, compared with control subjects or individuals with other psychiatric disorders. This magnification of corticotrophin-releasing factor levels is reduced by treatment with antidepressants and by effective electroconvulsive therapy. Further, postmortem brain tissue studies have revealed a marked exaggeration both in the number of CRF-producing neurons in the hypothalamus and in the expression of the corticotrophin-releasing factor gene (resulting in elevated corticotrophin-releasing factor synthesis) in depressed patients as compared with controls. Moreover, delivery of corticotrophin-releasing factor to the brains of laboratory animals produces behavioral effects that are cardinal features of depression in humans, namely, insomnia, decreased appetite, decreased libido and anxiety.

Geneticists have provided some of the oldest proof of a biological component to depression in many people. Depression and manic-depression frequently run in families. Thus, close blood relatives of patients with severe depressive or bipolar disorder are much more likely to suffer from those or related conditions than are members of the general population. Studies of identical and fraternal twins also support an inherited component. Illness in both members of a pair is much higher for manic-depression in identical twins than in fraternal and is somewhat elevated for depression alone.

In the past 20 years, genetic researchers have expended great effort trying to identify the genes which contribute to depression. So far, though, those genes have evaded discovery, perhaps because a predisposition to depression involves several genes, each of which makes only a small, hard-to-detect contribution. As a result, psychiatrists today have to choose antidepressant medications by intuition and trial and error; a situation that can put suicidal patients in jeopardy for weeks or months until the right compound is selected. Therefore, there is a strong need to successfully identify genes involved in depression; thus allowing researchers to understand the etiology of depression and address its cause, rather than symptoms.

#### Alzheimer's Disease

Alzheimer's disease is characterized by the onset in middle age of a slowly progressive dementia; there is loss of memory for past events, inability to develop new memories and impairment of intellect, all leading to a lessened capacity for dealing with the tasks and problems

of daily living. It is the most common cause of both presenile and senile dementia. Alzheimer's disease is not the non-specific degenerative disorder of the CNS that it was once thought to be, as neurochemical studies on postmortem material now reveal the degeneration to be selective for certain neuronal populations in the subcortical and cortical areas; other cell populations seem to be unaffected. Senile plaques and neurofibrillary tangles are the characteristic histological feature, found throughout the cerebral cortex and especially in certain regions of the limbic system (the amygdala and hippocampus), perhaps accounting for the memory loss so typical of the early phase of the disease. In addition, there is reduction of acetylcholine, norepinephrine, serotonin and somatostatin in the subcortical areas in Alzheimer's disease.

10           The activity of CAT, the enzyme involved in acetylcholine synthesis, is markedly decreased in Alzheimer's disease. This decrease does not occur in all areas of the brain, but does so particularly in the hippocampus and amygdala, which are some of the main sites where senile plaques and neurofibrillary tangles accumulate. The loss of such cortical cholinergic activity correlates well with the degree of dementia in patients with this disease. A further finding is that 15   nerve growth factor (NGF) is now known to be involved in the maintenance of cholinergic neurons in the forebrain; also, nicotine, a cholinomimetic compound, is able to stimulate dopaminergic neurons via their nicotinic receptors; thus, seemingly, to provide smokers with some protection against degeneration of the dopaminergic neurons. The forebrain cholinergic system degenerates not only in Alzheimer's disease, but also in alcohol-induced dementia, Pick's 20   disease, Lewy body dementia, progressive supranuclear palsy and in Parkinson's disease.

          In Alzheimer's disease there is a reduction of both serotonin and its receptor proteins in the temporal lobe of the brain, as revealed from studies on autopsy and biopsy material. The loss of serotonin is, however, less than in Parkinson's disease and it would be unlikely, therefore, that the severe memory loss of Alzheimer's disease could be accounted for on this basis alone, 25   although in Parkinson's disease there is an important difference in that the 5HT<sub>2</sub> receptor is not decreased. Of interest in this context, but not necessarily related, is the bradyphrenia (characterized by difficulty in concentration, slowing of thought processes and inability to associate ideas) of Parkinson's disease where serotonin is low in most of the cortical regions. In the Lewy body type of senile dementia it is common for visual hallucinations to occur, and it is 30   of great interest that in the temporal lobe the serotonergic activity is higher (as shown by the raised serotonergic:cholinergic ratio) in those patients who suffer from hallucinations compared with those who do not.

          In addition to the involvement of serotonin in Alzheimer's disease, patients also suffer from decreased levels of norepinephrine and several neuropeptides. It is in those patients with 35   Alzheimer's disease who also have depression that there is not only greatest reduction in the number of neurons within the locus ceruleus but also a markedly reduced norepinephrine content. There is also associated reduction in cortical somatostatin and corticotrophin-releasing factor,

and loss of the somatostatin content of neurons in the temporal cortex develops early in the condition.

There is no known definitive cure for Alzheimer's disease; therefore, treatment is aimed at relief of symptoms and protection from the effects of the deteriorating condition. Most treatments are still considered experimental or have had variable results. Treatment is also aimed at underlying disorders that contribute to confusion such as heart failure, hypoxia, thyroid disorders, anemia, nutritional disorders, infections, and psychiatric conditions such as depression. The correction of coexisting medical and psychiatric disorders often improves the patient's mental function.

#### 10        Parkinson's Disease

Parkinson's disease is a disabling progressive neurodegenerative disorder characterized by tremor, rigidity, bradykinesia, and loss of postural reflexes. In the United States, about a million people are believed to suffer from Parkinson's disease, and about 50,000 new cases are reported every year. Because the symptoms typically appear later in life, these Tables are expected to grow as the average age of the population increases over the next several decades. The disorder is most frequent among people in there 70s and 80s, and appears to be slightly more common in men than in women. Parkinson's disease is found all over the world. The rates vary from country to country, but it is not clear whether this reflects true ethnic or geographic differences or simply variations in data collection.

20        The pathology is not completely understood, but there appears to be consistent changes in the melanin-containing nerve cells in the brainstem (substantia nigra, locus ceruleus), where there are varying degrees of nerve cell loss with reactive gliosis along with eosinophilic intracytoplasmic inclusions (Lewy bodies). As a result, the primary neurochemical defect in Parkinson's disease is the loss of dopaminergic projections to the striatum. Moreover, the loss of these populations of neurons also leads to neurotransmitter deficits, but to a lesser extent than that which accompanies the massive degeneration of dopaminergic neurons. For example, norepinephrine, serotonin and acetylcholine are variably decreased in Parkinson's disease due to loss of neurons in the locus ceruleus, raphe nuclei and the nucleus basalis of Meynert. Thus, some of the secondary clinical features of Parkinson's disease have been ascribed to these neurotransmitter deficits.

30        The neurochemical defect associated with Parkinson's disease can be partially corrected by L-DOPA, which helps replace the brain's dopamine, but cannot reverse the progression of the disease. There is no specific biological test for the diagnosis of Parkinson's disease. Twin studies have shown variable results and suggest that the genetics of this disorder will prove to be complex. Despite the importance and severity of Parkinson's disease and many years of research, a cause has not been identified and there is neither means of preventing the disease nor a proven permanent cure.

Findings of considerable importance in this search would be the location of a genetic marker, determination of the probability of penetrance, determination of possible genetic heterogeneity, and evidence of multifactorial inheritance with environmental interaction. Genetic factors determining susceptibility to Parkinson's disease will enhance epidemiological studies and possibly lead to identification of susceptible groups and of significant risk factors.

#### Huntington's Disease

Huntington's disease is a hereditary neurodegenerative disease that generally develops subtly in a person's thirties or forties; though it can begin any time between childhood and old age. In the United States alone, about 30,000 people have Huntington's disease, while at least 150,000 others have a 50 percent risk of developing the disease and thousands more of their relatives live with the possibility that they, too, might develop Huntington's disease.

Huntington's disease is characterized by difficulties in three areas: a movement disorder, dementia, and psychiatric disturbances. The movement disorder consists of two parts: involuntary twitching movement which first tend to involve the fingers and toes and then progress to include the whole body, and difficulties with voluntary movements in the form of clumsiness, stiffness, or trouble with walking. Dementia refers to a gradual loss of intellectual abilities such as memory, concentration, problem solving, and judgment. Psychiatric disturbances do not strike every person with Huntington's disease, but when they do, usually take the form of depression, irritability, and apathy. Depression and other psychiatric conditions in people with Huntington's disease, which seem to result from damage to the brain, can be debilitating.

Loss of neurotransmitter receptors, especially glutamate and dopamine receptors, is one of the pathologic hallmarks of patients with Huntington's disease (Cha J.H. et al.; *Proc National Acad Sci USA* May 26;95(11):6480-5, 1998). In addition, deficiency of GABA permits excessive dopaminergic activity in the corpus striatum resulting in onset of Huntington's disease, on account of the imbalance generated between cholinergic and dopaminergic systems.

Researchers have identified a single gene product thought to be causal when mutated by a tri-nucleotide repeat expansion. However, there is at present no cure for Huntington's disease or even any direct treatments, although researchers are presently working on a number of treatments which may slow down the progression of the disease. In the early and middle stages of the disease, medications called neuroleptics, which are given in larger doses for psychiatric complaints, can be given in small doses to Huntington's disease patients to suppress the involuntary movements. Drugs that cause increased dopamine release in the brain and dopamine receptor agonists are used, but both precipitate nausea and vomiting as side effects and dopamine antagonists are anti-emetic.

#### Pharmacogenomics and CNS Disorders

The vast majority of common diseases, such as all of the CNS disorders described above, are polygenic, meaning multiple genes cause them. In addition, these diseases are modulated by environmental factors such as pollutants, chemicals and diet. This is why many diseases are considered to be multifactorial; they result from a synergistic combination of factors, both genetic and environmental. Therapeutic management and drug development could be markedly improved by the identification of specific genetic polymorphisms that determine and predict patient susceptibility to diseases or patient responses to drugs.

To assess the origins of individual variations in disease susceptibility or drug response, pharmacogenomics uses the genomic technologies to identify polymorphisms within genes which are part of biological pathways involved in disease susceptibility, etiology, and development, or more specifically in drug response pathways responsible for a drug's efficacy, tolerance or toxicity. Pharmacogenomics can also provide tools to refine the design of drug development by decreasing the incidence of adverse events in drug tolerance studies, by better defining patient subpopulations of responders and non-responders in efficacy studies and, by combining the results obtained therefrom, to further allow better enlightened individualized drug usage based on efficacy/tolerance prognosis. Pharmacogenomics can also provide tools to identify new targets for designing drugs and to optimize the use of already existing drugs, in order to either increase their response rate and/or exclude non-responders from corresponding treatment, or decrease their undesirable side effects and/or exclude from corresponding treatment patients with marked susceptibility to undesirable side effects. However, for pharmacogenomics to become clinically useful on a large scale, additional molecular tools and diagnostics tests must become available.

#### Genetic Analysis of Complex Traits

Until recently, the identification of genes linked with detectable traits has relied mainly on a statistical approach called linkage analysis. Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific trait throughout generations within a family. Linkage analysis involves the study of families with multiple affected individuals and is useful in the detection of inherited traits, which are caused by a single gene, or possibly a very small number of genes. Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and which have a high penetrance (the probability that a person with a given genotype will exhibit a trait). About 100 pathological trait-causing genes have been discovered using linkage analysis over the last 10 years. But, linkage studies have proven difficult when applied to complex genetic traits. Most traits of medical relevance do not follow simple Mendelian monogenic inheritance. However, complex diseases often aggregate in families, which suggests that there is a genetic component to be found. Such complex traits are often due to the combined action of multiple genes as well as environmental factors. Such complex traits include susceptibilities to heart disease, hypertension,



diabetes, cancer and inflammatory diseases. Drug efficacy, response and tolerance/toxicity can also be considered as multifactorial traits involving a genetic component in the same way as complex diseases. Linkage analysis cannot be applied to the study of such traits for which no large informative families are available. Moreover, because of their low penetrance, such  
5 complex traits do not segregate in a clear-cut Mendelian manner as they are passed from one generation to the next. Attempts to map such diseases have been plagued by inconclusive results, demonstrating the need for more sophisticated genetic tools.

Knowledge of genetic variation in the neuronal and endocrine systems is important for understanding why some people are more susceptible to disease or respond differently to  
10 treatments. Ways to identify genetic polymorphism and to analyze how they impact and predict disease susceptibility and response to treatment are needed.

Although the genes involved in the neuronal and endocrine systems represent major drug targets and are of high relevance to pharmaceutical research, we still have scant knowledge concerning the extent and nature of, sequence variation in these genes and their regulatory  
15 elements. In the case where polymorphisms have been identified the relevance of the variation is rarely understood. While polymorphisms hold promise for use as genetic markers in determining which genes contribute to multigenic or quantitative traits, suitable markers and suitable methods for exploiting those markers have not been found and brought to bare on the genes related to disorders of the brain and nervous system.

20 In the cases where polymorphisms have been identified, the relevance of the variation is rarely understood. While polymorphisms hold promise for use as genetic markers in determining which genes contribute to multigenic or quantitative traits, suitable markers and suitable methods for exploiting those markers have not been found and brought to bare on the genes related to central nervous system disorders.

25

#### SUMMARY OF THE INVENTION

The present invention is based on the discovery of a set of novel CNS disorder-related biallelic markers. See Table 7. These markers are located in the coding regions as well as non-coding regions adjacent to genes which express proteins associated with CNS disorders. The  
30 position of these markers and knowledge of the surrounding sequence has been used to design polynucleotide compositions which are useful in determining the identity of nucleotides at the marker position, as well as more complex association and haplotyping studies which are useful in determining the genetic basis for disease states involving the neuronal and endocrine systems. In addition, the compositions and methods of the invention find use in the identification of the  
35 targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterization of the differential efficacious responses to and side effects from pharmaceutical agents acting on CNS disorders. Further, the compositions and methods of the invention may be

employed in a process for screening for antagonists and/or agonists for the polypeptides of the invention. Such molecules may prove useful as therapeutics in the diagnosis and/or treatment of CNS disorders, particularly depression.

A first embodiment of the invention encompasses polynucleotides consisting of,  
 5 consisting essentially of, or comprising a contiguous span of nucleotides of a sequence selected as an individual or in any combination from the group consisting of SEQ ID NO: 1-542, the complements thereof, the sequences described in any one or more of Tables 8, 9, 10, 11, 12, 13 and 14 and the complements thereof, wherein said contiguous span is at least 6, 8, 10, 12, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 500 or 1000 nucleotides in length, to the extent that such a  
 10 length is consistent with the lengths of the particular Sequence ID. The present invention also relates to polynucleotides hybridizing under stringent or intermediate conditions to a sequence selected from the group consisting of SEQ ID NO: 1-542; and the complements thereof. In addition, the polynucleotides of the invention encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination:  
 15 Said contiguous span may optionally include the CNS disorder-related biallelic marker in said sequence; Optionally either the original or the alternative allele of Table 9 may be specified as being present at said CNS disorder-related biallelic marker; Optionally either the first or the second allele of Tables 8 or 10 may be specified as being present at said CNS disorder-related biallelic marker; Optionally, said polynucleotide may consist of, or consist essentially of a  
 20 contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a CNS disorder-related biallelic marker of said sequence, and optionally the original allele of Table 9 is present at said biallelic marker; Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of said polynucleotide or at the center of said  
 25 polynucleotide; Optionally, the 3' end of said contiguous span may be present at the 3' end of said polynucleotide; Optionally, biallelic marker may be present at the 3' end of said polynucleotide; Optionally, the 3' end of said polynucleotide may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500 or 1000 nucleotides upstream of a CNS disorder-related biallelic marker in said sequence, to the extent that such a distance is consistent with the  
 30 lengths of the particular Sequence ID; Optionally, the 3' end of said polynucleotide may be located 1 nucleotide upstream of a CNS disorder-related biallelic marker in said sequence; and Optionally, said polynucleotide may further comprise a label.

A second embodiment of the invention encompasses any polynucleotide of the invention attached to a solid support. In addition, the polynucleotides of the invention which are attached  
 35 to a solid support encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said polynucleotides may be specified as attached individually or in groups of at least 2, 5, 8, 10, 12,

15, 20, or 25 distinct polynucleotides of the inventions to a single solid support; Optionally, polynucleotides other than those of the invention may be attached to the same solid support as polynucleotides of the invention; Optionally, when multiple polynucleotides are attached to a solid support they may be attached at random locations, or in an ordered array; Optionally, said  
 5 ordered array may be addressable.

A third embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, determining the identity of one or more nucleotides at a CNS disorder-related biallelic marker. Microsequencing primers are provided in Table 12. In addition, the polynucleotides of the invention for use in determining the identity of one or more  
 10 nucleotides at a CNS disorder-related biallelic marker encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination. Optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID NO: 1-542; and the complements thereof; Optionally, said polynucleotide may comprise a sequence disclosed in  
 15 the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said determining may be performed in a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay; Optionally, said polynucleotide may be attached to a solid support, array, or addressable array; Optionally, said polynucleotide may be labeled.

20 A fourth embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, amplifying a segment of nucleotides comprising a CNS disorder-related biallelic marker. Amplification primers are provided in Table 13. In addition, the polynucleotides of the invention for use in amplifying a segment of nucleotides comprising a CNS disorder-related biallelic marker encompass polynucleotides with any further limitation  
 25 described in this disclosure, or those following, specified alone or in any combination:

Optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID 1-130; and the complements thereof; Optionally, said CNS disorder-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Table 7; Optionally, said CNS disorder-  
 30 related biallelic marker may be selected from the following biallelic markers: 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-

298, 99-28722-90 and 99-32306-409; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174; Optionally, said polynucleotide may comprise a sequence disclosed in the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said amplifying may be performed by a PCR or LCR. Optionally, said polynucleotide may be attached to a solid support, array, or addressable array. Optionally, said polynucleotide may be labeled.

10 A fifth embodiment of the invention encompasses methods of genotyping a biological sample comprising determining the identity of a nucleotide at a CNS disorder-related biallelic marker. In addition, the genotyping methods of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said CNS disorder-related biallelic marker may be in a sequence  
 15 selected individually or in any combination from the group consisting of SEQ ID NO: 1-542, and the complements thereof; Optionally, said CNS disorder-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Table 7; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers:  
 20 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-  
 25 88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174;  
 30 Optionally, said method further comprises determining the identity of a second nucleotide at said biallelic marker, wherein said first nucleotide and second nucleotide are not base paired (by Watson & Crick base pairing) to one another; Optionally, said biological sample is derived from a single individual or subject; Optionally, said method is performed *in vitro*; Optionally, said biallelic marker is determined for both copies of said biallelic marker present in said individual's  
 35 genome; Optionally, said biological sample is derived from multiple subjects or individuals; Optionally, said method further comprises amplifying a portion of said sequence comprising the biallelic marker prior to said determining step; Optionally, wherein said amplifying is performed

by PCR, LCR, or replication of a recombinant vector comprising an origin of replication and said portion in a host cell; Optionally, wherein said determining is performed by a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay.

A sixth embodiment of the invention comprises methods of estimating the frequency of an allele in a population comprising genotyping individuals from said population for a CNS disorder-related biallelic marker and determining the proportional representation of said biallelic marker in said population. In addition, the methods of estimating the frequency of an allele in a population of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ NO: 1-542; and the complements thereof; Optionally, said CNS disorder-related biallelic marker may be selected from the biallelic markers described in Table 7; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by determining the identity of the nucleotides for both copies of said biallelic marker present in the genome of each individual in said population and calculating the proportional representation of said nucleotide at said CNS disorder-related biallelic marker for the population; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by performing a genotyping method on a pooled biological sample derived from a representative number of individuals, or each individual, in said population, and calculating the proportional amount of said nucleotide compared with the total.

A seventh embodiment of the invention comprises methods of detecting an association between an allele and a phenotype, comprising the steps of a) determining the frequency of at least one CNS disorder-related biallelic marker allele in a trait positive population, b) determining the frequency of said CNS disorder-related biallelic marker allele in a control

population and; c) determining whether a statistically significant association exists between said genotype and said phenotype. In addition, the methods of detecting an association between an allele and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said

5 CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID NO: 1-542, and the complements thereof; Optionally, said CNS disorder-related biallelic marker may be selected from the biallelic markers described in Table 7; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a CNS disorder, a response to an agent acting

10 on a CNS disorder, or side effect to an agent acting on a CNS disorder; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID NO: 1-542 is determined in steps a) and b).

An eighth embodiment of the present invention encompasses methods of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising the steps of: a)

15 genotyping each individual in said population for at least one CNS disorder-related biallelic marker, b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said

20 frequency. In addition, the methods of estimating the frequency of a haplotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, or an expectation maximization algorithm; Optionally, said

25 second biallelic marker is a CNS disorder-related biallelic marker in a sequence selected from the group consisting of the biallelic markers of SEQ ID NO: 1-542, and the complements thereof; Optionally, said CNS disorder-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Table 7; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-27207-117, 99-

30 28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-

35 32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-4097; Optionally, said CNS disorder-related biallelic marker

may be selected from the following biallelic markers: 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the sequences of SEQ ID NO:

5 1-542 is determined in steps a) and b).

A ninth embodiment of the present invention encompasses methods of detecting an association between a haplotype and a phenotype, comprising the steps of: a) estimating the frequency of at least one haplotype in a trait positive population according to a method of estimating the frequency of a haplotype of the invention; b) estimating the frequency of said  
10 haplotype in a control population according to the method of estimating the frequency of a haplotype of the invention; and c) determining whether a statistically significant association exists between said haplotype and said phenotype. In addition, the methods of detecting an association between a haplotype and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any  
15 combination: Optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID NO: 1-542, and the complements thereof; Optionally, said CNS disorder-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Table 7; Optionally, said CNS disorder-related biallelic marker may be selected from the following  
20 biallelic markers: 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315,  
25 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409; Optionally, said CNS disorder-related biallelic marker may be selected from the following biallelic markers: 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-  
30 205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a CNS disorder, a response to an agent acting on a CNS disorder, or side effect to an agent acting on a CNS disorder; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID NO: 1-542 is  
35 included in the estimating steps a) and b).

A tenth embodiment of the present invention encompasses polypeptides encoded by SEQ ID NO: 543 or 544, as well as antisense analogs thereof and biologically active and

diagnostically or therapeutically useful fragments and derivatives thereof. The polypeptides of the present invention are of human origin. In accordance with a further aspect of the present invention, there is provided a method for producing such polypeptides by recombinant techniques which comprises culturing recombinant prokaryotic and/or eukaryotic host cells, containing a nucleic acid sequence encoding a polypeptide of the present invention, under conditions promoting expression of said protein and subsequent recovery of said protein. A further embodiment of the present invention encompasses antibodies against such polypeptides.

An eleventh embodiment of the present invention is a method for using one or more of the polypeptides according to the invention to screen for polypeptide antagonists and/or agonists and/or receptor ligands. A further embodiment of the present invention is a method of using such agonists to activate the polypeptides of the present invention for the treatment of conditions related to the underexpression of the polypeptide of the present invention, preferably depression. In accordance with another aspect of the present invention there is provided a method of using such antagonists for inhibiting the polypeptide of the present invention for treating conditions associated with overexpression of the polypeptides of the present invention.

A twelfth embodiment of the present invention encompasses non-naturally occurring synthetic, isolated and/or recombinant polypeptides which are fragments, consensus fragments and/or sequences having conservative amino acid substitutions, of at least one transmembrane domain, such that the polypeptides of the present invention may bind ligands, or which may also modulate, quantitatively or qualitatively, ligand binding to the polypeptides of the present invention. A further embodiment of the present invention encompasses synthetic or recombinant polypeptides, conservative substitution derivatives thereof, antibodies, anti-idiotypic antibodies, compositions and methods that can be useful as potential modulators of CNS-related protein function, by binding to ligands or modulating ligand binding, due to their expected biological properties, which may be used in diagnostic, therapeutic and/or research applications relating to CNS disorders. In yet a further embodiment of the present invention, there is provided synthetic, isolated or recombinant polypeptides which are designed to inhibit or mimic various polypeptides of the invention or fragments thereof, as receptor types and subtypes.

A thirteenth embodiment of the present invention encompasses a diagnostic assay for detecting a disease or susceptibility to a disease related to a mutation in a nucleic acid sequence encoding a polypeptide of the present invention. Preferably said disease is depression.

A fourteenth embodiment of the present invention is a method of administering a drug or a treatment comprising the steps of: a) obtaining a nucleic acid sample from an individual; b) determining the identity of the polymorphic base of at least one CNS disorder-related biallelic marker which is associated with a positive response to the treatment or the drug; or at least one biallelic CNS disorder-related marker which is associated with a negative response to the treatment or the drug; and c) administering the treatment or the drug to the individual if the



nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug. In addition, the methods of the present invention for administering a drug or a treatment encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ. ID. NO: 1-542 and the complements thereof-, or optionally, the administering step comprises administering the drug or the treatment to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

A fifteenth embodiment of the present invention is a method of selecting an individual for inclusion in a clinical trial of a treatment or drug comprising the steps of: a) obtaining a nucleic acid sample from an individual; b) determining the identity of the polymorphic base of at least one CNS disorder-related biallelic marker which is associated with a positive response to the treatment or the drug, or at least one CNS disorder-related biallelic marker which is associated with a negative response to the treatment or the drug in the nucleic acid sample, and c) including the individual in the clinical trial if the nucleic acid sample contains said CNS disorder-related biallelic marker associated with a positive response to the treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug. In addition, the methods of the present invention for selecting an individual for inclusion in a clinical trial of a treatment or drug encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said CNS disorder-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ. ID. NO: 1-542 and the complements thereof, optionally, the including step comprises administering the drug or the treatment to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

Additional embodiments are set forth in the Detailed Description of the Invention and in the Examples.

#### BRIEF DESCRIPTION OF THE TABLES

Tables 7A and 7C are charts containing a list of all of the CNS-related biallelic markers for each gene with an indication of the gene for which the marker is in closest physical proximity, an indication of whether the markers have been validated by microsequencing (with a Y indicating that the markers have been validated by microsequencing and an N indicating that it

has not), and an indication of the identity and frequency of the least common allele determined by genotyping (with a blank left to indicate that the frequency has not yet been reported for some markers).

Tables 7B and 7D contain all of the CNS-related biallelic markers provided in Tables 7A and 7C; however, they are provided in shorter, easier to search sequences of 47 nucleotides. Accordingly, Table 7A begins with SEQ ID NO: 1 and ends with SEQ ID NO: 130, while corresponding Table 7B begins with SEQ ID NO: 131 and ends with SEQ ID NO: 260. Also Table 7C begins with SEQ ID NO: 261 and ends with SEQ ID NO: 401, while corresponding Table 7D begins with SEQ ID NO: 402 and ends with SEQ ID NO: 542. Table 1 contains the first five markers listed in the sequence listing and their corresponding SEQ ID numbers in Tables 7A and 7C to illustrate the relationship between Tables 7A and 7B:

Table 1

<b>BIALLELIC MARKER ID</b>	<b>SEQ ID NO. IN TABLE 7A</b>	<b>BIALLELIC MARKER POSITION IN SEQ ID NO.</b>	<b>SEQ ID NO. IN TABLE 7B</b>	<b>BIALLELIC MARKER POSITION IN SEQ ID NO.</b>
99-27199-207	1	207	131	24
99-27207-117	2	117	132	24
99-27213-53	3	53	133	24
99-27218-333	4	333	134	24
99-28108-233	5	233	135	24

Tables 7B and 7D are the same as Tables 7A and 7C, respectively, in that they are a list of all of the CNS-related biallelic markers for each gene with an indication of the gene for which the marker is in closest physical proximity, an indication of whether the markers have been validated by microsequencing (with a Y indicating that the markers have been validated by microsequencing and an N indicating that it has not), and an indication of the identity and frequency of the least common allele determined by genotyping (with a blank left to indicate that the frequency has not yet been reported for some markers). However, the "Biallelic Marker Position in SEQ ID No." for all of the CNS-related biallelic markers provided in Tables 7B and 7D is position 24 (representing the midpoint of the 47mers that make up Tables 7B and 7D).

Tables 8, 9, and 10 are charts containing lists of the CNS disorder-related biallelic markers. Each marker is described by indicating its SEQ ID, the biallelic marker ID, and the two most common alleles. Table 8 is a chart containing a list of biallelic markers surrounded by preferred sequences. In the column labeled, "POSITION RANGE OF PREFERRED SEQUENCE" of Table 8 regions of particularly preferred sequences are listed for each SEQ ID, which contain a CNS disorder-related biallelic marker, as well as particularly preferred regions

of sequences that do not contain a CNS disorder-related biallelic marker but, which are in sufficiently close proximity to a CNS disorder-related biallelic marker to be useful as amplification or sequencing primers.

Table 11 is a chart listing particular sequences that are useful for designing some of the primers and probes of the invention. Each sequence is described by indicating its Sequence ID and the positions of the first and last nucleotides (position range) of the particular sequence in the Sequence ID.

Table 12 is a chart listing microsequencing primers which have been used to genotype CNS disorder-related biallelic markers (indicated by an \*) and other preferred microsequencing primers for use in genotyping CNS disorder-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible microsequencing primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are described by indicating their SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Table 13 is a chart listing amplification primers which have been used to amplify polynucleotides containing one or more CNS disorder-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible amplification primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are defined by the SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Table 14 is a chart listing preferred probes useful in genotyping CNS disorder-related biallelic markers by hybridization assays. The probes are 25-mers with a CNS disorder-related biallelic markers in the center position, and described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the probes in the Sequence ID. The probes complementary to the sequences in each position range in each Sequence ID are also understood to be a part of this preferred list even though they are not specified separately.

Table 15 is a table showing the results of single marker association tests between both biallelic marker alleles and genotypes of candidate genes and major depression.

Table 16 is a table showing the results of the LR rank of haplotypes using combinations of 2, 3 and 4 biallelic markers from each gene.

Table 17 is a table showing the rank of permutation tests for individual haplotypes confirming the statistical significance of the association between biallelic marker haplotypes from the candidate genes and major depression.

Table 18 is a table showing the results of single marker association tests between both biallelic marker alleles and genotypes of candidate genes and major depression using additional markers and a new population set as described in Example 4.

Table 19 is a table showing the results of the LR rank of haplotypes using combinations of 2, 3 and 4 biallelic markers from additional candidate genes and using data from a new population set as described in Example 4.

Table 20 is a table showing the rank of permutation tests for individual haplotypes from Table 19 confirming the statistical significance of the association between biallelic marker haplotypes from additional candidate genes and major depression.

## DETAILED DESCRIPTION OF THE INVENTION

### I. Candidate Genes of the Present Invention

Different approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and candidate gene association studies. Genome-wide association studies rely on the screening of genetic markers evenly spaced and covering the entire genome. Candidate region association studies rely on the screening of genetic markers evenly spaced covering a region identified as linked to the trait of interest. The candidate gene approach is based on the study of genetic markers specifically derived from genes potentially involved in the pathophysiology of a disease. In the present invention, genes involved in the central nervous system and/or the endocrine system have been chosen as candidate genes. The candidate genes of the present invention are listed in Table 2.

Table 2

Candidate Gene Name	Gene Symbol	Description
Serotonin receptor 6	5HTR6	A postsynaptic serotonin receptor.
Serotonin receptor 7	5HTR7	A postsynaptic serotonin receptor.
Neuronal nicotinic acid receptor $\alpha 7$	CHRNA7	An ion channel in the reward pathway.
Corticotrophin releasing factor receptor 1	CRFR1	A corticotrophin releasing factor receptor in the hypothalamus-pituitary-adrenal axis.
Mineralocorticoid receptor	MLR	A mineralocorticoid receptor.

Corticotrophin releasing factor receptor 2	CRFR2	A corticotrophin releasing factor receptor in the hypothalamus-pituitary-adrenal axis.
Glucocorticoid receptor	GRL	A glucocorticoid receptor in the hypothalamus-pituitary-adrenal axis.
Monoamine oxidase A	MAOA	Key enzyme in catecholamine metabolism.
Monoamine oxidase B	MAOB	Key enzyme in catecholamine metabolism.
Serotonin receptor 2C	5HTR2c	Postsynaptic receptor for serotonin.
Tyrosine hydroxylase	TH	The rate-limiting enzyme in the synthesis of dopamine and norepinephrine.
Corticotrophin releasing factor	CRF	A hormone released by the hypothalamus that stimulates the release of corticotrophin by the anterior pituitary gland.
Dopamine receptor 4	DRD4	A postsynaptic dopamine receptor.
Serotonin transporter	5HTT	A presynaptic membrane receptor that serves as a reuptake mechanism for serotonin.
Dopamine receptor 3	DRD3	A postsynaptic dopamine receptor.
Cytochrome P450 3A4	CYP3A4	A principal drug metabolizing enzyme.
Norepinephrine transporter	NET	A membrane protein responsible for termination of the action of synaptic norepinephrine.
Neurokinin or tachykinin receptor 1	NK1/TACR1	A receptor for the neuropeptide substance P.
Neuropeptide Y1 receptor	NPY1R	A receptor for the neuropeptide Y1. Belongs to family of g-protein coupled receptors with it highest similarity to tachykinins receptors.
Dopamine receptor 2	DRD2	G protein-coupled dopamine receptor.
Guanine nucleotide binding protein, $\beta 3$	Gbeta3	An important component of cAMP mediated signaling pathways.
Wolfram Syndrome 1 gene	WFS1	A gene that plays a role in the etiology of Wolfram syndrome.
Beta 1 adrenergic receptor	ADRB1R	An important component of the norepinephrine signaling pathway. Antidepressants are known to suppress expression.
Brain derived neurotrophic factor	BDNF	A protein known to affect the differentiation of dopaminergic and serotonergic neurons.

		Increased by antidepressants and electroconvulsive therapy.
Orphan G-protein coupled receptor	HM74	A putative chemokine receptor.
Vasopressin receptor 1A	AVPR1A	A receptor that stimulates adrenocorticotrophic hormone (ACTH) release in the anterior pituitary.
Serotonin receptor 1-A	5HT1A	A receptor that is misregulated in depression, as well as anxiety and stress.
Growth associated protein 43	GAP43	A protein known to play a role in synaptic plasticity. Increased levels in suicide victims.
Guanine nucleotide binding protein, $\alpha$ subunit, olfactory type	GOLF (GNAL)	A protein known to play a role in signaling: possibly in cAMP mediated signaling pathways and norepinephrine-related pathways.
Clock protein	CLOCK	A protein associated with sleeping patterns in humans.
Corticotrophin hormone binding protein	CRHBP	A protein capable of binding to corticotrophin releasing factor.
Dopamine transporter	DAT (SLC6A3)	A protein involved in the re-uptake of dopamine.
Phosphodiesterase type 4b	PDE4b	An enzyme believed to be involved in mediating central nervous system effects of therapeutic agents ranging from antidepressants to anti-inflammatory agents.
Catechol O-methyl transferase	COMT	An enzyme that catalyzes the transfer of a methyl group from s-adenosylmethionine to a catecholamine such as dopamine, epinephrine, or norepinephrine.
Melanin concentrating hormone receptor	SLC1	A transmembrane protein that serves as the functional receptor of melanin concentrating hormone.
Transcription factor	SEF2-1B (TCF4)	A transcription factor that binds to the e-box present in the somatostatin receptor 2 initiator element (sstr2-inr) to activate transcription (by similarity).

Heat shock protein	HSP70	A protein believed to interact with polypeptides during a variety of assembly processes in such a way as to prevent the formation of nonfunctional structures.
GABA-A receptor subunit	GABRG2	A receptor known to mediate inhibitory neurotransmission, complexing with DRD5 and promoting mutually inhibitory functional interactions between these receptor systems, putatively involved in the physiological dependence on alcohol, and in the maintenance of psychomotor disease states.
GABA-A receptor subunit 5	GABRA5	A receptor known to be part of the ligand-gated ionic channels protein family. Associated with bipolar disorder.

Both the central nervous system and the endocrine system play an important role in the pathophysiology of CNS disorders, moreover, these systems contain important drug targets and genetic polymorphisms in these genes are highly relevant in the response to a number of drugs.

- 5 The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular disease when some information concerning the pathophysiology of the disorder is available as is the case for many CNS disorders. However, it should be noted that all of the biallelic markers disclosed in the instant application can be employed as part of genome-wide association studies or as part of candidate region association
- 10 studies and such uses are specifically contemplated in the present invention and claims. All of the markers are known to be in close proximity to the genes with which they are listed in Table 7. For a portion of the markers, the precise position of the marker with respect to the various coding and non-coding elements of the genes has also been determined.

## 15 II. Definitions

Before describing the invention in greater detail, the following definitions are set forth to illustrate and define the meaning and scope of the terms used to describe the invention herein.

- As used interchangeably herein, the terms "nucleic acid molecule", "oligonucleotide", and "polynucleotide", unless specifically stated otherwise, include RNA or, DNA (either single
- 20 or double stranded, coding, complementary or antisense), or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form (although each of the above species may be particularly specified). The term "nucleotide" as used herein as an adjective to describe molecules comprising RNA, DNA, or RNA/DNA hybrid sequences of any length in

single-stranded or duplex form. More precisely, the expression "nucleotide sequence" encompasses the nucleic material itself and is thus not restricted to the sequence information (i.e. the succession of letters chosen among the four base letters) that biochemically characterizes a specific DNA or RNA molecule. The term "nucleotide" is also used herein as a noun to refer to individual nucleotides or varieties of nucleotides, meaning a molecule, or individual unit in a larger nucleic acid molecule, comprising a purine or pyrimidine, a ribose or deoxyribose sugar moiety, and a phosphate group, or phosphodiester linkage in the case of nucleotides within an oligonucleotide or polynucleotide. Although the term "nucleotide" is also used herein to encompass "modified nucleotides" which comprise at least one modifications (a) an alternative linking group, (b) an analogous form of purine, (c) an analogous form of pyrimidine, or (d) an analogous sugar, for examples of analogous linking groups, purine, pyrimidines, and sugars see for example PCT publication No. WO 95/04064. Preferred modifications of the present invention include, but are not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v) ybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art. Methylenemethylimino linked oligonucleosides as well as mixed backbone compounds having, may be prepared as described in U.S. Pat. Nos. 5,378,825; 5,386,023; 5,489,677; 5,602,240; and 5,610,289. Formacetal and thioformacetal linked oligonucleosides may be prepared as described in U.S. Pat. Nos. 5,264,562 and 5,264,564. Ethylene oxide linked oligonucleosides may be prepared as described in U.S. Pat. No. 5,223,618. Phosphinate oligonucleotides may be prepared as described in U.S. Pat. No. 5,508,270.. Alkyl phosphonate oligonucleotides may be prepared as described in U.S. Pat. No. 4,469,863. 3'-Deoxy-3'-methylene phosphonate oligonucleotides may be prepared as described in U.S. Pat. Nos. 5,610,289 or 5,625,050. Phosphoramidite oligonucleotides may be prepared as described in U.S. Pat. No. 5,256,775 or U.S. Pat. No. 5,366,878. Alkylphosphonothioate oligonucleotides may be prepared as described in published PCT applications WO 94/17093 and WO 94/02499. 3'-Deoxy-3'-amino phosphoramidate oligonucleotides may be prepared as described in U.S. Pat. No. 5,476,925. Phosphotriester



oligonucleotides may be prepared as described in U.S. Pat. No. 5,023,243. Borano phosphate oligonucleotides may be prepared as described in U.S. Pat. Nos. 5,130,302 and 5,177,198. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art.

The term "isolated" further requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

Specifically excluded from the definition of "isolated" are: naturally-occurring chromosomes (such as chromosome spreads), artificial chromosome libraries, genomic libraries, and cDNA libraries that exist either as an *in vitro* nucleic acid molecule preparation or as a transfected/transformed host cell preparation, wherein the host cells are either an *in vitro* heterogeneous preparation or plated as a heterogeneous population of single colonies. Also specifically excluded are the above libraries wherein a specified polynucleotide of the present invention makes up less than 5% of the number of nucleic acid molecule inserts in the vector molecules. Further specifically excluded are whole cell genomic DNA or whole cell RNA or mRNA preparations (including said whole cell preparations which are mechanically sheared or enzymatically digested). Further specifically excluded are the above whole cell preparations as either an *in vitro* preparation or as a heterogeneous mixture separated by electrophoresis (including blot transfers of the same) wherein the polynucleotide of the invention has not further been separated from the heterologous polynucleotides in the electrophoresis medium (e.g., further separating by excising a single band from a heterogeneous band population in an agarose gel or nylon blot).

As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately  $10^4$ - $10^6$  fold purification of the native message. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. Alternatively, purification may be expressed as "at least" a percent purity relative to heterologous polynucleotides (DNA, RNA

or both). As a preferred embodiment, the polynucleotides of the present invention are at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 96%, 98%, 99%, or 100% pure relative to heterologous polynucleotides. As a further preferred embodiment the polynucleotides have an "at least" purity ranging from any number, to the thousandth position, between 90% and 100% (e.g.,  
5 5' EST at least 99.995% pure) relative to heterologous polynucleotides. Additionally, purity of the polynucleotides may be expressed as a percentage (as described above) relative to all materials and compounds other than the carrier solution. Each number, to the thousandth position, may be claimed as individual species of purity.

The term "primer" denotes a specific oligonucleotide sequence which is complementary  
10 to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by DNA polymerase, RNA polymerase or reverse transcriptase.

The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., polynucleotide as defined herein) which can be used to identify a specific polynucleotide  
15 sequence present in samples, said nucleic acid segment comprising a nucleotide sequence complementary of the specific polynucleotide sequence to be identified.

The term "CNS disorder" refers to any condition linked to dysfunction of the central nervous system which is known in the art. A CNS disorder includes dysfunction of one or several physiological systems contributing to the function of the central nervous system, which  
20 includes the endocrine system and the peripheral nervous system. A CNS disorder further refers to disorders in neurotransmitter synthesis and degradation, neurotransmitter function, neurotransmitter receptor function, neurotransmitter signal transduction, neurotransmitter transporter function, motor neuron function, hormone synthesis and degradation, hormone function, hormone receptor function and hormone signal transduction. "CNS disorders" include  
25 mood disorders such as depression, bipolar disorder, anxiety, attention deficit disorder and schizophrenia. "CNS disorders" also include neurodegenerative disorders such as Parkinson's disease, Huntington's disease, Pick's disease, progressive supranuclear palsy, Lewy body dementia and Wolfram syndrome (diabetes insipidus, diabetes mellitus, optic atrophy and deafness). "CNS disorders" also include disorders of movement such as motor neuron disease as  
30 well as diseases involving the intellect such as Alzheimer's disease, Wernicke's encephalopathy and Jakob-Creutzfeldt disease. "CNS disorders" further include other disorders such as coma, head injury, cerebral infarction, epilepsy, alcoholism and states of mental retardation. All of the possible CNS disorders listed herein are included in, or may be excluded from, the present invention as individual species.

35 The term "depression" as used herein refers to both unipolar major depression (or major depressive disorder) and bipolar disorder.

An "agent acting on a CNS disorder" includes any drug or compound known in the art that addresses, reduces or alleviates one or more symptoms of a CNS disorder. "Agents acting on a CNS disorder" includes any drug or a compound modulating the activity or concentration of an enzyme or regulatory molecule involved in a CNS disorder that is known in the art. An agent acting on a CNS disorder includes but is not limited to tyrosine hydroxylase, monoamine oxidase A/B, dopamine  $\beta$ -hydroxylase, aldehyde dehydrogenase, phenylethanolamine N-methyltransferase, catechol o-methyltransferase, tryptophan hydroxylase, acetyl coenzyme A, proteinases, oestrogens, glucocorticoids, mineralocorticoids, nicotine, substance P and precursors to neurotransmitters such as tryptophan. "Agent acting on a CNS disorder" further refers to compounds modulating the synthesis, degradation, reuptake and action of neurotransmitters and hormones such as tricyclic antidepressants (TCAs), monoamine oxidase inhibitors (MAOIs), serotonin selective reuptake inhibitors (SSRIs), selective norepinephrine reuptake inhibitor (NRI) such as reboxetine, dual serotonin and norepinephrine reuptake inhibitor (SNRI), serotonin-2 antagonist/reuptake inhibitors (SARIs), noradrenergic and specific serotonergic antidepressants (NaSSAs), drugs that cause increased dopamine release in the brain such as levodopa, dopamine receptor agonists such as bromocriptine, dopamine antagonists such as metoclopramide, neuroleptic drugs such as phenothiazines, adrenergic agonists such as clonidine, N-methyl-D-aspartate antagonists such as phencyclidine, anticholinergic compounds, benzodiazepine drugs and anxiolytic compounds. Preferably, "agent acting on a CNS disorder" refers to the antidepressant drug Reboxetine.

The terms "response to an agent acting on a CNS disorder" refer to drug efficacy, including but not limited to the ability to metabolize a compound, the ability to convert a pro-drug to an active drug, and to the pharmacokinetics (absorption, distribution, elimination) and the pharmacodynamics (receptor-related) of a drug in an individual.

The terms "side effects to an agent acting on a CNS disorder" refer to adverse effects of therapy resulting from extensions of the principal pharmacological action of the drug or to idiosyncratic adverse reactions resulting from an interaction of the drug with unique host factors. "Side effects to an agent acting on a CNS disorder" include, but are not limited to autonomic side effects such as orthostatic hypotension, blurred vision, dry mouth, nasal congestion and constipation. "Side effects to an agent acting on a CNS disorder" also include anxiety, sleep disturbances, sexual dysfunction, gastrointestinal disturbances, nausea, diarrhea, orthostasis, dizziness, sedation, hypertension and shock.

The terms "trait" and "phenotype" are used interchangeably herein and refer to any visible, detectable or otherwise measurable property of an organism such as symptoms of, or susceptibility to a disease for example. Typically the terms "trait" or "phenotype" are used herein to refer to symptoms of, or susceptibility to a CNS disorder; or to refer to an individual's

response to an agent acting on a CNS disorder; or to refer to symptoms of, or susceptibility to side effects to an agent acting on a CNS disorder.

The term "allele" is used herein to refer to variants of a nucleotide sequence. A biallelic polymorphism has two forms. Typically the first identified allele is designated as the original allele whereas other alleles are designated as alternative alleles. Diploid organisms may be homozygous or heterozygous for an allelic form.

The term "heterozygosity rate" is used herein to refer to the incidence of individuals in a population, which are heterozygous at a particular allele. In a biallelic system the heterozygosity rate is on average equal to  $2P_a(1-P_a)$ , where  $P_a$  is the frequency of the least common allele. In order to be useful in genetic studies a genetic marker should have an adequate level of heterozygosity to allow a reasonable probability that a randomly selected person will be heterozygous.

The term "genotype" as used herein refers to the identity of the alleles present in an individual or a sample. In the context of the present invention a genotype preferably refers to the description of the biallelic marker alleles present in an individual or a sample. The term "genotyping" a sample or an individual for a biallelic marker consists of determining the specific allele or the specific nucleotide carried by an individual at a biallelic marker.

The term "mutation" as used herein refers to a difference in DNA sequence between or among different genomes or individuals which has a frequency below 1%.

The term "haplotype" refers to a combination of alleles present in an individual or a sample. In the context of the present invention a haplotype preferably refers to a combination of biallelic marker alleles found in a given individual and which may be associated with a phenotype.

The term "polymorphism" as used herein refers to the occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals. "Polymorphic" refers to the condition in which two or more variants of a specific genomic sequence can be found in a population. A "polymorphic site" is the locus at which the variation occurs. A single nucleotide polymorphism is a single base pair change. Typically a single nucleotide polymorphism is the replacement of one nucleotide by another nucleotide at the polymorphic site. Deletion of a single nucleotide or insertion of a single nucleotide, also give rise to single nucleotide polymorphisms. In the context of the present invention "single nucleotide polymorphism" preferably refers to a single nucleotide substitution. Typically, between different genomes or between different individuals, the polymorphic site may be occupied by two different nucleotides.

The terms "biallelic polymorphism" and "biallelic marker" are used interchangeably herein to refer to a polymorphism having two alleles at a fairly high frequency in the population, preferably a single nucleotide polymorphism. A "biallelic marker allele" refers to the nucleotide

variants present at a biallelic marker site. Typically the frequency of the less common allele of the biallelic markers of the present invention has been validated to be greater than 1%, preferably the frequency is greater than 10%, more preferably the frequency is at least 20% (i.e. heterozygosity rate of at least 0.32), even more preferably the frequency is at least 30% (i.e. heterozygosity rate of at least 0.42). A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker."

The location of nucleotides in a polynucleotide with respect to the center of the polynucleotide are described herein in the following manner. When a polynucleotide has an odd number of nucleotides, the nucleotide at an equal distance from the 3' and 5' ends of the polynucleotide is considered to be "at the center" of the polynucleotide, and any nucleotide immediately adjacent to the nucleotide at the center, or the nucleotide at the center itself is considered to be "within 1 nucleotide of the center." With an odd number of nucleotides in a polynucleotide any of the five nucleotide positions in the middle of the polynucleotide would be considered to be within 2 nucleotides of the center, and so on. When a polynucleotide has an even number of nucleotides, there would be a bond and not a nucleotide at the center of the polynucleotide. Thus, either of the two central nucleotides would be considered to be "within 1 nucleotide of the center" and any of the four nucleotides in the middle of the polynucleotide would be considered to be "within 2 nucleotides of the center", and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on.

The term "upstream" is used herein to refer to a location which is toward the 5' end of the polynucleotide from a specific reference point.

The terms "base paired" and "Watson & Crick base paired" are used interchangeably herein to refer to nucleotides which can be hydrogen bonded to one another by virtue of their sequence identities in a manner like that found in double-helical DNA with thymine or uracil residues linked to adenine residues by two hydrogen bonds and cytosine and guanine residues linked by three hydrogen bonds (See Stryer, L., *Biochemistry*, 4th edition, 1995).

The terms "complementary" or "complement thereof" are used herein to refer to the sequences of polynucleotides which is capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. This term is applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind.

As used herein the term "CNS disorder-related biallelic marker" relates to a set of biallelic markers in linkage disequilibrium with genes disclosed in Tables 7(A-D) which express proteins that are involved in the pathophysiology CNS disorders. The term CNS disorder-related biallelic marker encompasses all of the biallelic markers disclosed in Tables 7(A-D). The preferred CNS disorder-related biallelic marker alleles of the present invention include each one of the alleles described in Tables 7, 8, 9, and 10 individually or in groups consisting of all the possible combinations of the alleles included in Tables 7, 8, 9, and 10. In addition, Table 7 may include Tables 7A-7D, or Tables 7A, 7B, 7C or 7D as individual embodiments of the present invention or in any combination of the four.

The term "sequence described in Table 8" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 8. The SEQ ID that contains each "sequence described in Table 8" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Table 8." Unless otherwise noted the term "sequence described in Table 8" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "1<sup>ST</sup> ALLELE" and "2<sup>ND</sup> ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Table 8.

The term "sequence described in Table 9" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 9. Unless otherwise noted, the "sequences described in Table 9" consist of the entire sequence of each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Table 9" is to be construed as encompassing sequences that contain either of the two

alleles listed in the columns labeled, "ORIGINAL ALLELE" and "ALTERNATIVE ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Table 9.

The term "sequence described in Table 10" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 10. Unless otherwise noted, the "sequences described in Table 10" consist of the entire sequence of each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Table 10" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "1<sup>ST</sup> ALLELE" and "2<sup>ND</sup> ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Table 10:

The term "sequence described in Table 11" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 11. The SEQ ID that contains each "sequence described in Table 11" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION-RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Table 11."

The term "sequence described in Table 12" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 12. The SEQ ID that contains each "sequence described in Table 12" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF MICROSEQUENCING PRIMERS". The remaining half of the sequences described in Table 12 are complementary to the range of nucleotide positions within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS".

The term "sequence described in Table 13" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 13. The SEQ ID that contains each "sequence described in Table 13" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF AMPLIFICATION PRIMERS". The remaining half of the sequences described in Table 13 are complementary to the range of nucleotide positions within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS".

The term "sequence described in Table 14" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Table 14. The SEQ ID that contains each "sequence described in Table 14" is provided in the column labeled, "SEQ ID NO.". The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PROBES". The sequences which are complementary to the ranges listed in the column labeled, "POSITION RANGE OF PROBES" are also encompassed by the term, "sequence described in Table 14." Unless otherwise noted the term "sequence described in Table 14" is to be construed as encompassing sequences that contain either of the two alleles listed in the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Table 14.

The terms "biallelic marker described in Table" and "allele described in Table" are used herein to refer to any or all alleles which are listed in the allele feature in the appended Sequence Listing for each Sequence ID number referenced in the particular Table being mentioned.

The following abbreviations are used in this disclosure: serotonin receptor 6 gene is abbreviated 5HTR6; serotonin receptor 7 gene is abbreviated 5HTR7; neuronal nicotinic acid receptor  $\alpha 7$  gene is abbreviated CHRNA7; corticotrophin releasing factor receptor 1 gene is abbreviated CRFR1; mineralocorticoid receptor gene is abbreviated MLR; corticotrophin releasing factor receptor 2 gene is abbreviated CRFR2; glucocorticoid receptor gene is abbreviated GRL; monoamine oxidases A and B genes are abbreviated MAOA/B; serotonin receptor 2C gene is abbreviated 5HTR2c; tyrosine hydroxylase gene is abbreviated TH; corticotrophin releasing factor gene is abbreviated CRF; dopamine receptor 4 gene is abbreviated DRD4; serotonin transporter gene is abbreviated 5HTT; dopamine receptor 3 gene is abbreviated DRD3; cytochrome P450 3A4 gene is abbreviated CYP3A4; norepinephrine transporter gene is abbreviated NET; neurokinin or tachykinin receptor 1 gene is abbreviated NK1/TACR1; dopamine receptor 4 gene is abbreviated DRD2; guanine nucleotide binding protein,  $\beta 3$  gene is abbreviated Gbeta3; Wolfram Syndrome 1 gene is abbreviated WFS1; Beta 1 adrenergic receptor gene is abbreviated ADRB1R; Brain derived neurotrophic factor gene is abbreviated BDNF; Orphan G-protein coupled receptor gene is abbreviated HM74; Vasopressin receptor 1A gene is abbreviated AVPR1A; Serotonin receptor 1-A gene is abbreviated 5HT1A; Growth associated protein 43 gene is abbreviated GAP43; Guanine nucleotide binding protein,  $\alpha$  subunit, olfactory type gene is abbreviated GOLF (GNAL); Clock protein gene is abbreviated CLOCK; Corticotrophin hormone binding protein gene is abbreviated CRHBP; Dopamine transporter gene is abbreviated DAT (SLC6A3); Phosphodiesterase type 4b gene is abbreviated PDE4b; Catechol O-methyl transferase gene is abbreviated COMT; Melanin concentrating hormone receptor gene is abbreviated SLC1; Transcription factor gene is abbreviated SEF2-1B (TCF4); Heat shock protein gene is abbreviated HSP70; GABA-A receptor subunit gene is abbreviated GABRG2; and GABA-A receptor subunit 5 gene is abbreviated GABRA5.



### III. Biallelic Markers and Polynucleotides Comprising Biallelic Markers

#### A. Advantages of the Biallelic Markers of the Present Invention

5 The CNS disorder-related biallelic markers of the present invention offer a number of important advantages over other genetic markers such as RFLP (Restriction fragment length polymorphism) and VNTR (Variable Number of Tandem Repeats) markers.

The first generation of markers, were RFLPs, which are variations that modify the length of a restriction fragment. But methods used to identify and to type RFLPs are relatively wasteful of materials, effort, and time. The second generation of genetic markers were VNTRs, which can  
10 be categorized as either minisatellites or microsatellites. Minisatellites are tandemly repeated DNA sequences present in units of 5-50 repeats which are distributed along regions of the human chromosomes ranging from 0.1 to 20 kilobases in length. Since they present many possible alleles, their informative content is very high. Minisatellites are scored by performing Southern blots to identify the number of tandem repeats present in a nucleic acid sample from the  
15 individual being tested. However, there are only  $10^4$  potential VNTRs that can be typed by Southern blotting. Moreover, both RFLP and VNTR markers are costly and time-consuming to develop and assay in large numbers.

Single nucleotide polymorphism or biallelic markers can be used in the same manner as RFLPs and VNTRs but offer several advantages. Single nucleotide polymorphisms are densely  
20 spaced in the human genome and represent the most frequent type of variation. An estimated number of more than  $10^7$  sites are scattered along the  $3 \times 10^9$  base pairs of the human genome. Therefore, single nucleotide polymorphism occur at a greater frequency and with greater uniformity than RFLP or VNTR markers which means that there is a greater probability that such a marker will be found in close proximity to a genetic locus of interest. Single nucleotide  
25 polymorphisms are less variable than VNTR markers but are mutationally more stable.

Also, the different forms of a characterized single nucleotide polymorphism, such as the biallelic markers of the present invention, are often easier to distinguish and can therefore be typed easily on a routine basis. Biallelic markers have single nucleotide based alleles and they have only two common alleles, which allows highly parallel detection and automated scoring.  
30 The biallelic markers of the present invention offer the possibility of rapid, high-throughput genotyping of a large number of individuals.

Biallelic markers are densely spaced in the genome, sufficiently informative and can be assayed in large numbers. The combined effects of these advantages make biallelic markers extremely valuable in genetic studies. Biallelic markers can be used in linkage studies in  
35 families, in allele sharing methods, in linkage disequilibrium studies in populations, in association studies of case-control populations. An important aspect of the present invention is that biallelic markers allow association studies to be performed to identify genes involved in

complex traits. Association studies examine the frequency of marker alleles in unrelated case- and control-populations and are generally employed in the detection of polygenic or sporadic traits. Association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families (linkage studies). Biallelic markers  
5 in different genes can be screened in parallel for direct association with disease or response to a treatment. This multiple gene approach is a powerful tool for a variety of human genetic studies as it provides the necessary statistical power to examine the synergistic effect of multiple genetic factors on a particular phenotype, drug response, sporadic trait, or disease state with a complex genetic etiology.

#### 10 B. Polynucleotides of the Present Invention

The present invention encompasses polynucleotides for use as primers and probes in the methods of the invention. These polynucleotides may consist of, consist essentially of, or comprise a contiguous span of nucleotides of a sequence from any sequence in the Sequence Listing as well as sequences which are complementary thereto ("complements thereof"). The  
15 "contiguous span" may be at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID. It should be noted that the polynucleotides of the present invention are not limited to having the exact flanking sequences surrounding the polymorphic bases which, are enumerated in the Sequence Listing. Rather, it  
20 will be appreciated that the flanking sequences surrounding the biallelic markers, or any of the primers of probes of the invention which, are more distant from the markers, may be lengthened or shortened to any extent compatible with their intended use and the present invention specifically contemplates such sequences. It will be appreciated that the polynucleotides referred to in the Sequence Listing may be of any length compatible with their intended use. Also the  
25 flanking regions outside of the contiguous span need not be homologous to native flanking sequences which actually occur in human subjects. The addition of any nucleotide sequence, which is compatible with the nucleotides intended use is specifically contemplated. The contiguous span may optionally include the CNS disorder-related biallelic marker in said sequence. Biallelic markers generally consist of a polymorphism at one single base position.  
30 Each biallelic marker therefore corresponds to two forms of a polynucleotide sequence which, when compared with one another, present a nucleotide modification at one position. Usually, the nucleotide modification involves the substitution of one nucleotide for another. Optionally either the original or the alternative allele of the biallelic markers disclosed in Table 9, or the first or second allele disclosed in Table 8 and 10 may be specified as being present at the CNS disorder-  
35 related biallelic marker.

The invention also relates to polynucleotides that hybridize, under conditions of high or intermediate stringency, to a polynucleotide of a sequence from any sequence in the Sequence

Listing as well as sequences, which are complementary thereto. Preferably such polynucleotides are at least 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 nucleotides in length, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID. Preferred polynucleotides comprise a CNS disorder-related biallelic marker.

- 5 Optionally either the original or the alternative allele of the biallelic markers disclosed in Table 9 may be specified as being present at the CNS disorder-related biallelic marker. Conditions of high and intermediate stringency are further described herein.

The preferred polynucleotides of the invention include the sequence ranges included in any one the sequence ranges of Tables 8 and 11 to 14 individually or in groups consisting of all  
 10 the possible combinations of the ranges of included in Tables 8, and 11 to 14. The preferred polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence ranges included in any one of the sequence ranges of Tables 9, and 12 to 15 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range. The preferred  
 15 polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence complementary to the sequence ranges included in any one of the sequence ranges of Tables 8 and 11 to 14 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range.

- 20 The primers of the present invention may be designed from the disclosed sequences for any method known in the art. A preferred set of primers is fashioned such that the 3' end of the contiguous span of identity with the sequences of the Sequence Listing is present at the 3' end of the primer. Such a configuration allows the 3' end of the primer to hybridize to a selected nucleic acid sequence and dramatically increases the efficiency of the primer for amplification or  
 25 sequencing reactions. In a preferred set of primers the contiguous span is found in one of the sequences described in Table 11. Allele specific primers may be designed such that a biallelic marker is at the 3' end of the contiguous span and the contiguous span is present at the 3' end of the primer. Such allele specific primers tend to selectively prime an amplification or sequencing reaction so long as they are used with a nucleic acid sample that contains one of the two alleles  
 30 present at a biallelic marker. The 3' end of primer of the invention may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500, 1000, 2000 or 3000 to the extent that this distance is consistent with the particular Sequence ID, nucleotides upstream of a CNS disorder-related biallelic marker in said sequence or at any other location which is appropriate for their intended use in sequencing, amplification or the location of novel sequences or markers. A list  
 35 of preferred amplification primers is disclosed in Table 13. Primers with their 3' ends located 1 nucleotide upstream of a CNS disorder-related biallelic marker have a special utility as microsequencing assays. Preferred microsequencing primers are described in Tables 12.

The probes of the present invention may be designed from the disclosed sequences for any method known in the art, particularly methods which allow for testing if a particular sequence or marker disclosed herein is present. A preferred set of probes may be designed for use in the hybridization assays of the invention in any manner known in the art such that they selectively bind to one allele of a biallelic marker, but not the other under any particular set of assay conditions. Preferred hybridization probes may consist of, consist essentially of, or comprise a contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a CNS disorder-related biallelic marker of said sequence. Optionally the original allele or alternative allele disclosed in Table 9 and the first or second allele disclosed in Tables 8 and 10 may be specified as being present at the biallelic marker site. Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of the hybridization probe or at the center of said probe. A particularly preferred set of hybridization probes is disclosed in Table 14 or a sequence complementary thereto.

Any of the polynucleotides of the present invention can be labeled, if desired, by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioactive substances, fluorescent dyes or biotin. Preferably, polynucleotides are labeled at their 3' and 5' ends. A label can also be used to capture the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support. A capture label is attached to the primers or probes and can be a specific binding member which forms a binding pair with the solid's phase reagent's specific binding member (e.g. biotin and streptavidin). Therefore depending upon the type of label carried by a polynucleotide or a probe, it may be employed to capture or to detect the target DNA. Further, it will be understood that the polynucleotides, primers or probes provided herein, may, themselves, serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of a primer or probe to thereby immobilize the primer or probe to the solid phase. In cases where a polynucleotide probe itself serves as the binding member, those skilled in the art will recognize that the probe will contain a sequence or "tail" that is not complementary to the target. In the case where a polynucleotide primer itself serves as the capture label, at least a portion of the primer will be free to hybridize with a nucleic acid on a solid phase. DNA Labeling techniques are well known to the skilled technician.

Any of the polynucleotides, primers and probes of the present invention can be conveniently immobilized on a solid support. Solid supports are known to those skilled in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells, duracytes® and others. The solid support is not critical and can be selected by

one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and duracytes are all suitable examples. Suitable methods for immobilizing nucleic acids on solid phases include ionic, hydrophobic, covalent interactions and the like. A solid support, as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid support can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid support and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid support material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes® and other configurations known to those of ordinary skill in the art. The polynucleotides of the invention can be attached to or immobilized on a solid support individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the inventions to a single solid support. In addition, polynucleotides other than those of the invention may be attached to the same solid support as one or more polynucleotides of the invention.

Any polynucleotide provided herein may be attached in overlapping areas or at random locations on the solid support. Alternatively the polynucleotides of the invention may be attached in an ordered array wherein each polynucleotide is attached to a distinct region of the solid support which does not overlap with the attachment site of any other polynucleotide. Preferably, such an ordered array of polynucleotides is designed to be "addressable" where the distinct locations are recorded and can be accessed as part of an assay procedure. Addressable polynucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. The knowledge of the precise location of each polynucleotide's location makes these "addressable" arrays particularly useful in hybridization assays. Any addressable array technology known in the art can be employed with the polynucleotides of the invention. One particular embodiment of these polynucleotide arrays is known as the Genechips™, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092. These arrays may generally be produced using mechanical synthesis methods or light directed synthesis methods, which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis (Fodor et

al., Science, 251:767-777, 1991). The immobilization of arrays of oligonucleotides on solid supports has been rendered possible by the development of a technology generally identified as "Very Large Scale Immobilized Polymer Synthesis" (VLSIPS™) in which, typically, probes are immobilized in a high density array on a solid surface of a chip. Examples of VLSIPS™ technologies are provided in US Patents 5,143,854 and 5,412,087 and in PCT Publications WO 90/15070, WO 92/10092 and WO 95/11995, which describe methods for forming oligonucleotide arrays through techniques such as light-directed synthesis techniques. In designing strategies aimed at providing arrays of nucleotides immobilized on solid supports, further presentation strategies were developed to order and display the oligonucleotide arrays on the chips in an attempt to maximize hybridization patterns and sequence information. Examples of such presentation strategies are disclosed in PCT Publications WO 94/12305, WO 94/11530, WO 97/29212 and WO 97/31256.

Oligonucleotide arrays may comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-130; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of the biallelic markers of the present invention. Oligonucleotide arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-130; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for amplifying one or more alleles of the biallelic markers of Table 7. In other embodiments, arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-130; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for conducting microsequencing analyses to determine whether a sample contains one or more alleles of the biallelic markers of the invention. In still further embodiments, the oligonucleotide array may comprise at least one of the sequences selecting from the group consisting of SEQ ID No. 1-130; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500, 1000, 2000 or 3000 nucleotides in length, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of the biallelic markers of the present invention. In still further embodiments, the oligonucleotide array may comprise at least one of the novel sequences listed in the fifth column of Table 8 or the sequences complementary thereto or a fragment comprising at least 8, 10, 12, 15, 18, 20, 25, 35,

40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides thereof to the extent that fragments of these lengths are consistent with the lengths of the particular novel sequences.

The present invention also encompasses diagnostic kits comprising one or more polynucleotides of the invention, optionally with a portion or all of the necessary reagents and instructions for genotyping a test subject by determining the identity of a nucleotide at a CNS disorder-related biallelic marker. The determining of the identity may optionally be at a CNS disorder-related biallelic marker that predicts the response of a therapeutic agent, preferably Reboxetine, when administered to a patient suffering from depression. The polynucleotides of a kit may optionally be attached to a solid support, or be part of an array or addressable array of polynucleotides. The kit may provide for the determination of the identity of the nucleotide at a marker position by any method known in the art including, but not limited to, a sequencing assay method, a microsequencing assay method, a hybridization assay method, or an allele specific amplification method. Optionally such a kit may include instructions for scoring the results of the determination with respect to the test subjects' risk of contracting a CNS disorder, or likely response to an agent acting on CNS disorders, or chances of suffering from side effects to an agent acting on CNS disorders.

#### C. Polypeptides of the Invention

The polynucleotides which encode the WFS1 and the NET polypeptide may include: only the coding sequence for the mature polypeptide; the coding sequence for the polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence; the coding sequence for the polypeptide (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the mature polypeptide.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

As hereinabove indicated, the polynucleotides may have a coding sequence which is a naturally occurring allelic variant of the coding sequence of SEQ ID NO: 543 or 544. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

#### D. Host Cells

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the WFS1 or NET gene. The culture

conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included  
5 in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the  
10 host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

15 The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the E. coli. lac or trp, the phage lambda P.sub.L promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome  
20 binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin  
25 resistance in E. coli.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells,  
30 such as E. coli, Streptomyces, Salmonella typhimurium; fungal cells, such as yeast; insect cells such as Drosophila S2 and Spodoptera Sf9; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

#### E. Screening Assays

35 The polynucleotides of the present invention may be employed for producing polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include



chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli* lac or trp, the phage lambda P.sub.L promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* S2 and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3,

pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, PSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are  
5 PKK232-8 and PCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P.sub.R, P.sub.L and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the  
10 art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium  
15 phosphate transfection, DEAE-Dextran mediated transfection, or electroporation: (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

20 Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold  
25 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples including the SV40 enhancer on the late side of the replication origin bp  
30 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to  
35 direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\alpha$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is

assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, Wis., USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell*, 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The WFS1 and NET polypeptides can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The polypeptides of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

#### 15     F. Screening Assays

The WFS1 protein receptor of the present invention may be employed in a process for screening for antagonists and/or agonists for the receptor.

In general, such screening procedures involve providing appropriate cells which express the receptor on the surface thereof. In particular, a polynucleotide encoding the receptor of the present invention is employed to transfect cells to thereby express the WFS1 receptor. Such transfection may be accomplished by procedures as hereinabove described.

One such screening procedure involves the use of the melanophores which are transfected to express the WFS1 receptor of the present invention. Such a screening technique is described in PCT WO 92/01810 published Feb. 6, 1992.

25     Thus, for example, such assay may be employed for screening for a receptor antagonist by contacting the melanophore cells which encode the WFS1 receptor with both the receptor ligand and a compound to be screened. Inhibition of the signal generated by the ligand indicates that a compound is a potential antagonist for the receptor, i.e., inhibits activation of the receptor.

The screen may be employed for determining an agonist by contacting such cells with compounds to be screened and determining whether such compound generates a signal, i.e., activates the receptor.

Other screening techniques include the use of cells which express WFS1 receptor (for example, transfected CHO cells) in a system which measures extracellular pH changes caused by receptor activation, for example, as described in Science, volume 246, pages 181-296 (October 1989). For example, potential agonists or antagonists may be contacted with a cell which expresses the WFS1 receptor and a second messenger response, e.g. signal transduction or pH changes, may be measured to determine whether the potential agonist or antagonist is effective.

Another such screening technique involves introducing RNA encoding the WFS1 receptor into xenopus oocytes to transiently express the receptor. The receptor oocytes may then be contacted in the case of antagonist screening with the receptor ligand and a compound to be screened, followed by detection of inhibition of a calcium signal.

5 Another screening technique involves expressing the WFS1 receptor in which the receptor is linked to a phospholipase C or D. As representative examples of such cells, there may be mentioned endothelial cells, smooth muscle cells, embryonic kidney cells, etc. The screening for an antagonist or agonist may be accomplished as hereinabove described by detecting activation of the receptor or inhibition of activation of the receptor from the phospholipase  
10 second signal.

Another method involves screening for antagonists by determining inhibition of binding of labeled ligand to cells which have the receptor on the surface thereof. Such a method involves transfecting a eukaryotic cell with DNA encoding the WFS1 receptor such that the cell expresses the receptor on its surface and contacting the cell with a potential antagonist in the presence of a  
15 labeled form of a known ligand. The ligand can be labeled, e.g., by radioactivity. The amount of labeled ligand bound to the receptors is measured, e.g., by measuring radioactivity of the receptors. If the potential antagonist binds to the receptor as determined by a reduction of labeled ligand which binds to the receptors, the binding of labeled ligand to the receptor is inhibited.

The present invention also provides a method for determining whether a ligand not  
20 known to be capable of binding to a WFS1 receptor can bind to such receptor which comprises contacting a mammalian cell which expresses a WFS1 receptor with the ligand under conditions permitting binding of ligands to the WFS1 receptor, detecting the presence of a ligand which binds to the receptor and thereby determining whether the ligand binds to the WFS1 receptor. The systems hereinabove described for determining agonists and/or antagonists may also be  
25 employed for determining ligands which bind to the receptor.

In general, antagonists for WFS1 receptors which are determined by screening procedures may be employed for a variety of therapeutic purposes. For example, such antagonists have been employed for treatment of hypertension, angina pectoris, myocardial infarction, ulcers, asthma, allergies, psychoses, depression, migraine, vomiting, stroke, eating disorders, migraine  
30 headaches, cancer and benign prostatic hypertrophy.

Agonists for WFS1 receptors are also useful for therapeutic purposes, such as the treatment of Wolfram syndrome and/or depression.

Examples of WFS1 receptor antagonists include an antibody, or in some cases an oligonucleotide, which binds to the WFS1 receptor but does not elicit a second messenger  
35 response such that the activity of the WFS1 receptor is prevented. Antibodies include anti-idiotypic antibodies which recognize unique determinants generally associated with the antigen-binding site of an antibody.

Potential antagonists also include proteins which are closely related to the ligand of the WFS1 receptor, i.e. a fragment of the ligand, which have lost biological function and when binding to the WFS1 receptor, elicit no response.

A potential antagonist also includes an antisense construct prepared through the use of antisense technology. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix -see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al, Science, 241:456 (1988); and Dervan et al., Science, 251: 1360 (1991)), thereby preventing transcription and the production of WFS1 receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the WFS1 receptor (antisense-Okano, J. Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, Fla. (1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of WFS1 receptor.

Another potential antagonist is a small molecule which binds to the WFS1 receptor, making it inaccessible to ligands such that normal biological activity is prevented. Examples of small molecules include but are not limited to small peptides or peptide-like molecules.

Potential antagonists also include a soluble form of a WFS1 receptor, e.g. a fragment of the receptor, which binds to the ligand and prevents the ligand from interacting with membrane bound WFS1 receptors.

The WFS1 receptor and antagonists or agonists may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the polypeptide, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

#### G. Antibodies

The polypeptides, their fragments or other derivatives, or analogs thereof, or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment  
5 of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

#### IV. Methods for *De Novo* Identification of Biallelic Markers

10 Large fragments of human DNA, carrying genes of interest involved in CNS disorders; were cloned, sequenced and screened for biallelic markers. Biallelic markers within the candidate genes themselves as well as markers located on the same genomic fragment were identified. It will be clear to one of skill in the art that large fragments of human genomic DNA may be obtained from any appropriate source and may be cloned into a number of suitable  
15 vectors.

In a preferred embodiment of the invention, BAC (Bacterial Artificial Chromosomes) vectors were used to construct DNA libraries covering the entire human genome. Specific amplification primers were designed for each candidate gene and the BAC library was screened by PCR until there was at least one positive BAC clone per candidate gene. Genomic sequence,  
20 screened for biallelic markers, was generated by sequencing ends of BAC subclones. Details of a preferred embodiment are provided in Example 1. As a preferred alternative to sequencing the ends of an adequate number of BAC subclones, high throughput deletion-based sequencing vectors, which allow the generation of a high quality sequence information covering fragments of about 6kb, may be used. Having sequence fragments longer than 2.5 or 3kb enhances the  
25 chances of identifying biallelic markers therein. Methods of constructing and sequencing a nested set of deletions are disclosed in the related U.S. Patent Application entitled "High Throughput DNA Sequencing Vector" (Serial No. 09/058,746).

In another embodiment of the invention, genomic sequences of candidate genes were available in public databases allowing direct screening for biallelic markers.  
30 Any of a variety of methods can be used to screen a genomic fragment for single nucleotide polymorphisms such as differential hybridization with oligonucleotide probes, detection of changes in the mobility measured by gel electrophoresis or direct sequencing of the amplified nucleic acid. A preferred method for identifying biallelic markers involves comparative sequencing of genomic DNA fragments from an appropriate number of unrelated individuals.

35 In a first embodiment, DNA samples from unrelated individuals are pooled together, following which the genomic DNA of interest is amplified and sequenced. The nucleotide sequences thus obtained are then analyzed to identify significant polymorphisms. One of the

major advantages of this method resides in the fact that the pooling of the DNA samples substantially reduces the number of DNA amplification reactions and sequencing reactions, which must be carried out. Moreover, this method is sufficiently sensitive so that a biallelic marker obtained thereby usually demonstrates a sufficient frequency of its less common allele to  
5 be useful in conducting association studies. Usually, the frequency of the least common allele of a biallelic marker identified by this method is at least 10%.

In a second embodiment, the DNA samples are not pooled and are therefore amplified and sequenced individually. This method is usually preferred when biallelic markers need to be identified in order to perform association studies within candidate genes. Preferably, highly  
10 relevant gene regions such as promoter regions or exon regions may be screened for biallelic markers. A biallelic marker obtained using this method may show a lower degree of informativeness for conducting association studies, e.g. if the frequency of its less frequent allele may be less than about 10%. Such a biallelic marker will however be sufficiently informative to conduct association studies and it will further be appreciated that including less informative  
15 biallelic markers in the genetic analysis studies of the present invention, may allow in some cases the direct identification of causal mutations, which may, depending on their penetrance, be rare mutations.

The following is a description of the various parameters of a preferred method used by the inventors for the identification of the biallelic markers of the present invention.

#### 20     A. Genomic DNA Samples

The genomic DNA samples from which the biallelic markers of the present invention are generated are preferably obtained from unrelated individuals corresponding to a heterogeneous population of known ethnic background. The number of individuals from whom DNA samples are obtained can vary substantially, preferably from about 10 to about 1000, more preferably  
25 from about 50 to about 200 individuals. Usually, DNA samples are collected from at least about 100 individuals in order to have sufficient polymorphic diversity in a given population to identify as many markers as possible and to generate statistically significant results.

As for the source of the genomic DNA to be subjected to analysis, any test sample can be foreseen without any particular limitation. These test samples include biological samples, which  
30 can be tested by the methods of the present invention described herein, and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; fixed tissue specimens including tumor and non-tumor tissue and lymph node  
35 tissues; bone marrow aspirates and fixed cell specimens. The preferred source of genomic DNA used in the present invention is from peripheral venous blood of each donor. Techniques to prepare genomic DNA from biological samples are well known to the skilled technician. Details



of a preferred embodiment are provided in Example 1. The person skilled in the art can choose to amplify pooled or unpooled DNA samples.

#### B. DNA Amplification

The identification of biallelic markers in a sample of genomic DNA may be facilitated through the use of DNA amplification methods. DNA samples can be pooled or unpooled for the amplification step. DNA amplification techniques are well known to those skilled in the art. Various methods to amplify DNA fragments carrying biallelic markers are further described herein. The PCR technology is the preferred amplification technique used to identify new biallelic markers.

In a first embodiment, biallelic markers are identified using genomic sequence information generated by the inventors. Genomic DNA fragments, such as the inserts of the BAC clones described above, are sequenced and used to design primers for the amplification of 500 bp fragments. These 500 bp fragments are amplified from genomic DNA and are scanned for biallelic markers. Primers may be designed using the OSP software (Hillier L. and Green P., 1991). All primers may contain, upstream of the specific target bases, a common oligonucleotide tail that serves as a sequencing primer. Those skilled in the art are familiar with primer extensions, which can be used for these purposes.

In another embodiment of the invention, genomic sequences of candidate genes are available in public databases allowing direct screening for biallelic markers. Preferred primers, useful for the amplification of genomic sequences encoding the candidate genes, focus on promoters, exons and splice sites of the genes. A biallelic marker present in these functional regions of the gene has a higher probability to be a causal mutation.

Preferred primers include those disclosed in Table 13.

#### C. Sequencing of Amplified Genomic DNA and Identification of Single Nucleotide Polymorphisms

The amplification products generated as described above, are then sequenced using any method known and available to the skilled technician. Methods for sequencing DNA using either the dideoxy-mediated method (Sanger method) or the Maxam-Gilbert method are widely known to those of ordinary skill in the art. Such methods are for example disclosed in Maniatis et al. (Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Second Edition, 1989). Alternative approaches include hybridization to high-density DNA probe arrays as described in Chee et al. (Science 274, 610, 1996).

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. The products of the sequencing reactions are run on sequencing gels and the sequences are determined using gel image analysis. The polymorphism search is based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. Because each dideoxy

terminator is labeled with a different fluorescent molecule, the two peaks corresponding to a biallelic site present distinct colors corresponding to two different nucleotides at the same position on the sequence. However, the presence of two peaks can be an artifact due to background noise. To exclude such an artifact, the two DNA strands are sequenced and a comparison between the peaks is carried out. In order to be registered as a polymorphic sequence, the polymorphism has to be detected on both strands.

The above procedure permits those amplification products, which contain biallelic markers to be identified. The detection limit for the frequency of biallelic polymorphisms detected by sequencing pools of 100 individuals is approximately 0.1 for the minor allele, as verified by sequencing pools of known allelic frequencies. However, more than 90% of the biallelic polymorphisms detected by the pooling method have a frequency for the minor allele higher than 0.25. Therefore, the biallelic markers selected by this method have a frequency of at least 0.1 for the minor allele and less than 0.9 for the major allele. Preferably at least 0.2 for the minor allele and less than 0.8 for the major allele, more preferably at least 0.3 for the minor allele and less than 0.7 for the major allele, thus a heterozygosity rate higher than 0.18, preferably higher than 0.32, more preferably higher than 0.42.

In another embodiment, biallelic markers are detected by sequencing individual DNA samples; the frequency of the minor allele of such a biallelic marker may be less than 0.1.

The markers carried by the same fragment of genomic DNA, such as the insert in a BAC clone, need not necessarily be ordered with respect to one another within the genomic fragment to conduct association studies. However, in some embodiments of the present invention, the order of biallelic markers carried by the same fragment of genomic DNA are determined.

#### D. Validation of the Biallelic Markers of the Present Invention

The polymorphisms are evaluated for their usefulness as genetic markers by validating that both alleles are present in a population. Validation of the biallelic markers is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. Microsequencing is a preferred method of genotyping alleles. The validation by genotyping step may be performed on individual samples derived from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group can be as small as one individual if that individual is heterozygous for the allele in question.

Preferably the group contains at least three individuals, more preferably the group contains five or six individuals, so that a single validation test will be more likely to result in the validation of more of the biallelic markers that are being tested. It should be noted, however, that when the validation test is performed on a small group it may result in a false negative result if as a result of sampling error none of the individuals tested carries one of the two alleles. Thus, the validation process is less useful in demonstrating that a particular initial result is an artifact, than it is at demonstrating that there is a *bona fide* biallelic marker at a particular position in a

sequence. For an indication of whether a particular biallelic marker has been validated see Table 7. All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be performed solely with validated biallelic markers.

E. Evaluation of the Frequency of the Biallelic Markers of the Present Invention

5       The validated biallelic markers are further evaluated for their usefulness as genetic markers by determining the frequency of the least common allele at the biallelic marker site. The determination of the least common allele is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. This determination of frequency by genotyping step may be performed on individual samples derived  
10       from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group must be large enough to be representative of the population as a whole. Preferably the group contains at least 20 individuals, more preferably the group contains at least 50 individuals, most preferably the group contains at least 100 individuals. Of course the larger the group the greater the accuracy of the frequency determination because of reduced sampling  
15       error. For an indication of the frequency for the less common allele of a particular biallelic marker of the invention see Table 7. A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker." All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be performed solely with high quality biallelic markers.

20

V. Methods of Genotyping an Individual for Biallelic Markers

      Methods are provided to genotype a biological sample for one or more biallelic markers of the present invention, all of which may be performed *in vitro*. Such methods of genotyping comprise determining the identity of a nucleotide at a CNS disorder-related biallelic marker by  
25       any method known in the art. These methods find use in genotyping case-control populations in association studies as well as individuals in the context of detection of alleles of biallelic markers which, are known to be associated with a given trait, in which case both copies of the biallelic marker present in individual's genome are determined so that an individual may be classified as homozygous or heterozygous for a particular allele.

30       These genotyping methods can be performed nucleic acid samples derived from a single individual or pooled DNA samples.

      Genotyping can be performed using similar methods as those described above for the identification of the biallelic markers, or using other genotyping methods such as those further described below. In preferred embodiments, the comparison of sequences of amplified genomic  
35       fragments from different individuals is used to identify new biallelic markers whereas microsequencing is used for genotyping known biallelic markers in diagnostic and association study applications.

### A. Source of DNA for Genotyping

Any source of nucleic acids, in purified or non-purified form, can be utilized as the starting nucleic acid, provided it contains or is suspected of containing the specific nucleic acid sequence desired. DNA or RNA may be extracted from cells, tissues, body fluids and the like as described herein. While nucleic acids for use in the genotyping methods of the invention can be derived from any mammalian source, the test subjects and individuals from which nucleic acid samples are taken are generally understood to be human.

### B. Amplification of DNA Fragments Comprising Biallelic Markers

Methods and polynucleotides are provided to amplify a segment of nucleotides comprising one or more biallelic marker of the present invention. It will be appreciated that amplification of DNA fragments comprising biallelic markers may be used in various methods and for various purposes and is not restricted to genotyping. Nevertheless, many genotyping methods, although not all, require the previous amplification of the DNA region carrying the biallelic marker of interest. Such methods specifically increase the concentration or total number of sequences that span the biallelic marker or include that site and sequences located either distal or proximal to it. Diagnostic assays may also rely on amplification of DNA segments carrying a biallelic marker of the present invention.

Amplification of DNA may be achieved by any method known in the art. The established PCR (polymerase chain reaction) method or by developments thereof or alternatives. Amplification methods which can be utilized herein include but are not limited to Ligase Chain Reaction (LCR) as described in EP A 320 308 and EP A 439 182, Gap LCR (Wolcott, M.J., *Clin. Microbiol. Rev.* 5:370-386), the so-called "NASBA" or "3SR" technique described in Guatelli J.C. et al. (*Proc. Natl. Acad. Sci. USA* 87:1874-1878, 1990) and in Compton J. (*Nature* 350:91-92, 1991), Q-beta amplification as described in European Patent Application no 4544610, strand displacement amplification as described in Walker et al. (*Clin. Chem.* 42:9-13, 1996) and EP A 684 315 and, target mediated amplification as described in PCT Publication WO 9322461.

LCR and Gap LCR are exponential amplification techniques, both depend on DNA ligase to join adjacent primers annealed to a DNA molecule. In Ligase Chain Reaction (LCR), probe pairs are used which include two primary (first and second) and two secondary (third and fourth) probes, all of which are employed in molar excess to target. The first probe hybridizes to a first segment of the target strand and the second probe hybridizes to a second segment of the target strand, the first and second segments being contiguous so that the primary probes abut one another in 5' phosphate-3'hydroxyl relationship, and so that a ligase can covalently fuse or ligate the two probes into a fused product. In addition, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar abutting fashion. Of course, if the target is initially double stranded, the secondary probes also will hybridize to the target complement in the first instance. Once the

ligated strand of primary probes is separated from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary ligated product. It is important to realize that the ligated products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. A method for multiplex LCR has also been described (WO 9320227). Gap LCR (GLCR) is a version of LCR where the probes are not adjacent but are separated by 2 to 3 bases.

For amplification of mRNAs, it is within the scope of the present invention to reverse transcribe mRNA into cDNA followed by polymerase chain reaction (RT-PCR); or, to use a single enzyme for both steps as described in U.S. Patent No. 5,322,770 or, to use Asymmetric Gap LCR (RT-AGLCR) as described by Marshall R.L. et al. (*PCR Methods and Applications* 4:80-84, 1994). AGLCR is a modification of GLCR that allows the amplification of RNA.

Some of these amplification methods are particularly suited for the detection of single nucleotide polymorphisms and allow the simultaneous amplification of a target sequence and the identification of the polymorphic nucleotide as it is further described herein.

The PCR technology is the preferred amplification technique used in the present invention. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa (1997) and the publication entitled "PCR Methods and Applications" (1991, Cold Spring Harbor Laboratory Press). In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites. PCR has further been described in several patents including US Patents 4,683,195, 4,683,202 and 4,965,188.

The identification of biallelic markers as described above allows the design of appropriate oligonucleotides, which can be used as primers to amplify DNA fragments comprising the biallelic markers of the present invention. Amplification can be performed using the primers initially used to discover new biallelic markers which are described herein or any set of primers allowing the amplification of a DNA fragment comprising a biallelic marker of the present invention. Primers can be prepared by any suitable method. As for example, direct chemical synthesis by a method such as the phosphodiester method of Narang S.A. et al. (*Methods Enzymol.* 68:90-98, 1979), the phosphodiester method of Brown E.L. et al. (*Methods*

*Enzymol.* 68:109-151, 1979), the diethylphosphoramidite method of Beaucage et al. (*Tetrahedron Lett.* 22:1859-1862, 1981) and the solid support method described in EP 0 707 592.

In some embodiments the present invention provides primers for amplifying a DNA fragment containing one or more biallelic markers of the present invention. Preferred  
5 amplification primers are listed in Table 13. It will be appreciated that the primers listed are merely exemplary and that any other set of primers which produce amplification products containing one or more biallelic markers of the present invention.

The primers are selected to be substantially complementary to the different strands of each specific sequence to be amplified. The length of the primers of the present invention can  
10 range from 8 to 100 nucleotides, preferably from 8 to 50, 8 to 30 or more preferably 8 to 25 nucleotides. Shorter primers tend to lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer primers are expensive to produce and can sometimes self-hybridize to form hairpin structures. The formation of stable hybrids depends on the melting temperature ( $T_m$ ) of  
15 the DNA. The  $T_m$  depends on the length of the primer, the ionic strength of the solution and the G+C content. The higher the G+C content of the primer, the higher is the melting temperature because G:C pairs are held by three H bonds whereas A:T pairs have only two. The G+C content of the amplification primers of the present invention preferably ranges between 10 and 75 %, more preferably between 35 and 60 %, and most preferably between 40 and 55 %. The  
20 appropriate length for primers under a particular set of assay conditions may be empirically determined by one of skill in the art.

The spacing of the primers determines the length of the segment to be amplified. In the context of the present invention amplified segments carrying biallelic markers can range in size from at least about 25 bp to 35 kbp. Amplification fragments from 25-3000 bp are typical,  
25 fragments from 50-1000 bp are preferred and fragments from 100-600 bp are highly preferred. It will be appreciated that amplification primers for the biallelic markers may be any sequence which allow the specific amplification of any DNA fragment carrying the markers.

Amplification primers may be labeled or immobilized on a solid support as described in I.

#### C. Methods of Genotyping DNA samples for Biallelic Markers

30 Any method known in the art can be used to identify the nucleotide present at a biallelic marker site. Since the biallelic marker allele to be detected has been identified and specified in the present invention, detection will prove simple for one of ordinary skill in the art by employing any of a number of techniques. Many genotyping methods require the previous amplification of the DNA region carrying the biallelic marker of interest. While the  
35 amplification of target or signal is often preferred at present, ultrasensitive detection methods which do not require amplification are also encompassed by the present genotyping methods. Methods well-known to those skilled in the art that can be used to detect biallelic polymorphisms

include methods such as, conventional dot blot analyzes, single strand conformational polymorphism analysis (SSCP) described by Orita et al. (*Proc. Natl. Acad. Sci. U.S.A* 86:27776-2770, 1989), denaturing gradient gel electrophoresis (DGGE), heteroduplex analysis, mismatch cleavage detection, and other conventional techniques as described in Sheffield, V.C. et al. (*Proc. Natl. Acad. Sci. USA* 49:699-706, 1991), White et al. (*Genomics* 12:301-306, 1992), Grompe, M. et al. (*Proc. Natl. Acad. Sci. USA* 86:5855-5892, 1989) and Grompe, M. (*Nature Genetics* 5:111-117, 1993). Another method for determining the identity of the nucleotide present at a particular polymorphic site employs a specialized exonuclease-resistant nucleotide derivative as described in US patent 4,656,127.

Preferred methods involve directly determining the identity of the nucleotide present at a biallelic marker site by sequencing assay, enzyme-based mismatch detection assay, or hybridization assay. The following is a description of some preferred methods. A highly preferred method is the microsequencing technique. The term "sequencing assay" is used herein to refer to polymerase extension of duplex primer/template complexes and includes both traditional sequencing and microsequencing.

i) Sequencing assays

The nucleotide present at a polymorphic site can be determined by sequencing methods. In a preferred embodiment, DNA samples are subjected to PCR amplification before sequencing as described above. DNA sequencing methods are described herein.

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. Sequence analysis allows the identification of the base present at the biallelic marker site.

ii) Microsequencing assays

In microsequencing methods, a nucleotide at the polymorphic site that is unique to one of the alleles in a target DNA is detected by a single nucleotide primer extension reaction. This method involves appropriate microsequencing primers which, hybridize just upstream of a polymorphic base of interest in the target nucleic acid. A polymerase is used to specifically extend the 3' end of the primer with one single ddNTP (chain terminator) complementary to the selected nucleotide at the polymorphic site. Next the identity of the incorporated nucleotide is determined in any suitable way.

Typically, microsequencing reactions are carried out using fluorescent ddNTPs and the extended microsequencing primers are analyzed by electrophoresis on ABI 377 sequencing machines to determine the identity of the incorporated nucleotide as described in EP 412 883. Alternatively capillary electrophoresis can be used in order to process a higher number of assays simultaneously. An example of a typical microsequencing procedure that can be used in the context of the present invention is provided in Example 2.

Different approaches can be used to detect the nucleotide added to the microsequencing primer. A homogeneous phase detection method based on fluorescence resonance energy transfer has been described by Chen and Kwok (*Nucleic Acids Research* 25:347-353 1997) and Chen et al. (*Proc. Natl. Acad. Sci. USA* 94/20 10756-10761, 1997). In this method amplified genomic DNA fragments containing polymorphic sites are incubated with a 5'-fluorescein-labeled primer in the presence of allelic dye-labeled dideoxyribonucleoside triphosphates and a modified Taq polymerase. The dye-labeled primer is extended one base by the dye-terminator specific for the allele present on the template. At the end of the genotyping reaction, the fluorescence intensities of the two dyes in the reaction mixture are analyzed directly without separation or purification.

All these steps can be performed in the same tube and the fluorescence changes can be monitored in real time. Alternatively, the extended primer may be analyzed by MALDI-TOF Mass Spectrometry. The base at the polymorphic site is identified by the mass added onto the microsequencing primer (see Haff L.A. and Smirnov L.P., *Genome Research*, 7:378-388, 1997).

Microsequencing may be achieved by the established microsequencing method or by developments or derivatives thereof. Alternative methods include several solid-phase microsequencing techniques. The basic microsequencing protocol is the same as described previously, except that the method is conducted as a heterogenous phase assay, in which the primer or the target molecule is immobilized or captured onto a solid support. To simplify the primer separation and the terminal nucleotide addition analysis, oligonucleotides are attached to solid supports or are modified in such ways that permit affinity separation as well as polymerase extension. The 5' ends and internal nucleotides of synthetic oligonucleotides can be modified in a number of different ways to permit different affinity separation approaches, e.g., biotinylation. If a single affinity group is used on the oligonucleotides, the oligonucleotides can be separated from the incorporated terminator reagent. This eliminates the need of physical or size separation.

More than one oligonucleotide can be separated from the terminator reagent and analyzed simultaneously if more than one affinity group is used. This permits the analysis of several nucleic acid species or more nucleic acid sequence information per extension reaction. The affinity group need not be on the priming oligonucleotide but could alternatively be present on the template. For example, immobilization can be carried out via an interaction between biotinylated DNA and streptavidin-coated microtitration wells or avidin-coated polystyrene particles. In the same manner oligonucleotides or templates may be attached to a solid support in a high-density format. In such solid phase microsequencing reactions, incorporated ddNTPs can be radiolabeled (Syvänen, *Clinica Chimica Acta* 226:225-236, 1994) or linked to fluorescein (Livak and Hainer, *Human Mutation* 3:379-385, 1994). The detection of radiolabeled ddNTPs can be achieved through scintillation-based techniques. The detection of fluorescein-linked ddNTPs can be based on the binding of anti-fluorescein antibody conjugated with alkaline phosphatase, followed by incubation with a chromogenic substrate (such as *p*-nitrophenyl



phosphate). Other possible reporter-detection pairs include: ddNTP linked to dinitrophenyl (DNP) and anti-DNP alkaline phosphatase conjugate (Harju et al., *Clin. Chem.* 39/11 2282-2287, 1993) or biotinylated ddNTP and horseradish peroxidase-conjugated streptavidin with *o*-phenylenediamine as a substrate (WO 92/15712). As yet another alternative solid-phase  
5 microsequencing procedure, Nyren et al. (*Analytical Biochemistry* 208:171-175, 1993) described a method relying on the detection of DNA polymerase activity by an enzymatic luminometric inorganic pyrophosphate detection assay (ELIDA).

Pastinen et al. (*Genome research* 7:606-614, 1997) describe a method for multiplex  
detection of single nucleotide polymorphism in which the solid phase minisequencing principle  
10 is applied to an oligonucleotide array format. High-density arrays of DNA probes attached to a solid support (DNA chips) are further described herein.

In one aspect the present invention provides polynucleotides and methods to genotype one or more biallelic markers of the present invention by performing a microsequencing assay. Preferred microsequencing primers include those being featured in Table 12. It will be  
15 appreciated that the microsequencing primers listed in Table 12 are merely exemplary and that, any primer having a 3' end immediately adjacent to a polymorphic nucleotide may be used. Similarly, it will be appreciated that microsequencing analysis may be performed for any biallelic marker or any combination of biallelic markers of the present invention. One aspect of the present invention is a solid support which includes one or more microsequencing primers  
20 listed in Table 12, or fragments comprising at least 8, at least 12, at least 15, or at least 20 consecutive nucleotides thereof and having a 3' terminus immediately upstream of the corresponding biallelic marker, for determining the identity of a nucleotide at a biallelic marker site.

### iii) Mismatch detection assays based on polymerases and ligases

25 In one aspect the present invention provides polynucleotides and methods to determine the allele of one or more biallelic markers of the present invention in a biological sample, by mismatch detection assays based on polymerases and/or ligases. These assays are based on the specificity of polymerases and ligases. Polymerization reactions places particularly stringent requirements on correct base pairing of the 3' end of the amplification primer and the joining of  
30 two oligonucleotides hybridized to a target DNA sequence is quite sensitive to mismatches close to the ligation site, especially at the 3' end. The terms "enzyme based mismatch detection assay" are used herein to refer to any method of determining the allele of a biallelic marker based on the specificity of ligases and polymerases. Preferred methods are described below. Methods, primers and various parameters to amplify DNA fragments comprising biallelic markers of the  
35 present invention are further described herein.

#### 1. Allele specific amplification

Discrimination between the two alleles of a biallelic marker can also be achieved by allele specific amplification, a selective strategy, whereby one of the alleles is amplified without amplification of the other allele. This is accomplished by placing a polymorphic base at the 3' end of one of the amplification primers. Because the extension forms from the 3' end of the primer, a mismatch at or near this position has an inhibitory effect on amplification. Therefore, under appropriate amplification conditions, these primers only direct amplification on their complementary allele. Designing the appropriate allele-specific primer and the corresponding assay conditions are well within the ordinary skill in the art.

## 2. Ligation/amplification based methods

The "Oligonucleotide Ligation Assay" (OLA) uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of target molecules. One of the oligonucleotides is biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate that can be captured and detected. OLA is capable of detecting biallelic markers and may be advantageously combined with PCR as described by Nickerson D.A. et al. (*Proc. Natl. Acad. Sci. U.S.A.* 87:8923-8927, 1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Other methods which are particularly suited for the detection of biallelic markers include LCR (ligase chain reaction), Gap LCR (GLCR) which are described herein. As mentioned above LCR uses two pairs of probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides, is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependant ligase. In accordance with the present invention, LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a biallelic marker site. In one embodiment, either oligonucleotide will be designed to include the biallelic marker site. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide(s) that is complementary to the biallelic marker on the oligonucleotide. In an alternative embodiment, the oligonucleotides will not include the biallelic marker, such that when they hybridize to the target molecule, a "gap" is created as described in WO 90/01069. This gap is then "filled" with complementary dNTPs (as mediated by DNA polymerase), or by an additional pair of oligonucleotides. Thus at the end of each cycle, each single strand has a complement capable of serving as a target during the next cycle and exponential allele-specific amplification of the desired sequence is obtained.

Ligase/Polymerase-mediated Genetic Bit Analysis<sup>TM</sup> is another method for determining the identity of a nucleotide at a preselected site in a nucleic acid molecule (WO 95/21271). This

method involves the incorporation of a nucleoside triphosphate that is complementary to the nucleotide present at the preselected site onto the terminus of a primer molecule, and their subsequent ligation to a second oligonucleotide. The reaction is monitored by detecting a specific label attached to the reaction's solid phase or by detection in solution.

5            iv) Hybridization assay methods

A preferred method of determining the identity of the nucleotide present at a biallelic marker site involves nucleic acid hybridization. The hybridization probes, which can be conveniently used in such reactions, preferably include the probes defined herein. Any hybridization assay may be used including Southern hybridization, Northern hybridization, dot blot hybridization and solid-phase hybridization (see Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989).

Hybridization refers to the formation of a duplex structure by two single stranded nucleic acids due to complementary base pairing. Hybridization can occur between exactly complementary nucleic acid strands or between nucleic acid strands that contain minor regions of mismatch. Specific probes can be designed that hybridize to one form of a biallelic marker and not to the other and therefore are able to discriminate between different allelic forms. Allele-specific probes are often used in pairs, one member of a pair showing perfect match to a target sequence containing the original allele and the other showing a perfect match to the target sequence containing the alternative allele. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Stringent, sequence specific hybridization conditions, under which a probe will hybridize only to the exactly complementary target sequence are well known in the art (Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989).

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10<sup>6</sup> cpm of <sup>32</sup>P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Sodium citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2

x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68°C for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then  
5 hybridized at a temperature of 60°C in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50°C and the hybridized probes are detectable by autoradiography. Other conditions of high and intermediate stringency which may be used are well known in the art and as cited in Sambrook et al. (Molecular Cloning - A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y.,  
10 1989) and Ausubel et al. (Current Protocols in Molecular Biology, Green Publishing Associates and Wiley-Interscience, N.Y., 1989).

Although such hybridizations can be performed in solution, it is preferred to employ a solid-phase hybridization assay. The target DNA comprising a biallelic marker of the present invention may be amplified prior to the hybridization reaction. The presence of a specific allele  
15 in the sample is determined by detecting the presence or the absence of stable hybrid duplexes formed between the probe and the target DNA. The detection of hybrid duplexes can be carried out by a number of methods. Various detection assay formats are well known which utilize detectable labels bound to either the target or the probe to enable detection of the hybrid duplexes. Typically, hybridization duplexes are separated from unhybridized nucleic acids and  
20 the labels bound to the duplexes are then detected. Those skilled in the art will recognize that wash steps may be employed to wash away excess target DNA or probe. Standard heterogeneous assay formats are suitable for detecting the hybrids using the labels present on the primers and probes.

Two recently developed assays allow hybridization-based allele discrimination with no  
25 need for separations or washes (see Landegren U. et al., *Genome Research*, 8:769-776, 1998). The TaqMan assay takes advantage of the 5' nuclease activity of Taq DNA polymerase to digest a DNA probe annealed specifically to the accumulating amplification product. TaqMan probes are labeled with a donor-acceptor dye pair that interacts via fluorescence energy transfer. Cleavage of the TaqMan probe by the advancing polymerase during amplification dissociates the  
30 donor dye from the quenching acceptor dye, greatly increasing the donor fluorescence. All reagents necessary to detect two allelic variants can be assembled at the beginning of the reaction and the results are monitored in real time (see Livak et al., *Nature Genetics*, 9:341-342, 1995). In an alternative homogeneous hybridization-based procedure, molecular beacons are used for allele discriminations. Molecular beacons are hairpin-shaped oligonucleotide probes that report  
35 the presence of specific nucleic acids in homogeneous solutions. When they bind to their targets they undergo a conformational reorganization that restores the fluorescence of an internally quenched fluorophore (Tyagi et al., *Nature Biotechnology*, 16:49-53, 1998).

The polynucleotides provided herein can be used in hybridization assays for the detection of biallelic marker alleles in biological samples. These probes are characterized in that they preferably comprise between 8 and 50 nucleotides, and in that they are sufficiently complementary to a sequence comprising a biallelic marker of the present invention to hybridize thereto and preferably sufficiently specific to be able to discriminate the targeted sequence for only one nucleotide variation. The GC content in the probes of the invention usually ranges between 10 and 75 %, preferably between 35 and 60 %, and more preferably between 40 and 55 %. The length of these probes can range from 10, 15, 20, or 30 to at least 100 nucleotides, preferably from 10 to 50, more preferably from 18 to 35 nucleotides. A particularly preferred probe is 25 nucleotides in length. Preferably the biallelic marker is within 4 nucleotides of the center of the polynucleotide probe. In particularly preferred probes the biallelic marker is at the center of said polynucleotide. Shorter probes may lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer probes are expensive to produce and can sometimes self-hybridize to form hairpin structures. Methods for the synthesis of oligonucleotide probes have been described above and can be applied to the probes of the present invention.

Preferably the probes of the present invention are labeled or immobilized on a solid support. Labels and solid supports are further described in I. Detection probes are generally nucleic acid sequences or uncharged nucleic acid analogs such as, for example peptide nucleic acids which are disclosed in International Patent Application WO 92/20702; morpholino analogs which are described in U.S. Patents Numbered 5,185,444; 5,034,506 and 5,142,047. The probe may have to be rendered "non-extendable" in that additional dNTPs cannot be added to the probe. In and of themselves analogs usually are non-extendable and nucleic acid probes can be rendered non-extendable by modifying the 3' end of the probe such that the hydroxyl group is no longer capable of participating in elongation. For example, the 3' end of the probe can be functionalized with the capture or detection label to thereby consume or otherwise block the hydroxyl group. Alternatively, the 3' hydroxyl group simply can be cleaved, replaced or modified, U.S. Patent Application Serial No. 07/049,061 filed April 19, 1993 describes modifications, which can be used to render a probe non-extendable.

The probes of the present invention are useful for a number of purposes. They can be used in Southern hybridization to genomic DNA or Northern hybridization to mRNA. The probes can also be used to detect PCR amplification products. By assaying the hybridization to an allele specific probe, one can detect the presence or absence of a biallelic marker allele in a given sample.

High-Throughput parallel hybridizations in array format are specifically encompassed within "hybridization assays" and are described below.

i. Hybridization to addressable arrays of oligonucleotides

Hybridization assays based on oligonucleotide arrays rely on the differences in hybridization stability of short oligonucleotides to perfectly matched and mismatched target sequence variants. Efficient access to polymorphism information is obtained through a basic structure comprising high-density arrays of oligonucleotide probes attached to a solid support (the chip) at selected positions. Each DNA chip can contain thousands to millions of individual synthetic DNA probes arranged in a grid-like pattern and miniaturized to the size of a dime.

The chip technology has already been applied with success in numerous cases. For example, the screening of mutations has been undertaken in the BRCA1 gene, in *S. cerevisiae* mutant strains, and in the protease gene of HIV-1 virus (Hacia et al., *Nature Genetics*, 14(4):441-447, 1996; Shoemaker et al., *Nature Genetics*, 14(4):450-456, 1996 ; Kozal et al., *Nature Medicine*, 2:753-759, 1996). Chips of various formats for use in detecting biallelic polymorphisms can be produced on a customized basis by Affymetrix (GeneChip™), Hyseq (HyChip and HyGnostics), and Protogene Laboratories.

In general, these methods employ arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual which, target sequences include a polymorphic marker. EP785280 describes a tiling strategy for the detection of single nucleotide polymorphisms. Briefly, arrays may generally be "tiled" for a large number of specific polymorphisms. By "tiling" is generally meant the synthesis of a defined set of oligonucleotide probes which is made up of a sequence complementary to the target sequence of interest, as well as preselected variations of that sequence, e.g., substitution of one or more given positions with one or more members of the basis set of monomers, i.e. nucleotides. Tiling strategies are further described in PCT application No. WO 95/11995. In a particular aspect, arrays are tiled for a number of specific, identified biallelic marker sequences. In particular the array is tiled to include a number of detection blocks, each detection block being specific for a specific biallelic marker or a set of biallelic markers. For example, a detection block may be tiled to include a number of probes, which span the sequence segment that includes a specific polymorphism. To ensure probes that are complementary to each allele, the probes are synthesized in pairs differing at the biallelic marker. In addition to the probes differing at the polymorphic base, monosubstituted probes are also generally tiled within the detection block. These monosubstituted probes have bases at and up to a certain number of bases in either direction from the polymorphism, substituted with the remaining nucleotides (selected from A, T, G, C and U). Typically the probes in a tiled detection block will include substitutions of the sequence positions up to and including those that are 5 bases away from the biallelic marker. The monosubstituted probes provide internal controls for the tiled array, to distinguish actual hybridization from artefactual cross-hybridization. Upon completion of hybridization with the target sequence and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data from the scanned array is

then analyzed to identify which allele or alleles of the biallelic marker are present in the sample. Hybridization and scanning may be carried out as described in PCT application No. WO 92/10092 and WO 95/11995 and US patent No. 5,424,186.

Thus, in some embodiments, the chips may comprise an array of nucleic acid sequences of fragments of about 15 nucleotides in length. In further embodiments, the chip may comprise an array including at least one of the sequences selected from the group consisting of SEQ ID No. 1-130 and the sequences complementary thereto, or a fragment thereof at least about 8 consecutive nucleotides, preferably 10, 15, 20, more preferably 25, 30, 40, 47, or 50 consecutive nucleotides. In some embodiments, the chip may comprise an array of at least 2, 3, 4, 5, 6, 7, 8 or more of these polynucleotides of the invention. Solid supports and polynucleotides of the present invention attached to solid supports are further described in I.

#### v) Integrated systems

Another technique, which may be used to analyze polymorphisms, includes multicomponent integrated systems, which miniaturize and compartmentalize processes such as PCR and capillary electrophoresis reactions in a single functional device. An example of such technique is disclosed in US patent 5,589,136, which describes the integration of PCR amplification and capillary electrophoresis in chips.

Integrated systems can be envisaged mainly when microfluidic systems are used. These systems comprise a pattern of microchannels designed onto a glass, silicon, quartz, or plastic wafer included on a microchip. The movements of the samples are controlled by electric, electroosmotic or hydrostatic forces applied across different areas of the microchip. For genotyping biallelic markers, the microfluidic system may integrate nucleic acid amplification, microsequencing, capillary electrophoresis and a detection method such as laser-induced fluorescence detection.

25

#### VI. Methods of Genetic Analysis Using the Biallelic Markers of the Present Invention

Different methods are available for the genetic analysis of complex traits (see Lander and Schork, *Science*, 265, 2037-2048, 1994). The search for disease-susceptibility genes is conducted using two main methods: the linkage approach in which evidence is sought for cosegregation between a locus and a putative trait locus using family studies, and the association approach in which evidence is sought for a statistically significant association between an allele and a trait or a trait causing allele (Khoury J. et al., *Fundamentals of Genetic Epidemiology*, Oxford University Press, NY, 1993). In general, the biallelic markers of the present invention find use in any method known in the art to demonstrate a statistically significant correlation between a genotype and a phenotype. The biallelic markers may be used in parametric and non-parametric linkage analysis methods. Preferably, the biallelic markers of the present invention are used to identify genes associated with detectable traits using association studies, an approach

35

which does not require the use of affected families and which permits the identification of genes associated with complex and sporadic traits.

The genetic analysis using the biallelic markers of the present invention may be conducted on any scale. The whole set of biallelic markers of the present invention or any subset of biallelic markers of the present invention may be used. In some embodiments a subset of biallelic markers corresponding to one or several candidate genes of the present invention may be used. In other embodiments a subset of biallelic markers corresponding to CNS disorder candidate genes may be used. Alternatively, a subset of biallelic markers of the present invention localised on a specific chromosome segment may be used. Further, any set of genetic markers including a biallelic marker of the present invention may be used. A set of biallelic polymorphisms that, could be used as genetic markers in combination with the biallelic markers of the present invention, has been described in WO 98/20165. As mentioned above, it should be noted that the biallelic markers of the present invention may be included in any complete or partial genetic map of the human genome. These different uses are specifically contemplated in the present invention and claims.

#### A. Linkage Analysis

Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific trait throughout generations within a family. Thus, the aim of linkage analysis is to detect marker loci that show cosegregation with a trait of interest in pedigrees.

##### i. Parametric methods

When data are available from successive generations there is the opportunity to study the degree of linkage between pairs of loci. Estimates of the recombination fraction enable loci to be ordered and placed onto a genetic map. With loci that are genetic markers, a genetic map can be established, and then the strength of linkage between markers and traits can be calculated and used to indicate the relative positions of markers and genes affecting those traits (Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data*, Sinauer Assoc., Inc., Sunderland, MA, USA, 1996). The classical method for linkage analysis is the logarithm of odds (lod) score method (see Morton N.E., *Am.J. Hum. Genet.*, 7:277-318, 1955; Ott J., *Analysis of Human Genetic Linkage*, John Hopkins University Press, Baltimore, 1991). Calculation of lod scores requires specification of the mode of inheritance for the disease (parametric method). Generally, the length of the candidate region identified using linkage analysis is between 2 and 20Mb. Once a candidate region is identified as described above, analysis of recombinant individuals using additional markers allows further delineation of the candidate region. Linkage analysis studies have generally relied on the use of a maximum of 5,000 microsatellite markers, thus limiting the maximum theoretical attainable resolution of linkage analysis to about 600 kb on average.



Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and which have a high penetrance (i.e., the ratio between the number of trait positive carriers of allele  $a$  and the total number of  $a$  carriers in the population). However, parametric linkage analysis suffers from a variety of drawbacks. First, it is limited by its reliance on the choice of a genetic model suitable for each studied trait. Furthermore, as already mentioned, the resolution attainable using linkage analysis is limited, and complementary studies are required to refine the analysis of the typical 2Mb to 20Mb regions initially identified through linkage analysis. In addition, parametric linkage analysis approaches have proven difficult when applied to complex genetic traits, such as those due to the combined action of multiple genes and/or environmental factors. It is very difficult to model these factors adequately in a lod score analysis. In such cases, too large an effort and cost are needed to recruit the adequate number of affected families required for applying linkage analysis to these situations, as recently discussed by Risch, N. and Merikangas, K. (*Science*, 273:1516-1517, 1996).

#### ii. Non-parametric methods

The advantage of the so-called non-parametric methods for linkage analysis is that they do not require specification of the mode of inheritance for the disease, they tend to be more useful for the analysis of complex traits. In non-parametric methods, one tries to prove that the inheritance pattern of a chromosomal region is not consistent with random Mendelian segregation by showing that affected relatives inherit identical copies of the region more often than expected by chance. Affected relatives should show excess "allele sharing" even in the presence of incomplete penetrance and polygenic inheritance. In non-parametric linkage analysis the degree of agreement at a marker locus in two individuals can be measured either by the number of alleles identical by state (IBS) or by the number of alleles identical by descent (IBD). Affected sib pair analysis is a well-known special case and is the simplest form of these methods.

The biallelic markers of the present invention may be used in both parametric and non-parametric linkage analysis. Preferably biallelic markers may be used in non-parametric methods which allow the mapping of genes involved in complex traits. The biallelic markers of the present invention may be used in both IBD- and IBS- methods to map genes affecting a complex trait. In such studies, taking advantage of the high density of biallelic markers, several adjacent biallelic marker loci may be pooled to achieve the efficiency attained by multi-allelic markers (Zhao et al., *Am. J. Hum. Genet.*, 63:225-240, 1998).

However, both parametric and non-parametric linkage analysis methods analyse affected relatives, they tend to be of limited value in the genetic analysis of drug responses or in the analysis of side effects to treatments. This type of analysis is impractical in such cases due to the lack of availability of familial cases. In fact, the likelihood of having more than one individual in a family being exposed to the same drug at the same time is extremely low.

#### B. Population Association Studies

The present invention comprises methods for identifying one or several genes among a set of candidate genes that are associated with a detectable trait using the biallelic markers of the present invention. In one embodiment the present invention comprises methods to detect an association between a biallelic marker allele or a biallelic marker haplotype and a trait. Further, the invention comprises methods to identify a trait causing allele in linkage disequilibrium with any biallelic marker allele of the present invention.

As described above, alternative approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and candidate gene association studies. In a preferred embodiment, the biallelic markers of the present invention are used to perform candidate gene association studies. The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular trait when some information concerning the biology of the trait is available. Further, the biallelic markers of the present invention may be incorporated in any map of genetic markers of the human genome in order to perform genome-wide association studies. Methods to generate a high-density map of biallelic markers has been described in US Provisional Patent application serial number 60/082,614. The biallelic markers of the present invention may further be incorporated in any map of a specific candidate region of the genome (a specific chromosome or a specific chromosomal segment for example).

As mentioned above, association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families. Association studies are extremely valuable as they permit the analysis of sporadic or multifactor traits. Moreover, association studies represent a powerful method for fine-scale mapping enabling much finer mapping of trait causing alleles than linkage studies. Studies based on pedigrees often only narrow the location of the trait causing allele. Association studies using the biallelic markers of the present invention can therefore be used to refine the location of a trait causing allele in a candidate region identified by Linkage Analysis methods. Moreover, once a chromosome segment of interest has been identified, the presence of a candidate gene such as a candidate gene of the present invention, in the region of interest can provide a shortcut to the identification of the trait causing allele. Biallelic markers of the present invention can be used to demonstrate that a candidate gene is associated with a trait. Such uses are specifically contemplated in the present invention and claims.

i. Determining the frequency of a biallelic marker allele or of a biallelic marker haplotype in a population

Association studies explore the relationships among frequencies for sets of alleles between loci.

1) Determining the frequency of an allele in a population

Allelic frequencies of the biallelic markers in a population can be determined using one of the methods described above under the heading "Methods for genotyping an individual for biallelic markers", or any genotyping procedure suitable for this intended purpose. Genotyping pooled samples or individual samples can determine the frequency of a biallelic marker allele in a population. One way to reduce the number of genotypings required is to use pooled samples. A major obstacle in using pooled samples is in terms of accuracy and reproducibility for determining accurate DNA concentrations in setting up the pools. Genotyping individual samples provides higher sensitivity, reproducibility and accuracy and; is the preferred method used in the present invention. Preferably, each individual is genotyped separately and simple gene counting is applied to determine the frequency of an allele of a biallelic marker or of a genotype in a given population.

## 2) Determining the frequency of a haplotype in a population

The gametic phase of haplotypes is unknown when diploid individuals are heterozygous at more than one locus. Using genealogical information in families gametic phase can sometimes be inferred (Perlin et al., *Am. J. Hum. Genet.*, 55:777-787, 1994). When no genealogical information is available different strategies may be used. One possibility is that the multiple-site heterozygous diploids can be eliminated from the analysis, keeping only the homozygotes and the single-site heterozygote individuals, but this approach might lead to a possible bias in the sample composition and the underestimation of low-frequency haplotypes. Another possibility is that single chromosomes can be studied independently, for example, by asymmetric PCR amplification (see Newton et al., *Nucleic Acids Res.*, 17:2503-2516, 1989; Wu et al., *Proc. Natl. Acad. Sci. USA*, 86:2757, 1989) or by isolation of single chromosome by limit dilution followed by PCR amplification (see Ruano et al., *Proc. Natl. Acad. Sci. USA*, 87:6296-6300, 1990). Further, a sample may be haplotyped for sufficiently close biallelic markers by double PCR amplification of specific alleles (Sarkar, G. and Sommer S.S., *Biotechniques*, 1991). These approaches are not entirely satisfying either because of their technical complexity, the additional cost they entail, their lack of generalisation at a large scale, or the possible biases they introduce. To overcome these difficulties, an algorithm to infer the phase of PCR-amplified DNA genotypes introduced by Clark A.G. (*Mol. Biol. Evol.*, 7:111-122, 1990) may be used. Briefly, the principle is to start filling a preliminary list of haplotypes present in the sample by examining unambiguous individuals, that is, the complete homozygotes and the single-site heterozygotes. Then other individuals in the same sample are screened for the possible occurrence of previously recognized haplotypes. For each positive identification, the complementary haplotype is added to the list of recognized haplotypes, until the phase information for all individuals is either resolved or identified as unresolved. This method assigns a single haplotype to each multiheterozygous individual, whereas several haplotypes are possible when there are more than one heterozygous site. Alternatively, one can use methods estimating haplotype frequencies in a population without

assigning haplotypes to each individual. Preferably, a method based on an expectation-maximization (EM) algorithm (Dempster et al., *J. R. Stat. Soc.*, 39B: 1-38, 1977) leading to maximum-likelihood estimates of haplotype frequencies under the assumption of Hardy-Weinberg proportions (random mating) is used (see Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). The EM algorithm is a generalized iterative maximum-likelihood approach to estimation that is useful when data are ambiguous and/or incomplete. The EM algorithm is used to resolve heterozygotes into haplotypes. Haplotype estimations are further described below under the heading "Statistical methods". Any other method known in the art to determine or to estimate the frequency of a haplotype in a population may also be used.

10     ii. Linkage disequilibrium analysis

Linkage disequilibrium is the non-random association of alleles at two or more loci and represents a powerful tool for mapping genes involved in disease traits (see Ajioka R.S. et al., *Am. J. Hum. Genet.*, 60:1439-1447, 1997). Biallelic markers, because they are densely spaced in the human genome and can be genotyped in more numerous numbers than other types of genetic markers (such as RFLP or VNTR markers), are particularly useful in genetic analysis based on linkage disequilibrium. The biallelic markers of the present invention may be used in any linkage disequilibrium analysis method known in the art.

Briefly, when a disease mutation is first introduced into a population (by a new mutation or the immigration of a mutation carrier), it necessarily resides on a single chromosome and thus on a single "background" or "ancestral" haplotype of linked markers. Consequently, there is complete disequilibrium between these markers and the disease mutation: one finds the disease mutation only in the presence of a specific set of marker alleles. Through subsequent generations recombinations occur between the disease mutation and these marker polymorphisms, and the disequilibrium gradually dissipates. The pace of this dissipation is a function of the recombination frequency, so the markers closest to the disease gene will manifest higher levels of disequilibrium than those further away. When not broken up by recombination, "ancestral" haplotypes and linkage disequilibrium between marker alleles at different loci can be tracked not only through pedigrees but also through populations. Linkage disequilibrium is usually seen as an association between one specific allele at one locus and another specific allele at a second locus.

The pattern or curve of disequilibrium between disease and marker loci is expected to exhibit a maximum that occurs at the disease locus. Consequently, the amount of linkage disequilibrium between a disease allele and closely linked genetic markers may yield valuable information regarding the location of the disease gene. For fine-scale mapping of a disease locus, it is useful to have some knowledge of the patterns of linkage disequilibrium that exist between markers in the studied region. As mentioned above the mapping resolution achieved through the analysis of linkage disequilibrium is much higher than that of linkage studies. The

high density of biallelic markers combined with linkage disequilibrium analysis provides powerful tools for fine-scale mapping. Different methods to calculate linkage disequilibrium are described below under the heading "Statistical Methods".

### iii. Population-based case-control studies of trait-marker associations

5 As mentioned above, the occurrence of pairs of specific alleles at different loci on the same chromosome is not random and the deviation from random is called linkage disequilibrium. Association studies focus on population frequencies and rely on the phenomenon of linkage disequilibrium. If a specific allele in a given gene is directly involved in causing a particular trait, its frequency will be statistically increased in an affected (trait positive) population, when  
10 compared to the frequency in a trait negative population or in a random control population. As a consequence of the existence of linkage disequilibrium, the frequency of all other alleles present in the haplotype carrying the trait-causing allele will also be increased in trait positive individuals compared to trait negative individuals or random controls. Therefore, association between the trait and any allele (specifically a biallelic marker allele) in linkage disequilibrium with the trait-  
15 causing allele will suffice to suggest the presence of a trait-related gene in that particular region. Case-control populations can be genotyped for biallelic markers to identify associations that narrowly locate a trait causing allele. As any marker in linkage disequilibrium with one given marker associated with a trait will be associated with the trait. Linkage disequilibrium allows the relative frequencies in case-control populations of a limited number of genetic polymorphisms  
20 (specifically biallelic markers) to be analyzed as an alternative to screening all possible functional polymorphisms in order to find trait-causing alleles. Association studies compare the frequency of marker alleles in unrelated case-control populations, and represent powerful tools for the dissection of complex traits.

#### 1) Case-control populations (inclusion criteria)

25 Population-based association studies do not concern familial inheritance but compare the prevalence of a particular genetic marker, or a set of markers, in case-control populations. They are case-control studies based on comparison of unrelated case (affected or trait positive) individuals and unrelated control (unaffected or trait negative or random) individuals. Preferably the control group is composed of unaffected or trait negative individuals. Further, the  
30 control group is ethnically matched to the case population. Moreover, the control group is preferably matched to the case-population for the main known confusion factor for the trait under study (for example age-matched for an age-dependent trait). Ideally, individuals in the two samples are paired in such a way that they are expected to differ only in their disease status. In the following "trait positive population", "case population" and "affected population" are used  
35 interchangeably.

An important step in the dissection of complex traits using association studies is the choice of case-control populations (see Lander and Schork, *Science*, 265, 2037-2048, 1994). A

major step in the choice of case-control populations is the clinical definition of a given trait or phenotype. Any genetic trait may be analyzed by the association method proposed here by carefully selecting the individuals to be included in the trait positive and trait negative phenotypic groups. Four criteria are often useful: clinical phenotype, age at onset, family history and severity. The selection procedure for continuous or quantitative traits (such as blood pressure for example) involves selecting individuals at opposite ends of the phenotype distribution of the trait under study, so as to include in these trait positive and trait negative populations individuals with non-overlapping phenotypes. Preferably, case-control populations consist of phenotypically homogeneous populations. Trait positive and trait negative populations consist of phenotypically uniform populations of individuals representing each between 1 and 98%, preferably between 1 and 80%, more preferably between 1 and 50%, and more preferably between 1 and 30%, most preferably between 1 and 20% of the total population under study, and selected among individuals exhibiting non-overlapping phenotypes. The clearer the difference between the two trait phenotypes, the greater the probability of detecting an association with biallelic markers. The selection of those drastically different but relatively uniform phenotypes enables efficient comparisons in association studies and the possible detection of marked differences at the genetic level, provided that the sample sizes of the populations under study are significant enough.

In preferred embodiments, a first group of between 50 and 300 trait positive individuals, preferably about 100 individuals, are recruited according to their phenotypes. A similar number of trait negative individuals are included in such studies.

In the present invention, typical examples of inclusion criteria include a CNS disorder or the evaluation of the response to a drug acting on a CNS disorder or side effects to treatment with drugs acting on a CNS disorder.

Suitable examples of association studies using biallelic markers including the biallelic markers of the present invention, are studies involving the following populations:

a case population suffering from a CNS disorder and a healthy unaffected control population, or

a case population treated with agents acting on a CNS disorder suffering from side-effects resulting from the treatment and a control population treated with the same agents showing no side-effects, or

a case population treated with agents acting on a CNS disorder showing a beneficial response and a control population treated with same agents showing no beneficial response.

## 2) Association analysis

The general strategy to perform association studies using biallelic markers derived from a region carrying a candidate gene is to scan two groups of individuals (case-control populations)

in order to measure and statistically compare the allele frequencies of the biallelic markers of the present invention in both groups.

If a statistically significant association with a trait is identified for at least one or more of the analyzed biallelic markers, one can assume that: either the associated allele is directly responsible for causing the trait (the associated allele is the trait causing allele), or more likely the associated allele is in linkage disequilibrium with the trait causing allele. The specific characteristics of the associated allele with respect to the candidate gene function usually gives further insight into the relationship between the associated allele and the trait (causal or in linkage disequilibrium). If the evidence indicates that the associated allele within the candidate gene is most probably not the trait causing allele but is in linkage disequilibrium with the real trait causing allele, then the trait causing allele can be found by sequencing the vicinity of the associated marker.

Association studies are usually run in two successive steps. In a first phase, the frequencies of a reduced number of biallelic markers from one or several candidate genes are determined in the trait positive and trait negative populations. In a second phase of the analysis, the identity of the candidate gene and the position of the genetic loci responsible for the given trait is further refined using a higher density of markers from the relevant region. However, if the candidate gene under study is relatively small in length, as it is the case for many of the candidate genes analyzed included in the present invention, a single phase may be sufficient to establish significant associations.

### 3) Haplotype analysis

As described above, when a chromosome carrying a disease allele first appears in a population as a result of either mutation or migration, the mutant allele necessarily resides on a chromosome having a set of linked markers: the ancestral haplotype. This haplotype can be tracked through populations and its statistical association with a given trait can be analyzed. Complementing single point (allelic) association studies with multi-point association studies also called haplotype studies increases the statistical power of association studies. Thus, a haplotype association study allows one to define the frequency and the type of the ancestral carrier haplotype. A haplotype analysis is important in that it increases the statistical power of an analysis involving individual markers.

In a first stage of a haplotype frequency analysis, the frequency of the possible haplotypes based on various combinations of the identified biallelic markers of the invention is determined. The haplotype frequency is then compared for distinct populations of trait positive and control individuals. The number of trait positive individuals, which should be, subjected to this analysis to obtain statistically significant results usually ranges between 30 and 300, with a preferred number of individuals ranging between 50 and 150. The same considerations apply to the number of unaffected individuals (or random control) used in the study. The results of this

first analysis provide haplotype frequencies in case-control populations, for each evaluated haplotype frequency a p-value and an odd ratio are calculated. If a statistically significant association is found the relative risk for an individual carrying the given haplotype of being affected with the trait under study can be approximated.

5           4) Interaction analysis

The biallelic markers of the present invention may also be used to identify patterns of biallelic markers associated with detectable traits resulting from polygenic interactions. The analysis of genetic interaction between alleles at unlinked loci requires individual genotyping using the techniques described herein. The analysis of allelic interaction among a selected set of  
10 biallelic markers with appropriate level of statistical significance can be considered as a haplotype analysis. Interaction analysis consists in stratifying the case-control populations with respect to a given haplotype for the first loci and performing a haplotype analysis with the second loci with each subpopulation.

Statistical methods used in association studies are further described below in IV.C.

15           iv. Testing for linkage in the presence of association

The biallelic markers of the present invention may further be used in TDT (transmission/disequilibrium test). TDT tests for both linkage and association and is not affected by population stratification. TDT requires data from affected individuals and their parents or data from unaffected sibs instead of from parents (see Spielmann S. et al., *Am. J. Hum. Genet.*,  
20 52:506-516, 1993; Schaid D.J. et al., *Genet. Epidemiol.*, 13:423-450, 1996; Spielmann S. and Ewens W.J., *Am. J. Hum. Genet.*, 62:450-458, 1998). Such combined tests generally reduce the false – positive errors produced by separate analyses.

C. Statistical Methods

In general, any method known in the art to test whether a trait and a genotype show a  
25 statistically significant correlation may be used.

i. Methods in linkage analysis

Statistical methods and computer programs useful for linkage analysis are well-known to those skilled in the art (see Terwilliger J.D. and Ott J., *Handbook of Human Genetic Linkage*, John Hopkins University Press, London, 1994; Ott J., *Analysis of Human Genetic Linkage*, John  
30 Hopkins University Press, Baltimore, 1991).

ii. Methods to estimate haplotype frequencies in a population

As described above, when genotypes are scored, it is often not possible to distinguish heterozygotes so that haplotype frequencies cannot be easily inferred. When the gametic phase is not known, haplotype frequencies can be estimated from the multilocus genotypic data. Any  
35 method known to person skilled in the art can be used to estimate haplotype frequencies (see Lange K., *Mathematical and Statistical Methods for Genetic Analysis*, Springer, New York, 1997; Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data*, Sinauer



*Assoc., Inc., Sunderland, MA, USA, 1996*). Preferably, maximum-likelihood haplotype frequencies are computed using an Expectation- Maximization (EM) algorithm (see Dempster et al., *J. R. Stat. Soc.*, 39B:1-38, 1977; Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). This procedure is an iterative process aiming at obtaining maximum-likelihood estimates of haplotype frequencies from multi-locus genotype data when the gametic phase is unknown. Haplotype estimations are usually performed by applying the EM algorithm using for example the EM-HAPLO program (Hawley M.E. et al., *Am. J. Phys. Anthropol.*, 18:104, 1994) or the Arlequin program (Schneider et al., *Arlequin: a software for population genetics data analysis*, University of Geneva, 1997). The EM algorithm is a generalized iterative maximum likelihood approach to estimation and is briefly described below.

In what follows, phenotypes will refer to multi-locus genotypes with unknown haplotypic phase. Genotypes will refer to multi-locus genotypes with known haplotypic phase.

Suppose one has a sample of  $N$  unrelated individuals typed for  $K$  markers. The data observed are the unknown-phase  $K$ -locus phenotypes that can be categorized with  $F$  different phenotypes. Further, suppose that we have  $H$  possible haplotypes (in the case of  $K$  biallelic markers, we have for the maximum number of possible haplotypes  $H=2^K$ ).

For phenotype  $j$  with  $c_j$  possible genotypes, we have:

$$P_j = \sum_{i=1}^{c_j} P(\text{genotype}(i)) = \sum_{i=1}^{c_j} P(h_k, h_l). \quad \text{Equation 1}$$

Here,  $P_j$  is the probability of the  $j^{\text{th}}$  phenotype, and  $P(h_k, h_l)$  is the probability of the  $i^{\text{th}}$  genotype composed of haplotypes  $h_k$  and  $h_l$ . Under random mating (*i.e.* Hardy-Weinberg Equilibrium),  $P(h_k, h_l)$  is expressed as:

$$\begin{aligned} P(h_k, h_l) &= P(h_k)^2 \text{ for } h_k = h_l, \text{ and} \\ P(h_k, h_l) &= 2P(h_k)P(h_l) \text{ for } h_k \neq h_l. \end{aligned} \quad \text{Equation 2}$$

The E-M algorithm is composed of the following steps: First, the genotype frequencies are estimated from a set of initial values of haplotype frequencies. These haplotype frequencies are denoted  $P_1^{(0)}, P_2^{(0)}, P_3^{(0)}, \dots, P_H^{(0)}$ . The initial values for the haplotype frequencies may be obtained from a random number generator or in some other way well known in the art. This step is referred to the Expectation step. The next step in the method, called the Maximization step, consists of using the estimates for the genotype frequencies to re-calculate the haplotype frequencies. The first iteration haplotype frequency estimates are denoted by  $P_1^{(1)}, P_2^{(1)}, P_3^{(1)}, \dots, P_H^{(1)}$ . In general, the Expectation step at the  $s^{\text{th}}$  iteration consists of calculating the probability of placing each phenotype into the different possible genotypes based on the haplotype frequencies of the previous iteration:

$$P(h_k, h_l)^{(s)} = \frac{n_j}{N} \left[ \frac{P_j(h_k, h_l)^{(s)}}{P_j} \right], \quad \text{Equation 3}$$

where  $n_j$  is the number of individuals with the  $j^{\text{th}}$  phenotype and  $P_j(h_k, h_l)^{(s)}$  is the probability of genotype  $h_k h_l$  in phenotype  $j$ . In the Maximization step, which is equivalent to the gene-counting method (Smith, *Ann. Hum. Genet.*, 21:254-276, 1957), the haplotype frequencies are re-estimated based on the genotype estimates:

$$P_t^{(s+1)} = \frac{1}{2} \sum_{j=1}^F \sum_{i=1}^{c_j} \delta_{it} P_j(h_k, h_l)^{(s)}. \quad \text{Equation 4}$$

Here,  $\delta_{it}$  is an indicator variable which counts the number of occurrences that haplotype  $t$  is present in  $i^{\text{th}}$  genotype; it takes on values 0, 1, and 2.

The E-M iterations cease when the following criterion has been reached. Using Maximum Likelihood Estimation (MLE) theory, one assumes that the phenotypes  $j$  are distributed multinomially. At each iteration  $s$ , one can compute the likelihood function  $L$ . Convergence is achieved when the difference of the log-likelihood between two consecutive iterations is less than some small number, preferably  $10^{-7}$ .

### iii. Methods to calculate linkage disequilibrium between markers

A number of methods can be used to calculate linkage disequilibrium between any two genetic positions, in practice linkage disequilibrium is measured by applying a statistical association test to haplotype data taken from a population.

Linkage disequilibrium between any pair of biallelic markers comprising at least one of the biallelic markers of the present invention ( $M_i, M_j$ ) having alleles ( $a_i/b_i$ ) at marker  $M_i$  and alleles ( $a_j/b_j$ ) at marker  $M_j$  can be calculated for every allele combination ( $a_i, a_j; a_i, b_j; b_i, a_j$  and  $b_i, b_j$ ), according to the Piazza formula :

$$\Delta_{aiaj} = \sqrt{\theta 4} - \sqrt{(\theta 4 + \theta 3)(\theta 4 + \theta 2)}, \text{ where :}$$

$\theta 4 = --$  = frequency of genotypes not having allele  $a_i$  at  $M_i$  and not having allele  $a_j$  at  $M_j$

$\theta 3 = - +$  = frequency of genotypes not having allele  $a_i$  at  $M_i$  and having allele  $a_j$  at  $M_j$

$\theta 2 = + -$  = frequency of genotypes having allele  $a_i$  at  $M_i$  and not having allele  $a_j$  at  $M_j$

Linkage disequilibrium (LD) between pairs of biallelic markers ( $M_i, M_j$ ) can also be calculated for every allele combination ( $a_i, a_j; a_i, b_j; b_i, a_j$  and  $b_i, b_j$ ), according to the maximum-likelihood estimate (MLE) for delta (the composite genotypic disequilibrium coefficient), as described by Weir (Weir B.S., *Genetic Data Analysis*, Sinauer Ass. Eds, 1996). The MLE for the composite linkage disequilibrium is:

$$D_{aiaj} = (2n_1 + n_2 + n_3 + n_4/2)/N - 2(\text{pr}(a_i) \cdot \text{pr}(a_j))$$

Where  $n_1 = \Sigma$  phenotype ( $a_i/a_i, a_j/a_j$ ),  $n_2 = \Sigma$  phenotype ( $a_i/a_i, a_j/b_j$ ),  $n_3 = \Sigma$  phenotype ( $a_i/b_i, a_j/a_j$ ),  $n_4 = \Sigma$  phenotype ( $a_i/b_i, a_j/b_j$ ) and  $N$  is the number of individuals in the sample.

This formula allows linkage disequilibrium between alleles to be estimated when only genotype, and not haplotype, data are available.

Another means of calculating the linkage disequilibrium between markers is as follows. For a couple of biallelic markers,  $M_i (a_i/b_i)$  and  $M_j (a_j/b_j)$ , fitting the Hardy-Weinberg equilibrium, one can estimate the four possible haplotype frequencies in a given population according to the approach described above.

The estimation of gametic disequilibrium between  $a_i$  and  $a_j$  is simply:

$$D_{a_i a_j} = pr(haplotype(a_i, a_j)) - pr(a_i).pr(a_j).$$

Where  $pr(a_i)$  is the probability of allele  $a_i$  and  $pr(a_j)$  is the probability of allele  $a_j$  and where  $pr(haplotype(a_i, a_j))$  is estimated as in Equation 3 above.

For a couple of biallelic marker only one measure of disequilibrium is necessary to describe the association between  $M_i$  and  $M_j$ .

Then a normalised value of the above is calculated as follows:

$$D'_{a_i a_j} = D_{a_i a_j} / \max(-pr(a_i).pr(a_j), -pr(b_i).pr(b_j)) \text{ with } D_{a_i a_j} < 0$$

$$D'_{a_i a_j} = D_{a_i a_j} / \max(pr(b_i).pr(a_j), pr(a_i).pr(b_j)) \text{ with } D_{a_i a_j} > 0$$

The skilled person will readily appreciate that other LD calculation methods can be used without undue experimentation.

Linkage disequilibrium among a set of biallelic markers having an adequate heterozygosity rate can be determined by genotyping between 50 and 1000 unrelated individuals, preferably between 75 and 200, more preferably around 100.

#### iv. Testing for association

Methods for determining the statistical significance of a correlation between a phenotype and a genotype, in this case an allele at a biallelic marker or a haplotype made up of such alleles, may be determined by any statistical test known in the art and with any accepted threshold of statistical significance being required. The application of particular methods and thresholds of significance are well within the skill of the ordinary practitioner of the art.

Testing for association is performed by determining the frequency of a biallelic marker allele in case and control populations and comparing these frequencies with a statistical test to determine if there is a statistically significant difference in frequency which would indicate a correlation between the trait and the biallelic marker allele under study. Similarly, a haplotype analysis is performed by estimating the frequencies of all possible haplotypes for a given set of biallelic markers in case and control populations, and comparing these frequencies with a statistical test to determine if there is a statistically significant correlation between the haplotype and the phenotype (trait) under study. Any statistical tool useful to test for a statistically significant association between a genotype and a phenotype may be used. Preferably the statistical test employed is a chi-square test with one degree of freedom. A p-value is then

determined (the P-value is the probability that a statistic as large or larger than the observed one would occur by chance).

### 1) Statistical significance

In preferred embodiments, significance for diagnostic purposes, either as a positive basis for further diagnostic tests or as a preliminary starting point for early preventive therapy, the p value related to a biallelic marker association is preferably about  $1 \times 10^{-2}$  or less, more preferably about  $1 \times 10^{-4}$  or less, for a single biallelic marker analysis and about  $1 \times 10^{-3}$  or less, still more preferably  $1 \times 10^{-6}$  or less and most preferably of about  $1 \times 10^{-8}$  or less, for a haplotype analysis involving several markers. These values are believed to be applicable to any association studies involving single or multiple marker combinations.

The skilled person can use the range of values set forth above as a starting point in order to carry out association studies with biallelic markers of the present invention. In doing so, significant associations between the biallelic markers of the present invention and CNS disorders can be revealed and used for diagnosis and drug screening purposes.

### 2) Phenotypic permutation

In order to confirm the statistical significance of the first stage haplotype analysis described above, it might be suitable to perform further analyses in which genotyping data from case-control individuals are pooled and randomized with respect to the trait phenotype. Each individual genotyping data is randomly allocated to two groups, which contain the same number of individuals as the case-control populations used to compile the data obtained in the first stage. A second stage haplotype analysis is preferably run on these artificial groups, preferably for the markers included in the haplotype of the first stage analysis showing the highest relative risk coefficient. This experiment is re-iterated preferably at least between 100 and 10000 times. The repeated iterations allow the determination of the percentage of obtained haplotypes with a significant p-value level.

### 3) Assessment of statistical association

To address the problem of false positives similar analysis may be performed with the same case-control populations in random genomic regions. Results in random regions and the candidate region are compared as described in US Provisional Patent Application entitled "Methods, software and apparatus for identifying genomic regions harbouring a gene associated with a detectable trait".

### v. Evaluation of risk factors

The association between a risk factor (in genetic epidemiology the risk factor is the presence or the absence of a certain allele or haplotype at marker loci) and a disease is measured by the odds ratio (OR) and by the relative risk (RR). If  $P(R^+)$  is the probability of developing the disease for individuals with risk factor R and  $P(R^-)$  is the probability for individuals without the risk factor, then the relative risk is simply the ratio of the two probabilities, that is:

$$RR = P(R^+)/P(R^-)$$

In case-control studies, direct measures of the relative risk cannot be obtained because of the sampling design. However, the odds ratio allows a good approximation of the relative risk for low-incidence diseases and can be calculated:

$$OR = \left[ \frac{F^+}{1 - F^+} \right] / \left[ \frac{F^-}{1 - F^-} \right]$$

$$5 \quad OR = [F^+/(1-F^+)] / [F^-/(1-F^-)]$$

$F^+$  is the frequency of the exposure to the risk factor in cases and  $F^-$  is the frequency of the exposure to the risk factor in controls.  $F^+$  and  $F^-$  are calculated using the allelic or haplotype frequencies of the study and further depend on the underlying genetic model (dominant, recessive, additive...).

10 One can further estimate the attributable risk (AR) which describes the proportion of individuals in a population exhibiting a trait due to a given risk factor. This measure is important in quantitating the role of a specific factor in disease etiology and in terms of the public health impact of a risk factor. The public health relevance of this measure lies in estimating the proportion of cases of disease in the population that could be prevented if the exposure of interest  
15 were absent. AR is determined as follows:

$$AR = P_E (RR - 1) / (P_E (RR - 1) + 1)$$

AR is the risk attributable to a biallelic marker allele or a biallelic marker haplotype.  $P_E$  is the frequency of exposure to an allele or a haplotype within the population at large; and RR is the relative risk which is approximated with the odds ratio when the trait under study has a relatively  
20 low incidence in the general population.

#### D. Association of Biallelic Markers of the Invention with Major Depression

In the context of the present invention, an association between biallelic marker alleles from candidate genes of the present invention and a CNS disorder was demonstrated. The considered CNS disorder was major depression.

25 Depression is a serious medical illness that affects 340 million people worldwide. In contrast to the normal emotional experiences of sadness, loss, or passing mood states, clinical depression is persistent and can interfere significantly with an individual's ability to function. Many neurochemical findings are coming to light implicating a biological basis for the depression, at least for certain subtypes. Abnormalities of monoamine function as well as over  
30 stimulation of the HPA axis have been recognized in depression for many years. Patterns of clustering and segregation in depressive families have suggested a genetic component to depression. However, the lack of a defined and specific depression phenotype and of suitable markers for genetic analysis is proving to be a major hurdle for reliably identifying genes associated with depression. As a result, psychiatrists today have to choose antidepressant

medications by intuition and trial and error; a situation that can put suicidal patients in jeopardy for weeks or months until the right compound is selected. Clearly, there is a strong need to successfully identify genes involved in depression; thus allowing researchers to understand the etiology of depression and address its cause, rather than symptoms.

5 As mentioned above, both the nervous system and endocrine system play a major role in the etiology of depression. More specifically, the neurotransmitters dopamine, norepinephrine and serotonin as well as the hormones corticotrophin releasing factor, glucocorticoids, mineralocorticoids and various neuropeptides are thought to play a major role in the pathophysiology of depression.

10 In order to investigate and identify a genetic origin of depression, a candidate gene scan for depression was conducted. The rationale of this approach was to: 1) select candidate genes potentially involved in the pathophysiology of interest, in this case major depression, 2) to identify biallelic markers in those genes and finally 3) to measure the frequency of biallelic marker alleles in order to determine if some alleles are more frequent in depressed populations  
15 than in non-affected populations. Results were further validated by haplotype studies. Significant associations between biallelic marker alleles from the serotonin receptor 6 (5HTR6), serotonin 7 (5HTR7), serotonin transporter (5HTT), dopamine receptor 3 (DRD3), norepinephrine transporter (NET), guanine nucleotide binding protein,  $\beta 3$  (Gbeta3), glucocorticoid receptor (GRL), drug metabolizing enzyme cytochrome P450 3A4 (CYP3A4) and  
20 Wolfram Syndrome 1 (WFS1) genes and depression were demonstrated in the context of the present invention. Association studies are further described in Examples 3, 4 and 5.

This information is extremely valuable. The knowledge of a potential genetic predisposition, even if this predisposition is not absolute, might contribute in a very significant manner to treatment efficacy of depressed patients and to the development of diagnostic tools.

25 E. Identification of Biallelic Markers in Linkage Disequilibrium with the Biallelic Markers of the Invention

Once a first biallelic marker has been identified in a genomic region of interest, the practitioner of ordinary skill in the art, using the teachings of the present invention, can easily identify additional biallelic markers in linkage disequilibrium with this first marker. As  
30 mentioned before any marker in linkage disequilibrium with a first marker associated with a trait will be associated with the trait. Therefore, once an association has been demonstrated between a given biallelic marker and a trait, the discovery of additional biallelic markers associated with this trait is of great interest in order to increase the density of biallelic markers in this particular region. The causal gene or mutation will be found in the vicinity of the marker or set of markers  
35 showing the highest correlation with the trait.

Identification of additional markers in linkage disequilibrium with a given marker involves: (a) amplifying a genomic fragment comprising a first biallelic marker from a plurality

of individuals; (b) identifying of second biallelic markers in the genomic region harboring said first biallelic marker; (c) conducting a linkage disequilibrium analysis between said first biallelic marker and second biallelic markers; and (d) selecting said second biallelic markers as being in linkage disequilibrium with said first marker. Subcombinations comprising steps (b) and (c) are also contemplated.

Methods to identify biallelic markers and to conduct linkage disequilibrium analysis are described herein and can be carried out by the skilled person without undue experimentation. The present invention then also concerns biallelic markers which are in linkage disequilibrium with the specific biallelic markers shown in Table 7 and which are expected to present similar characteristics in terms of their respective association with a given trait.

#### F. Identification of Functional Mutations

Once a positive association is confirmed with a biallelic marker of the present invention, the associated candidate gene can be scanned for mutations by comparing the sequences of a selected number of trait positive and trait negative individuals. In a preferred embodiment, functional regions such as exons and splice sites, promoters and other regulatory regions of the candidate gene are scanned for mutations. Preferably, trait positive individuals carry the haplotype shown to be associated with the trait and trait negative individuals do not carry the haplotype or allele associated with the trait. The mutation detection procedure is essentially similar to that used for biallelic site identification.

The method used to detect such mutations generally comprises the following steps: (a) amplification of a region of the candidate gene comprising a biallelic marker or a group of biallelic markers associated with the trait from DNA samples of trait positive patients and trait negative controls; (b) sequencing of the amplified region; (c) comparison of DNA sequences from trait-positive patients and trait-negative controls; and (d) determination of mutations specific to trait-positive patients. Subcombinations which comprise steps (b) and (c) are specifically contemplated.

It is preferred that candidate polymorphisms be then verified by screening a larger population of cases and controls by means of any genotyping procedure such as those described herein, preferably using a microsequencing technique in an individual test format.

Polymorphisms are considered as candidate mutations when present in cases and controls at frequencies compatible with the expected association results.

#### VII. Biallelic Markers of the Invention in Methods of Genetic Diagnostics

The biallelic markers of the present invention can also be used to develop diagnostics tests capable of identifying individuals who express a detectable trait as the result of a specific genotype or individuals whose genotype places them at risk of developing a detectable trait at a subsequent time. The trait analyzed using the present diagnostics may be any detectable trait,

including a CNS disorder, a response to an agent acting on a CNS disorder or side effects to an agent acting on a CNS disorder.

The diagnostic techniques of the present invention may employ a variety of methodologies to determine whether a test subject has a biallelic marker pattern associated with an increased risk of developing a detectable trait or whether the individual suffers from a detectable trait as a result of a particular mutation, including methods which enable the analysis of individual chromosomes for haplotyping, such as family studies, single sperm DNA analysis or somatic hybrids.

The present invention provides diagnostic methods to determine whether an individual is at risk of developing a disease or suffers from a disease resulting from a mutation or a polymorphism in a candidate gene of the present invention. The present invention also provides methods to determine whether an individual is likely to respond positively to an agent acting on a CNS disorder or whether an individual is at risk of developing an adverse side effect to an agent acting on a CNS disorder.

These methods involve obtaining a nucleic acid sample from the individual and, determining, whether the nucleic acid sample contains at least one allele or at least one biallelic marker haplotype, indicative of a risk of developing the trait or indicative that the individual expresses the trait as a result of possessing a particular candidate gene polymorphism or mutation (trait-causing allele).

Preferably, in such diagnostic methods, a nucleic acid sample is obtained from the individual and this sample is genotyped using methods described herein. The diagnostics may be based on a single biallelic marker or on a group of biallelic markers.

In each of these methods, a nucleic acid sample is obtained from the test subject and the biallelic marker pattern of one or more of the biallelic markers listed in Table 7 is determined.

In one embodiment, PCR amplification is conducted on the nucleic acid sample to amplify regions in which polymorphisms associated with a detectable phenotype have been identified. The amplification products are sequenced to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype. The primers used to generate amplification products may comprise the primers listed in Table 13. Alternatively, the nucleic acid sample is subjected to microsequencing reactions as described above to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype resulting from a mutation or a polymorphism in a candidate gene. The primers used in the microsequencing reactions may include the primers listed in Table 12. In another embodiment, the nucleic acid sample is contacted with one or more allele specific oligonucleotide probes which, specifically hybridize to one or more candidate gene alleles associated with a detectable phenotype. The probes used in the hybridization assay may include the probes listed in Table 14.



In a preferred embodiment the identity of the nucleotide present at, at least one, 5HTR6 related biallelic marker selected from the group consisting of 99-27207-117, 99-28110-75, and 99-28134-215, is determined and the detectable trait is depression.

5 In a preferred embodiment the identity of the nucleotide present at, at least one, 5HTR7 related biallelic marker selected from the group consisting of 99-32181-192 and 99-28106-185, is determined and the detectable trait is depression.

In a preferred embodiment the identity of the nucleotide present at, at least one, GRL related biallelic marker selected from the group consisting of 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, and 99-30853-364, is determined and the detectable trait is depression.

10 In a preferred embodiment the identity of the nucleotide present at, at least one, NET related biallelic marker selected from the group consisting of 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, and 16-50-196, is determined and the detectable trait is depression.

15 In a preferred embodiment the identity of the nucleotide present at, at least one, DRD3 related biallelic marker selected from the group consisting of 8-19-372, is determined and the detectable trait is depression.

In a preferred embodiment the identity of the nucleotide present at, at least one, CYP3A4 related biallelic marker selected from the group consisting of 12-254-180, 10-214-279, and 10-217-91, is determined and the detectable trait is depression.

In a preferred embodiment the identity of the nucleotide present at, at least one, 5HTT related biallelic marker selected from the group consisting of 18-194-130, 18-186-391, 18-198-252, and 18-242-300, is determined and the detectable trait is depression.

In a preferred embodiment the identity of the nucleotide present at, at least one, Gbeta3 related biallelic marker selected from the group consisting of 20-205-302, 19-58-162, 19-9-45, 19-22-74, and 19-88-185, is determined and the detectable trait is depression.

In a preferred embodiment the identity of the nucleotide present at, at least one, WFS1 related biallelic marker selected from the group consisting of 19-18-310, 19-19-174, 19-17-188, and 19-16-127, is determined and the detectable trait is depression.

30 Diagnostic kits comprising polynucleotides of the present invention are further described in section I.

These diagnostic methods are extremely valuable as they can, in certain circumstances, be used to initiate preventive treatments or to allow an individual carrying a significant haplotype to foresee warning signs such as minor symptoms. In diseases in which attacks may be extremely violent and sometimes fatal if not treated on time, such as asthma, the knowledge of a potential predisposition, even if this predisposition is not absolute, might contribute in a very significant manner to treatment efficacy. Similarly, a diagnosed predisposition to a potential side

effect could immediately direct the physician toward a treatment for which such side effects have not been observed during clinical trials.

Diagnostics, which analyze and predict response to a drug or side effects to a drug, may be used to determine whether an individual should be treated with a particular drug. For example, if the diagnostic indicates a likelihood that an individual will respond positively to treatment with a particular drug, the drug may be administered to the individual. Conversely, if the diagnostic indicates that an individual is likely to respond negatively to treatment with a particular drug, an alternative course of treatment may be prescribed. A negative response may be defined as either the absence of an efficacious response or the presence of toxic side effects.

Clinical drug trials represent another application for the markers of the present invention. One or more markers indicative of response to an agent acting on a CNS disorder or to side effects to an agent acting on a CNS disorder may be identified using the methods described above. Thereafter, potential participants in clinical trials of such an agent may be screened to identify those individuals most likely to respond favorably to the drug and exclude those likely to experience side effects. In that way, the effectiveness of drug treatment may be measured in individuals who respond positively to the drug, without lowering the measurement as a result of the inclusion of individuals who are unlikely to respond positively in the study and without risking undesirable safety problems.

#### VIII. DNA Typing Methods and Systems

The present invention also encompasses a DNA typing system having a much higher discriminatory power than currently available typing systems. The systems and associated methods are particularly applicable in the identification of individuals for forensic science and paternity determinations. These applications have become increasingly important; in forensic science, for example, the identification of individuals by polymorphism analysis has become widely accepted by courts as evidence.

While forensic geneticists have developed many techniques to compare homologous segments of DNA to determine if the segments are identical or if they differ in one or more nucleotides, each technique still has certain disadvantages. In particular, the techniques vary widely in terms of expense of analysis, time required to carry out an analysis and statistical power.

##### RFLP analysis methods

The best known and most widespread method in forensic DNA typing is the restriction fragment length polymorphism (RFLP) analysis. In RFLP testing, a repetitive DNA sequence referred to as a variable number tandem repeat (VNTR) which varies between individuals is analyzed. The core repeat is typically a sequence of about 15 base pairs in length; and highly polymorphic VNTR loci can have an average of about 20 alleles. DNA restriction sites located

on either site of the VNTR are exploited to create DNA fragments from about 0.5Kb to less than 10Kb which are then separated by electrophoresis, indicating the number of repeats found in the individual at the particular loci. RFLP methods generally consist of (1) extraction and isolation of DNA, (2) restriction endonuclease digestion; (3) separation of DNA fragments by electrophoresis; (4) capillary transfer; (5) hybridization with radiolabelled probes; (6) autoradiography; and (7) interpretation of results (Lee, H.C. et al., Am. J. Forensic. Med. Pathol. 15(4): 269-282 (1994)). RFLP methods generally combine analysis at about 5 loci and have much higher discriminate potential than other available test due the highly polymorphic nature of the VNTRs. However, autoradiography is costly and time consuming and an analysis generally takes weeks or months for turnaround. Additionally, a large amount of sample DNA is required, which is often not available at a crime scene. Furthermore, the reliability of the system and its credibility as evidence is decreased because the analysis of tightly spaced bands on electrophoresis results in a high rate of error.

#### PCR methods

PCR based methods offer an alternative to RFLP methods. In a first method called AmpFLP, DNA fragments containing VNTRs are amplified and then separated electrophoretically, without the restriction step of RFLP method. While this method allows small quantities of sample DNA to be used, decreases analysis time by avoiding autoradiography, and retains high discriminatory potential, it nevertheless requires electrophoretic separation which takes substantial time and introduces an significant error rate. In another AmpFLP method, short tandem repeats (STRs) of 2 to 8 base pairs are analyzed. STRs are more suitable to analysis of degraded DNA samples since they require smaller amplified fragments but have the disadvantage of requiring separation of the amplified fragments. While STRs are far less informative than longer repeats, similar discriminatory potential can be achieved if enough STRs are used in a single analysis.

Other methods include sequencing of mitochondrial DNA, which is especially suitable for situations where sample DNA is very degraded or in small quantities. However, only a small region of 1Kb of the mitochondrial DNA referred to as the D-Loop locus has been found useful for typing because of its polymorphic nature, resulting in lower discriminatory potential than with RFLP or AmpFLP methods. Furthermore, DNA sequencing is expensive to carry out on a large number of samples.

Further available methods include dot-blot methods, which involve using allele specific oligonucleotide probes which hybridize sequence specifically to one allele of a polymorphic site. Systems include the HLA DQ-alpha kit developed by Cetus Corp. which has a discriminatory value of about 1 in 20, and a dot-blot strip referred to as the Polymarker strip combining five genetic loci for a discriminatory value of about one in a few thousand. (Weedn, V., Clinics in Lab. Med. 16(1): 187-196 (1996)).

In addition to difficulties in analysis and time consuming laboratory procedures, it remains desirable for all DNA typing systems to have a higher discriminatory power. Several applications exist in which even the most discriminating tests need improvement in order to remove the considerable remaining doubt resulting from such analyses. Table 3 below lists characteristics of currently available forensic testing systems (Weedn, (1996)) and compares them with the method of the invention.

Table 3

<i>Test type</i>	<i>Technology</i>	<i>Turnaround time</i>	<i>Discriminatory potential</i>	<i>Sensitivity (amount DNA)</i>	<i>Sample</i>
RFLP	VNTR (autoradiography)	Weeks or months	$10^6$ to $10^9$	10ng	Highly intact DNA
AmpFLP	VNTR (PCR based)	Days	$10^3$ to $10^6$	100pg	Moderate degradation
Dot blot (ex. HLADQA1)	Sequence specific oligonucleotide probes	Days	$10^1$ to $10^3$	1ng	Moderate degradation
Mitochondrial DNA	D-loop sequence (PCR based)	Days	$10^2$	1pg	Severe degradation
Present marker set	Biallelic Markers (set of 13, set of 100, set of 200, set of 270)	Hours to Days (throughput dependent)	$10^6$ , $10^{47}$ , $10^{238}$	100pg	Moderate degradation

#### Applications

As described above, an important application of DNA typing tests is to determine whether a DNA sample (e.g. from a crime scene) originated from an individual suspected of leaving said DNA sample.

There are several applications for DNA typing which require a particularly powerful genotyping system. In a first application, a high powered typing system is advantageous when for example a suspect is identified by searching a DNA profile database such as that maintained by the U.S. Federal Bureau of Investigation. Since databases may contain large numbers of data entries that are expected to increase consistently, currently used forensic systems can be expected to identify several matching DNA profiles due to their relative lack of power. While database searches generally reinforce the evidence by excluding other possible suspects, low powered typing systems resulting in the identification of several individuals may often tend to diminish the overall case against a defendant.

In another application, a target population is systematically tested to identify an individual having the same DNA profile as that of a DNA sample. In such a situation, a defendant is chosen at random based on DNA profile from a large population of innocent individuals. Since the population tested can often be large enough that at least one positive match is identified, and it is usually not possible to exhaustively test a population, the usefulness of the evidence will depend on the level of significance of the forensic test. In order to render such an application useful as a sole or primary source of evidence, DNA typing systems of extremely high discriminatory potential are required.

In yet another application, it is desirable to be able to discriminate between related individuals. Because related individuals will be expected to share a large portion of alleles at polymorphic sites, a very high powered DNA typing assay would be required to discriminate between them. This can have important effects if a sample is found to match the defendant's DNA profile and no evidence that the perpetrator is a relative can be found.

Accordingly, there is a need in this art for a rapid, simple, inexpensive and accurate technique having a very high resolution value to determine relationships between individuals and differences in degree of relationships. Also, there is a need in the art for a very accurate genetic relationship test procedure which uses very small amounts of an original DNA sample, yet produces very accurate results.

The present invention thus involves methods for the identification of individuals comprising determining the identity of the nucleotides at a set of genetic markers in a biological sample, wherein said set of genetic markers comprises at least one CNS disorder-related marker. The present invention provides an extensive set of biallelic markers allowing a higher discriminatory potential than the genetic markers used in current forensic typing systems. Also, biallelic markers can be genotyped in individuals with much higher efficiency and accuracy than the genetic markers used in current forensic typing systems. In preferred embodiments, the invention comprises determining the identity of a nucleotide at a CNS disorder-related marker by single nucleotide primer extension, which does not require electrophoresis as in techniques described above and results in lower rate of experimental error. As shown in Table 3, above, in comparison with PCR based VNTR based methods which allow discriminatory potential of thousands to millions, and RFLP based methods which allow discriminatory potential of merely millions to billions under optimal assumptions, the biallelic marker based method of the present invention provides a radical increase in discriminatory potential.

Any suitable set of genetic markers and biallelic markers of the invention may be used, and may be selected according to the discriminatory power desired. Biallelic markers, sets of biallelic markers, probes, primers, and methods for determining the identity of said biallelic markers are further described herein.

Discriminatory potential of biallelic marker typing

### Calculating discriminatory potential

The discriminatory potential of the forensic test can be determined in terms of the profile frequency, also referred to as the random match probability, by applying the product rule. The product rule involves multiplying the allelic frequencies of all the individual alleles tested, and multiplying by an additional factor of 2 for each heterozygous locus.

In one example discussed below, the discriminatory potential of biallelic marker typing can be considered in the context of forensic science. In order to determine the discriminatory potential with respect to the numbers of biallelic markers to be used in a genetic typing system, the formulas and calculations below assume that (1) the population under study is sufficiently large (so that we can assume no consanguinity); (2) all markers chosen are not correlated, so that the product rule (Lander and Budlowle (1992)) can be applied; and (3) the ceiling rule can be applied or that the allelic frequencies of markers in the population under study are known with sufficient accuracy.

As noted in Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data*, Sinauer Assoc., Inc., Sunderland, MA, USA, 1996, the example assumes a crime has been committed and a sample of DNA from the perpetrator (P) is available for analysis. The genotype of this DNA sample can be determined for several genetic markers, and the profile A of the perpetrator can thereby be determined.

In this example, one suspect (S) is available for typing. The same set of genetic markers, such as the biallelic markers of the invention, are typed and the same profile A is obtained for (S) and (P). Two hypotheses are thus presented as follows:

- (1) either S is P (event C)
- (2) either S is not P (event  $\bar{C}$ ).

The ratio L of both probabilities can then be calculated using the following equation:

$$L = \frac{pr(S = A, P = A / C)}{pr(S = A, P = A / \bar{C})}$$

L can then further be calculated by the following equation:

$$L = \frac{1}{pr(P = A / S = A, \bar{C})} \quad (1) \text{ Equation 1}$$

These probabilities as well as L can be calculated in several settings, notably for different kinship coefficients between P and S for a genetic marker (see Weir, (1996)).

Assuming that all genetic markers chosen are independent of each other, the global ratio L for a set of genetic markers will be the product over each genetic marker of all L.

It is further possible to estimate the mean number of biallelic markers or VNTRs required to have a ratio L equal to  $10^8$  or  $10^6$  by calculating the expectancy of the random variable L using the following equation:

$$E(L) = \prod_{i=1}^N E(L_i) \text{ where } N \text{ is the number of loci}$$

$$E(L_i) = \sum_{j=1}^{G_i} \text{pr}(P = A_{ij} / S = A_{ij}, \bar{C}) \cdot L_{ij}, \text{ where } A_{ij} \text{ is the genotype } j \text{ at the } i\text{th marker,}$$

$L_{ij}$  the ratio associated with such genotype,  $G_i$  being the number of genotypes at locus  $i$ .

From equation 1, it can easily be derived that the expectancy of  $L_i$  is  $G_i$ , the number of possible genotypes of this marker.

The general expectancy for a set of genetic markers can then be expressed by the following equation:

$$E(L) = \prod_{i=1}^N G_i \quad (2) \text{ Equation 2}$$

#### Biallelic marker-based DNA typing systems

Using the equations described above, it is possible to select biallelic marker-based DNA typing systems having a desired discriminatory potential.

Using biallelic markers,  $E(L)$  can thus be expressed as  $3^N$ . When using VNTR-based DNA typing systems, assuming the VNTRs have 10 alleles,  $E(L)$  can be expressed as  $55^N$ . Based on these results, the number of biallelic markers or VNTRs needed to obtain, in mean, a ratio of at least  $10^6$  or  $10^8$  can be calculated, and are set forth below in Table 4.

Table 4

Marker sets	$L=10^6$	$L=10^8$
Biallelic	13	17
5-allele markers (e.g. VNTR)	5	7
10-allele markers (e.g. VNTR)	4	5

15

Thus, in a first embodiment, DNA typing systems and methods of the invention may comprise genotyping a set of at least 13 or at least 17 biallelic markers to obtain a ratio of at least  $10^6$  or  $10^8$ , assuming a flat distribution of  $L$  across the biallelic markers. In preferred embodiments, a greater number of biallelic markers is genotyped to obtain a higher  $L$  value.

Preferably at least 1, 2, 3, 4, 5, 10, 13, 15, 17, 20, 25, 30, 40, 50, 70, 85, 100, 150, 200, 250 or all of the CNS disorder-related markers are genotyped. Said DNA typing systems of the invention would result in  $L$  values as listed in Table 5 below as an indication of the discriminate potential of the systems of the invention.

Table 5

Number of biallelic markers	$L$
-----------------------------	-----

50	$7.2 * 10^{23}$
100	$5 * 10^{47}$
271	$3^{271}$

In situations where the distribution of L is not flat, such as in the worst case when the perpetrator is homozygous for the major allele at each genetic locus and L thus takes the lowest value, a larger number of biallelic markers is required for the same discriminatory potential.

- 5 Therefore, in preferred embodiments, DNA typing systems and methods of the invention using a larger number of biallelic markers allow for uneven distributions of L across the biallelic markers. For example, assuming unrelated individuals, a set of independent markers having an allelic frequency of 0.1/0.9, and the genetic profile of a homozygote at each genetic loci for the major allele, 66 biallelic markers are required to obtain a ratio of  $10^6$ , and 88 biallelic markers are
- 10 required to obtain a ratio of  $10^8$ . Thus, in preferred embodiments based on the use of markers having a major allele of sufficiently high frequency, this is a first estimation of the upper bound of markers required in a DNA typing system.

- In further embodiments, it is also desirable to have the ability to discriminate between relatives. Although unrelated individuals have a low probability of sharing genetic profiles, the
- 15 probability is greatly increased for relatives. For example, the DNA profile of a suspect matches the DNA profile of a sample at a crime scene, and the probability of obtaining the same DNA profile if left by an untyped relative is required. Table 6 below (Weir (1996)) lists probabilities for several different types of relationships, assuming alleles  $A_i$  and  $A_j$ , and population
- 20 frequencies  $p_i$  and  $p_j$ , and lists likelihood ratios assuming genetic loci having allele frequencies of 0.1.

Table 6

Genotype	Relationship	$\Pr(p=A S=A)$	L
$A_i A_j$	Full brothers	$(1+p_i+p_j+2p_i p_j)/4$	3.3
	Father and son	$(p_i+p_j)/2$	10.0
	Half brothers	$(p_i+p_j+4p_i p_j)/4$	16.7
	Uncle and nephew	$(1+p_i+p_j+2p_i p_j)/4$	16.7
	First cousins	$(1+p_i+p_j+12p_i p_j)/8$	25.0
	Unrelated	$2p_i p_j$	50.0
$A_j A_j$	Full brothers	$(1+p_j)^2/4$	3.3



Father and son	$P_i$	10.0
Half brothers	$P_i (1+p_i)/2$	18.2
Uncle and nephew	$P_i (1+p_i)/2$	18.2
First cousins	$P_i (1+3p_i)/4$	30.8
Unrelated	$p_i^2$	100.0

In one example, where the suspect is the full brother of the perpetrator, the number of required biallelic markers will be 187 assuming the profile is that of a homozygote for the major allele at each biallelic marker.

5 In yet further embodiments, the DNA typing systems and methods of the present invention may further take into account effects of subpopulations on the discriminatory potential. In embodiments described above for example, DNA typing systems consider close familial relationships, but do not take into account membership in the same population. While population membership is expected to have little effect, the invention may further comprise genotyping a  
10 larger set of biallelic markers to achieve higher discriminatory potential. Alternatively, a larger set of biallelic markers may be optimized for typing selected populations; alternatively, the ceiling principle may be used to study allele frequencies from individuals in various populations of interest, taking for any particular genotype the maximum allele frequency found among the populations.

15 The invention thus encompasses methods for genotyping comprising determining the identity of a nucleotide at least 13, 15, 17, 20, 25, 30, 40, 50, 66, 70, 85, 88, 100, 187, 200, or 250, 500, 700, 1000 or 2000 biallelic markers in a biological sample, wherein at least 1, 2, 3, 4, 5, 10, 13, 17, 20, 25, 30, 40, 50, 70, 85, 100, 150, 200, 250 or all of said biallelic markers are CNS disorder-related markers selected from the group consisting of SEQ ID NOS: 1-271.

20 Any markers known in the art may be used with the CNS disorder-related markers of the present invention in the DNA typing methods and systems described herein, for example in anyone of the following web sites offering collections of SNPs and information about those SNPs:

*The Genetic Annotation Initiative* (<http://cgap.nci.nih.gov/GAI/>). An NIH run site  
25 which contains information on candidate SNPs thought to be related to cancer and tumorigenesis generally.

*dbSNP Polymorphism Repository* (<http://www.ncbi.nlm.nih.gov/SNP/>). A more comprehensive NIH-run database containing information on SNPs with broad applicability in biomedical research.

30 *HUGO Mutation Database Initiative*  
(<http://ariel.ucs.unimelb.edu.au:80/~cotton/mdi.htm>). A database meant to provide systematic

access to information about human mutations including SNPs. This site is maintained by the Human Genome Organisation (HUGO).

*Human SNP Database* (<http://www-genome.wi.mit.edu/SNP/human/index.html>).

Managed by the Whitehead Institute for Biomedical Research Genome Institute, this site contains  
5 information about SNPs resulting from the many Whitehead research projects on mapping and sequencing.

*SNPs in the Human-Genome SNP database* (<http://www.ihc.wustl.edu/SNP>). This website provides access to SNPs that have been organized by chromosomes and cytogenetic location. The site is run by Washington University.

10 *HGBase* (<http://hgbase.cgr.ki.se/>). HGBASE is an attempt to summarize all known sequence variations in the human genome, to facilitate research into how genotypes affect common diseases, drug responses, and other complex phenotypes, and is run by the Karolinska Institute of Sweden.

*The SNP Consortium Database* (<http://snp.cshl.org/db/snp/map>). A collection of SNPs  
15 and related information resulting from the collaborative effort of a number of large pharmaceutical and information processing companies.

GeneSNPs (<http://www.genome.utah.edu/genesnps/>). Run by the University of Utah, this site contains information about SNPs resulting from the U. S. National Institute of Environmental Health's initiative to understand the relationship between genetic variation and response to  
20 environmental stimuli and xenobiotics.

In addition, biallelic markers provided in the following patents and patent applications may also be used with the map-related biallelic markers of the invention in the DNA typing methods and systems described above: US Serial No. 60/206,615, filed 24 March 2000; US  
25 Serial No. 60/216,745, filed 30 June 2000; WIPO Serial No. PCT/IB00/00184, filed 11 February 2000; WIPO Serial No. PCT/IB98/01193, filed 17 July 1998; PCT Publication No. WO 99/54500, filed 21 April 1999; and WIPO Serial No. PCT/IB00/00403, filed 24 March 2000.

Biallelic markers, sets of biallelic markers, probes, primers, and methods for determining the identity of a nucleotide at said biallelic markers are also encompassed and are further described herein, and may encompass any further limitation described in this disclosure, alone or  
30 in any combination.

Forensic matching by microsequencing is further described in Example 6 below.

Throughout this application, various publications, patents, and published patent applications are cited. The disclosures of the publications, patents, and published patent  
35 specifications referenced in this application are hereby incorporated by reference into the present disclosure to more fully describe the state of the art to which this invention pertains.

### EXAMPLES

Several of the methods of the present invention are described in the following examples, which are offered by way of illustration and not by way of limitation. Many other modifications and variations of the invention as herein set forth can be made without departing from the spirit and scope thereof and therefore only such limitations should be imposed as are indicated by the appended claims.

#### Example 1: *De Novo* Identification of Biallelic Markers

The biallelic markers set forth in this application were isolated from human genomic sequences. To identify biallelic markers, genomic fragments were amplified, sequenced and compared in a plurality of individuals.

#### DNA samples

Donors were unrelated and healthy. They represented a sufficient diversity for being representative of a French heterogeneous population. The DNA from 100 individuals was extracted and tested for the *de novo* identification of biallelic markers.

DNA samples were prepared peripheral venous blood as follows. 30 ml of peripheral venous blood were taken from each donor in the presence of EDTA. Cells (pellet) were collected after centrifugation for 10 minutes at 2000 rpm. Red cells were lysed in a lysis solution (50 ml final volume: 10 mM Tris pH7.6; 5 mM MgCl<sub>2</sub>; 10 mM NaCl). The solution was centrifuged (10 minutes, 2000 rpm) as many times as necessary to eliminate the residual red cells present in the supernatant, after resuspension of the pellet in the lysis solution. The pellet of white cells was lysed overnight at 42°C with 3.7 ml of lysis solution composed of: (a) 3 ml TE 10-2 (Tris-HCl 10 mM, EDTA 2 mM) / NaCl 0.4 M; (b) 200 µl SDS 10%; and (c) 500 µl proteinase K (2 mg proteinase K in TE 10-2 / NaCl 0.4 M).

For the extraction of proteins, 1 ml saturated NaCl (6M) (1/3.5 v/v) was added. After vigorous agitation, the solution was centrifuged for 20 minutes at 10000 rpm. For the precipitation of DNA, 2 to 3 volumes of 100% ethanol were added to the previous supernatant, and the solution was centrifuged for 30 minutes at 2000 rpm. The DNA solution was rinsed three times with 70% ethanol to eliminate salts, and centrifuged for 20 minutes at 2000 rpm. The pellet was dried at 37°C, and resuspended in 1 ml TE 10-1 or 1 ml water. The DNA concentration was evaluated by measuring the optical density (OD) at 260 nm (1 unit OD = 50 µg/ml DNA). To determine the presence of proteins in the DNA solution, the OD 260 / OD 280 ratio was determined. Only DNA preparations having a OD 260 / OD 280 ratio between 1.8 and 2 were used in the subsequent examples described below. DNA pools were constituted by mixing equivalent quantities of DNA from each individual.

Amplification of genomic DNA by PCR

Amplification of specific genomic sequences was carried out on pooled DNA samples obtained as described above.

Amplification primers

5 The primers used for the amplification of human genomic DNA fragments were defined with the OSP software (Hillier & Green, 1991). Preferably, primers included, upstream of the specific bases targeted for amplification, a common oligonucleotide tail useful for sequencing. Primers PU contain the following additional PU 5' sequence : TGTAACGACGGCCAGT; primers RP contain the following RP 5' sequence : CAGGAAACAGCTATGACC. Primers are  
10 listed in Table 12.

Amplification

PCR assays were performed using the following protocol:

	Final volume	25 µl
15	DNA	2 ng/µl
	MgCl <sub>2</sub>	2 mM
	dNTP (each)	200 µM
	primer (each)	2.9 ng/µl
	Ampli Taq Gold DNA polymerase	0.05 unit/µl
20	PCR buffer (10x = 0.1 M TrisHCl pH8.3 0.5M KCl)	1x

DNA amplification was performed on a Genius II thermocycler. After heating at 94°C for 10 min, 40 cycles were performed. Cycling times and temperatures were: 30 sec at 94°C, 55°C for 1 min and 30 sec at 72°C. Holding for 7 min at 72°C allowed final elongation. The  
25 quantities of the amplification products obtained were determined on 96-well microtiter plates, using a fluorometer and Picogreen as intercalant agent (Molecular Probes).

Sequencing of amplified genomic DNA and identification of biallelic polymorphisms

Sequencing of the amplified DNA was carried out on ABI 377 sequencers. The  
30 sequences of the amplification products were determined using automated dideoxy terminator sequencing reactions with a dye terminator cycle sequencing protocol. The products of the sequencing reactions were run on sequencing gels and the sequences were determined using gel image analysis (ABI Prism DNA Sequencing Analysis software 2.1.2 version).

The sequence data were further evaluated to detect the presence of biallelic markers  
35 within the amplified fragments. The polymorphism search was based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. However, the presence of two peaks can be an artifact due to background noise.

To exclude such an artifact, the two DNA strands were sequenced and a comparison between the two strands was carried out. In order to be registered as a polymorphic sequence, the polymorphism had to be detected on both strands. Further, some biallelic single nucleotide polymorphisms were confirmed by microsequencing as described below.

5 Biallelic markers were identified in the analyzed fragments and are shown in Table 7.

#### Example 2: Genotyping of Biallelic Markers

The biallelic markers identified as described above were further confirmed and their respective frequencies were determined through microsequencing. Microsequencing was carried  
10 out on individual DNA samples obtained as described herein.

#### Microsequencing primers

Amplification of genomic DNA fragments from individual DNA samples was performed as described in Example 1 using the same set of PCR primers (Table 12). Microsequencing was  
15 carried out on the amplified fragments using specific primers. See Table 13. The preferred primers used in microsequencing had about 19 nucleotides in length and hybridized just upstream of the considered polymorphic base.

The microsequencing reactions were performed as follows: 5 µl of PCR products were added to 5 µl purification mix (2U SAP (Shrimp alkaline phosphate) (Amersham E70092X)); 2U  
20 Exonuclease I (Amersham E70073Z); and 1 µl SAP buffer (200 mM Tris-HCl pH8, 100 mM MgCl<sub>2</sub>) in a microtiter plate. The reaction mixture was incubated 30 minutes at 37°C, and denatured 10 minutes at 94°C afterwards. To each well was then added 20 µl of microsequencing reaction mixture containing: 10 pmol microsequencing oligonucleotide (19mers, GENSET, crude synthesis, 5 OD), 1 U Thermosequenase (Amersham E79000G), 1.25  
25 µl Thermosequenase buffer (260 mM Tris HCl pH 9.5, 65 mM MgCl<sub>2</sub>), and the two appropriate fluorescent ddNTPs complementary to the nucleotides at the polymorphic site corresponding to both polymorphic bases (11.25 nM TAMRA-ddTTP ; 16.25 nM ROX-ddCTP ; 1.675 nM REG-ddATP ; 1.25 nM RHO-ddGTP ; Perkin Elmer, Dye Terminator Set 401095). After 4 minutes at 94°C, 20 PCR cycles of 15 sec at 55°C, 5 sec at 72°C, and 10 sec at 94°C were carried out in a  
30 Tetrad PTC-225 thermocycler (MJ Research). The microtiter plate was centrifuged 10 sec at 1500 rpm. The unincorporated dye terminators were removed by precipitation with 19 µl MgCl<sub>2</sub> 2mM and 55 µl 100 % ethanol. After 15 minute incubation at room temperature, the microtiter plate was centrifuged at 3300 rpm 15 minutes at 4°C. After discarding the supernatants, the microplate was evaporated to dryness under reduced pressure (Speed Vac). Samples were  
35 resuspended in 2.5 µl formamide EDTA loading buffer and heated for 2 min at 95°C. 0.8 µl microsequencing reaction were loaded on a 10 % (19:1) polyacrylamide sequencing gel. The

data were collected by an ABI PRISM 377 DNA sequencer and processed using the GENESCAN software (Perkin Elmer).

#### Frequency of biallelic markers

Frequencies are reported for the less common allele only and are shown in Table 7.

5

#### Example 3: Association Study Between Major Depression and the Biallelic Markers of Candidate Genes

##### Collection of DNA samples from affected and non-affected individuals

- 10 The disease trait followed in this association study was major depression, a complex disorder believed to involve several neurotransmitter pathways including those utilizing norepinephrine and serotonin. The depressed patient population consists of 140 individuals that participated in a clinical study for the evaluation of the anti-depressant compound Reboxetine (Montgomery S.A. and Schatzberg A.F.; *Journal Clin. Psychiatry* 59(suppl 14): 3-7, 1998).
- 15 Approximately 90% of these individuals were from a Caucasian ethnic background. The control population consisted of 94 individuals from a Caucasian population that had been found not to have any personal or family evidence of psychiatric disease.

##### Genotyping of affected and control individuals

- The general strategy was to individually determine allele frequencies of biallelic markers
- 20 in all individuals from each population described above. Allele frequencies of the biallelic markers were determined by performing microsequencing reactions on amplified DNA fragments obtained from genomic PCR performed on DNA samples from each individual. Genomic PCR and microsequencing were performed as detailed above in Examples 1 and 2.

- 25 Frequency of the biallelic markers alleles and genotypes of candidate gene and association with major depression

- Frequencies of biallelic marker alleles were compared in the case-control populations described above. The data in Table 15 show the p-value obtained for each marker typed for each candidate gene for individual alleles and genotypes. Nine markers from 7 of 19 candidate genes
- 30 were significant at the 5% level for allele frequency differences while seven markers from 6 of 19 candidate genes were significant at the 5% level for genotype frequency differences. In 4 cases, the same marker was significant at the 5% level for both allele and genotype frequency differences. This occurred for markers from the genes 5HTR6, 5HTR7, NET, and Gbeta3. These genes all participate in the mechanism of either serotonin or norepinephrine
- 35 neurotransmission.

##### Haplotype frequency analysis

The results of the haplotype analysis using combinations of 2, 3, and 4 biallelic markers from each gene are shown in Tables 17 and 18. Haplotype analyses for the candidate genes were performed by estimating the frequencies of all 2, 3, and 4 marker haplotypes in the depressed and control populations. Haplotype estimations were performed by applying the Expectation-  
 5 Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995). Estimated haplotype frequencies in the depressed and control populations were compared by means of permutation tests based on individual haplotypes (Permutation test) as well as the distribution of frequencies from all possible haplotypes derived from a particular combination of given markers (Omnibus LR test).

10 The results of the Omnibus LR test are shown in Table 16. Listed are the top 10 marker combinations for each category of 4, 3, and 2 marker combinations and boxed in a double line border are the top 5% of each category (by p-value based on phenotypic reiteration of at least 1000 simulations). It is remarkable that several of the same genes identified by single marker association tests also appear in the top 5% of the Omnibus LR test. In particular, markers from  
 15 the genes NET and Gbeta3 appear as top 5% in each category of combinations for the Omnibus LR test.

The results of the Permutation test for individual haplotypes are shown in Table 17. Listed are the top 20 haplotypes for each category of 4, 3, and 2 marker haplotypes and boxed in a double line border are the top 1% of each category (by p-value based on phenotypic reiteration  
 20 of at least 1000 simulations). Again it is remarkable that several of the same genes identified by single marker association tests and Omnibus LR test also contribute haplotypes that appear in the top 1% of the Permutation test for individual haplotypes. Of all genes, only NET contributes to the top percentiles of each category of testing (individual markers for allele and genotype frequencies, Omnibus LR 4,3 and 2 marker combinations, and Permutation test for individual 4,  
 25 3, and 2 marker haplotypes). However several other genes contribute to several testing categories including previously mentioned Gbeta3 and 5HTR7 as well as WFS1, GRL, 5HTT and DRD3.

Two preferred haplotypes can be constructed from markers derived from the NET gene. One consists of markers 99-28788/300, 99-32061/304, and 99-32121/242 each manifesting the G  
 30 allele. The GGG haplotype is present in only 1% of depressed cases vs. 7% of controls. While this haplotype is low in overall frequency, the p-value by permutation test is  $2 \times 10^{-4}$  and the p-value for this group of markers is  $2 \times 10^{-3}$  by Omnibus LR test suggesting that the result is highly significant. A second haplotype consists of markers 16-3/199, 16-28/93, and 16-50/196 manifesting alleles TCT respectively. The haplotype TCT is present in only 30% of cases vs.  
 35 43% of controls. The p-value by permutation test is  $9 \times 10^{-4}$  and the p-value for this group of markers is  $8.9 \times 10^{-4}$  by Omnibus LR test, also indicating a high level of significance.

Another example of a preferred haplotype comes from markers 16-16/285, 16-17/121, and 16-106/364 which are derived from the gene Gbeta3. The haplotype TTC is present in 21% of cases vs. 35% of controls. The p-value by permutation test is  $1 \times 10^{-3}$  and the p-value for this group of markers is  $1 \times 10^{-4}$  by Omnibus LR test, indicating a high level of significance.

5

Example 4: Association Study Between Major Depression and the Biallelic Markers of Candidate Genes

The association analysis of Example 3 was repeated using a different population set as described below. In general, these estimates agreed with the frequencies observed in the first screening within a few percent. Statistical assessments of haplotype frequency differences between depressed cases and controls were made by Omnibus LR tests and individual haplotype tests.

For Omnibus analyses, WFS1 marker combinations showed the most significant ( $p < 0.01$ ) differences between the depressed cases and controls for 2, 3, and 4 locus haplotypes. Strongest among these associations were combinations of markers spanning the core exonic region of the WFS1 gene including 19-17/188, 19-19/174, and 24-243/346. Several NET marker combinations showed significant associations ( $p < 0.05$ ) including those from the 5' flanking region and those from the exonic region. When compared to the distribution of Omnibus p-values observed in the 1<sup>st</sup> screening, 11 WFS1 marker combinations would have been among the top 5% of observed Omnibus p-values whereas 2 NET marker combinations would have been among the top 5%.

For individual haplotypes, haplotype GT from WFS1 markers 19-17/188 and 24-243/346 showed an 11% difference (37% cases vs. 26% controls,  $p < 0.001$ ). A similar difference was observed for haplotype GC from WFS1 markers 19-17/188 and 19-19/174 and GCT from all three markers ( $p < 0.005$ ). Several NET haplotypes showed >10% frequency differences between cases and controls ( $p < 0.01$ ). When compared to the distribution of individual haplotype p-values observed in the first screening, 6 WFS1 marker combinations would have been among the top 1% of observed individual haplotype p-values.

Frequency of the biallelic markers alleles and genotypes of candidate gene and association with major depression

Frequencies of biallelic marker alleles were compared in the case-control populations described above. The data in Table 18 show the p-value obtained for each marker typed for each candidate gene for individual alleles and genotypes. Nine markers from 7 of 19 candidate genes were significant at the 5% level for allele frequency differences while seven markers from 6 of 19 candidate genes were significant at the 5% level for genotype frequency differences. In 4 cases, the same marker was significant at the 5% level for both allele and genotype frequency differences. This occurred for markers from the genes 5HTR6, 5HTR7, and WFS1.



Haplotype frequency analysis

The results of the haplotype analysis using combinations of 2, 3, and 4 biallelic markers from each gene are shown in Tables 19 and 20. Haplotype analyses for the candidate genes were performed by estimating the frequencies of all 2, 3, and 4 marker haplotypes in the depressed and control populations. Haplotype estimations were performed by applying the Expectation-  
 5 Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995). Estimated haplotype frequencies in the depressed and control populations were compared by means of permutation tests based on individual haplotypes (Permutation test) as well as the distribution of frequencies from all possible haplotypes derived from a particular combination of  
 10 given markers (Omnibus LR test).

The results of the Omnibus LR test are shown in Table 19. Listed are the top 10 marker combinations for each category of 4, 3, and 2 marker combinations and boxed in a double line border are the top 5% of each category (by p-value based on phenotypic reiteration of at least 1000 simulations). It is remarkable that several of the same genes identified by single marker  
 15 association tests also appear in the top 5% of the Omnibus LR test. In particular, markers from the gene WFS1 appears as top 5% in each category of combinations for the Omnibus LR test.

The results of the Permutation test for individual haplotypes are shown in Table 20. Listed are the top 20 haplotypes for each category of 4, 3, and 2 marker haplotypes and boxed in a double line border are the top 1% of each category (by p-value based on phenotypic reiteration  
 20 of at least 1000 simulations). Again it is remarkable that several of the same genes identified by single marker association tests and Omnibus LR test also contribute haplotypes that appear in the top 1% of the Permutation test for individual haplotypes. Of all genes, WFS1 contributes to the top percentiles of nearly all categories of testing (individual markers for allele and genotype frequencies, Omnibus LR 4,3 and 2 marker combinations, and Permutation test for individual 3  
 25 and 2 marker haplotypes). However several other genes contribute to several testing categories including previously mentioned 5HTR7 as well as NET, GRL, 5HTT and DRD3.

A preferred haplotype can be constructed from markers derived from the WFS1 gene. This consists of markers 19-17/188, 19-19/174, and 24-243/176 manifesting alleles GCT respectively. The GCT haplotype is present in 34% of depressed cases vs. 24% of controls.  
 30 While this haplotype is low in overall frequency, the p-value by permutation test is  $3 \times 10^{-3}$  and the p-value for this group of markers is  $1 \times 10^{-3}$  by Omnibus LR test suggesting that the result is highly significant.

Example 5: Response to Reboxetine in Depressed Patients

35 Single point analyses were also performed on data from the candidate genes to determine Reboxetine response among depressed patients as compared to controls. Two markers from NET

(99-32061/304 and 99-32121/242) showed allelic and genotypic association ( $p < 0.05$ ). A single marker from Gbeta3 (18-355/67) showed allelic association with drug response ( $p = 0.05$ ).

Multipoint analyses on the data revealed Omnibus LR-based associations to be minimal for these genes with only two marker combinations from NET achieving a level of significance of  $p < 0.05$ . At the individual haplotype level, a number of NET haplotypes achieved this level of significance with 10-15% responder/non-responder differences in haplotype frequencies. Also of note is the observation that a few individual haplotypes from Gbeta3 showed a remarkable level of significance ( $p < 0.0005$ ) corresponding to a nearly infinite relative risk (15-20% in non-responders vs. 0% in responders). This difference in estimated haplotype frequency is based largely on the observation that one particular haplotype cannot be unambiguously detected in the 204 responder haplotypes although there are at least 9 copies in 182 non-responder haplotypes.

In conclusion, modest association is present between NET and drug response. In addition, select individual haplotypes from Gbeta3 show a strong statistical association with drug response.

#### Example 6: Forensic Matching by Microsequencing

DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the sequences of SEQ ID NOS: 1 to 542 is then utilized according to the methods described herein to amplify DNA of approximately 500 bases in length from the forensic specimen. The alleles present at each of the selected biallelic markers site according to biallelic markers SEQ ID NOS: 1 to 542 are then identified according Example 2. A simple database comparison of the analysis results determines the differences, if any, between the sequences from a subject individual or from a database and those from the forensic sample. In a preferred method, statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 13, 17, 20, 25, 30, 40, 50, 66, 70, 85, 88, 100, 187, 200 or 250 biallelic markers are used to test identity between the suspect and the sample.

In accordance with the regulations relating to Sequence Listings, the following codes have been used in the Sequence Listing to indicate the locations of biallelic markers within the sequences and to identify each of the alleles present at the polymorphic base. The code "r" in the sequences indicates that one allele of the polymorphic base is a guanine, while the other allele is an adenine. The code "y" in the sequences indicates that one allele of the polymorphic base is a thymine, while the other allele is a cytosine. The code "m" in the sequences indicates that one

allele of the polymorphic base is an adenine, while the other allele is an cytosine. The code "k" in the sequences indicates that one allele of the polymorphic base is a guanine, while the other allele is a thymine. The code "s" in the sequences indicates that one allele of the polymorphic base is a guanine, while the other allele is a cytosine. The code "w" in the sequences indicates that one

5 allele of the polymorphic base is an adenine, while the other allele is an thymine.

**TABLE 7A**

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO- SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY	
5HTR6	99-27199-207	1	207	Y	T	0.30
5HTR6	99-27207-117	2	117	Y	C	0.37
5HTR6	99-27213-53	3	53	Y		
5HTR6	99-27218-333	4	333	Y		
5HTR6	99-28108-233	5	233	Y		
5HTR6	99-28109-275	6	275	N		
5HTR6	99-28110-75	7	74	Y	T	0.48
5HTR6	99-28125-81	8	81	Y		
5HTR6	99-28134-215	9	215	Y	T	0.37
5HTR6	99-28137-96	10	96	Y		
5HTR6	99-32204-305	11	305	N		
5HTR7	99-28149-118	12	118	Y	C	0.31
5HTR7	99-28160-285	13	285	Y	G	0.49
5HTR7	99-28171-458	14	457	Y	A	0.38
5HTR7	99-28173-395	15	395	Y		
5HTR7	99-32177-113	16	113	Y		
5HTR7	99-32181-192	17	192	Y	C	0.38
5HTR7	99-32193-258	18	257	Y	T	0.65
CHRNA7	99-28722-90	19	90	Y	C	0.32
CHRNA7	99-28730-351	20	351	Y	A	0.38
CHRNA7	99-32306-409	21	407	Y	G	0.33
CRFR1	99-27088-246	22	246	Y	A	0.38
CRFR1	99-27090-203	23	204	Y	G	0.22
CRFR1	99-27091-220	24	221	Y	A	0.49
CRFR1	99-27093-145	25	145	N		
CRFR1	99-27094-406	26	406	Y	T	0.21
CRFR1	99-27096-410	27	410	N		
CRFR1	99-27097-83	28	83	Y	T	0.47
CRFR1	99-27098-162	29	162	N		
CRFR1	99-27550-48	30	48	Y	A	0.26
CRFR1	99-27558-335	31	335	Y		
CRFR1	99-27561-106	32	106	Y		
CRFR1	99-27562-366	33	364	N		
MLR	16-31-738	34	738	Y	G	0.47
MLR	99-27110-301	35	300	Y		
MLR	99-27563-400	36	400	Y	A	0.44
MLR	99-27573-443	37	443	Y		
MLR	99-28732-133	38	133	Y	A	0.31
MLR	99-28735-56	39	56	Y	T	0.30
MLR	99-28736-399	40	399	Y		
MLR	99-28738-319	41	319	Y	C	0.37
MLR	99-28739-364	42	364	Y		
CRFR2	99-27875-185	43	185	Y	C	0.40
CRFR2	99-27880-176	44	176	Y	T	0.44
CRFR2	99-28747-371	45	373	Y	C	0.44
CRFR2	99-28753-353	46	352	Y	C	0.39
CRFR2	99-28755-206	47	207	Y	G	0.41
CRFR2	99-32333-366	48	366	N	C	
GRL	16-38-323	49	323	Y	A	0.33
GRL	99-28484-179	50	179	Y	A	0.40

**TABLE 7A (cont)**

GRL	99-30853-364	51	364	Y	G	0.42
GRL	99-28485-198	52	198	Y	G	0.20
GRL	99-30858-354	53	354	Y	T	0.16
GRL	99-32002-313	54	311	Y	A	0.48
GRL	18-15-366	55	366	Y		
GRL	18-20-174	56	174	Y	G	0.27
GRL	18-31-178	57	178	Y	C	0.35
GRL	18-38-395	58	395	Y	T	0.37
MAOA	18-2-192	59	192	Y	T	0.32
MAOB	99-26921-210	60	211	Y	G	0.48
MAOA	16-215-80	61	250	Y	T	0.33
MAOA-B	18-132-368	62	368	Y	C	0.34
MAOA	18-133-293	63	292	Y	A	0.27
5HTR2c	18-12-191	64	191	Y	A	0.14
5HTR2c	18-11-137	65	138	Y	G	0.27
5HTR2c	18-93-96	66	96	Y		
TH	16-115-343	67	343	Y	C	0.24
TH	16-42-140	68	140	Y	G	0.30
TH	18-251-176	69	176	Y	T	0.43
TH	18-269-44	70	44	Y	A	0.38
CRF	16-218-624	71	624	N		
CRF	18-393-330	72	330	Y		
CRF	18-394-402	73	402	Y		
DRD4	16-217-55	74	55	Y		
DRD4	18-284-139	75	139	Y		
DRD4	18-285-305	76	305	Y		
DRD4	18-289-239	77	239	Y		
DRD4	18-291-91	78	91	Y		
5HTT	18-186-391	79	391	Y	T	0.47
5HTT	18-194-130	80	130	Y	T	0.48
5HTT	18-198-252	81	252	Y	A	0.49
5HTT	18-242-300	82	299	Y	G	0.46
DRD3	8-15-126	83	1501	Y	G	0.30
DRD3	8-19-372	84	1501	Y	A	0.28
DRD3	99-2409-298	85	428	Y	A	0.40
DRD3	99-339-54	86	1501	Y	G	0.46
CYP3A4-7	12-254-180	87	311	Y	G	0.46
CYP3A4-7	10-214-279	88	1501	Y	C	0.12
CYP3A4-7	10-217-91	89	1501	Y	T	0.07
NET	99-28779-168	90	168	Y		
NET	99-28788-300	91	300	Y	A	0.47
NET	99-32052-262	92	263	Y		
NET	99-32121-242	93	244	Y	G	0.48
NET	99-32059-169	94	169	N		
NET	99-32061-304	95	304	Y	A	0.39
NET	99-32065-303	96	303	Y		
NET	99-32123-118	97	118	Y		
NET	99-32148-315	98	314	Y		
NET	16-2-76	99	95	Y	A	0.27
NET	16-28-93	100	120	Y	C	0.44
NET	16-3-199	101	342	Y	C	0.32
NET	16-50-197	102	197	Y	C	0.21
NET	16-1-59	103	181	Y		
NET	16-2-187	104	206	Y		
TACR1	99-28761-311	105	311	Y	A	0.22

**TABLE 7A (cont)**

TACR1	99-28771-86	106	86	Y	T	0.48
TACR1	99-28791-291	107	291	Y	A	0.26
TACR1	99-32077-66	108	66	Y		
TACR1	99-32078-466	109	467	Y		
TACR1	99-32376-426	110	426	Y		
TACR1	99-32361-419	111	420	Y	T	0.48
DRD2	16-21-228	112	228	Y	A	0.16
DRD2	16-22-156	113	156	Y	C	0.45
DRD2	16-23-404	114	404	Y	G	0.47
DRD2	16-24-175	115	175	Y	A	0.16
DRD2	16-25-286	116	286	Y	T	0.37
DRD2	16-25-279	117	279	Y		
DRD2	16-23-393	118	393	Y		
Gbeta3	16-106-364	119	364	Y	T	0.01
Gbeta3	16-16-285	120	285	Y	T	0.38
Gbeta3	16-17-121	121	121	Y	T	0.36
Gbeta3	16-84-185	122	185	Y	C	0.40
Gbeta3	16-87-74	123	74	Y	A	0.34
Gbeta3	16-91-333	124	333	Y	A	0.43
WFS1	16-128-142	125	142	Y	C	0.27
WFS1	16-133-205	126	245	Y	G	0.34
WFS1	16-135-181	127	232	Y	A	0.28
WFS1	16-145-405	128	455	Y	C	0.11
WFS1	16-177-320	129	320	Y	A	0.07
WFS1	16-4-354	130	354	Y	C	0.36

**TABLE 7B**

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO- SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY	
5HTR6	99-27199-207	131	24	Y	T	0.30
5HTR6	99-27207-117	132	24	Y	C	0.37
5HTR6	99-27213-53	133	24	Y		
5HTR6	99-27218-333	134	24	Y		
5HTR6	99-28108-233	135	24	Y		
5HTR6	99-28109-275	136	24	N		
5HTR6	99-28110-75	137	24	Y	T	0.48
5HTR6	99-28125-81	138	24	Y		
5HTR6	99-28134-215	139	24	Y	T	0.37
5HTR6	99-28137-96	140	24	Y		
5HTR6	99-32204-305	141	24	N		
5HTR7	99-28149-118	142	24	Y	C	0.31
5HTR7	99-28160-285	143	24	Y	G	0.49
5HTR7	99-28171-458	144	24	Y	A	0.38
5HTR7	99-28173-395	145	24	Y		
5HTR7	99-32177-113	146	24	Y		
5HTR7	99-32181-192	147	24	Y	C	0.38
5HTR7	99-32193-258	148	24	Y	T	0.65
CHRNA7	99-28722-90	149	24	Y	C	0.32
CHRNA7	99-28730-351	150	24	Y	A	0.38
CHRNA7	99-32306-409	151	24	Y	G	0.33
CRFR1	99-27088-246	152	24	Y	A	0.38
CRFR1	99-27090-203	153	24	Y	G	0.22

**TABLE 7B (cont)**

CRFR1	99-27091-220	154	24	Y	A	0.49
CRFR1	99-27093-145	155	24	N		
CRFR1	99-27094-406	156	24	Y	T	0.21
CRFR1	99-27096-410	157	24	N		
CRFR1	99-27097-83	158	24	Y	T	0.47
CRFR1	99-27098-162	159	24	N		
CRFR1	99-27550-48	160	24	Y	A	0.26
CRFR1	99-27558-335	161	24	Y		
CRFR1	99-27561-106	162	24	Y		
CRFR1	99-27562-366	163	24	N		
MLR	16-31-738	164	24	Y	G	0.47
MLR	99-27110-301	165	24	Y		
MLR	99-27563-400	166	24	Y	A	0.44
MLR	99-27573-443	167	24	Y		
MLR	99-28732-133	168	24	Y	A	0.31
MLR	99-28735-56	169	24	Y	T	0.30
MLR	99-28736-399	170	24	Y		
MLR	99-28738-319	171	24	Y	C	0.37
MLR	99-28739-364	172	24	Y		
CRFR2	99-27875-185	173	24	Y	C	0.40
CRFR2	99-27880-176	174	24	Y	T	0.44
CRFR2	99-28747-371	175	24	Y	C	0.44
CRFR2	99-28753-353	176	24	Y	C	0.39
CRFR2	99-28755-206	177	24	Y	G	0.41
CRFR2	99-32333-366	178	24	N	C	
GRL	16-38-323	179	24	Y	A	0.33
GRL	99-28484-179	180	24	Y	A	0.40
GRL	99-30853-364	181	24	Y	G	0.42
GRL	99-28485-198	182	24	Y	G	0.20
GRL	99-30858-354	183	24	Y	T	0.16
GRL	99-32002-313	184	24	Y	A	0.48
GRL	18-15-366	185	24	Y		
GRL	18-20-174	186	24	Y	G	0.27
GRL	18-31-178	187	24	Y	C	0.35
GRL	18-38-395	188	24	Y	T	0.37
MAOA	18-2-192	189	24	Y	T	0.32
MAOB	99-26921-210	190	24	Y	G	0.48
MAOA	16-215-80	191	24	Y	T	0.33
MAOA-B	18-132-368	192	24	Y	C	0.34
MAOA	18-133-293	193	24	Y	A	0.27
5HTR2c	18-12-191	194	24	Y	A	0.14
5HTR2c	18-11-137	195	24	Y	G	0.27
5HTR2c	18-93-96	196	24	Y		
TH	16-115-343	197	24	Y	C	0.24
TH	16-42-140	198	24	Y	G	0.30
TH	18-251-176	199	24	Y	T	0.43
TH	18-269-44	200	24	Y	A	0.38
CRF	16-218-624	201	24	N		
CRF	18-393-330	202	24	Y		
CRF	18-394-402	203	24	Y		
DRD4	16-217-55	204	24	Y		
DRD4	18-284-139	205	24	Y		
DRD4	18-285-305	206	24	Y		
DRD4	18-289-239	207	24	Y		
DRD4	18-291-91	208	24	Y		

**TABLE 7B (cont)**

5HTT	18-186-391	209	24	Y	T	0.47
5HTT	18-194-130	210	24	Y	T	0.48
5HTT	18-198-252	211	24	Y	A	0.49
5HTT	18-242-300	212	24	Y	G	0.46
DRD3	8-15-126	213	24	Y	G	0.30
DRD3	8-19-372	214	24	Y	A	0.28
DRD3	99-2409-298	215	24	Y	A	0.40
DRD3	99-339-54	216	24	Y	G	0.46
CYP3A4-7	12-254-180	217	24	Y	G	0.46
CYP3A4-7	10-214-279	218	24	Y	C	0.12
CYP3A4-7	10-217-91	219	24	Y	T	0.07
NET	99-28779-168	220	24	Y		
NET	99-28788-300	221	24	Y	A	0.47
NET	99-32052-262	222	24	Y		
NET	99-32121-242	223	24	Y	G	0.48
NET	99-32059-169	224	24	N		
NET	99-32061-304	225	24	Y	A	0.39
NET	99-32065-303	226	24	Y		
NET	99-32123-118	227	24	Y		
NET	99-32148-315	228	24	Y		
NET	16-2-76	229	24	Y	A	0.27
NET	16-28-93	230	24	Y	C	0.44
NET	16-3-199	231	24	Y	C	0.32
NET	16-50-197	232	24	Y	C	0.21
NET	16-1-59	233	24	Y		
NET	16-2-187	234	24	Y		
TACR1	99-28761-311	235	24	Y	A	0.22
TACR1	99-28771-86	236	24	Y	T	0.48
TACR1	99-28791-291	237	24	Y	A	0.26
TACR1	99-32077-66	238	24	Y		
TACR1	99-32078-466	239	24	Y		
TACR1	99-32376-426	240	24	Y		
TACR1	99-32361-419	241	24	Y	T	0.48
DRD2	16-21-228	242	24	Y	A	0.16
DRD2	16-22-156	243	24	Y	C	0.45
DRD2	16-23-404	244	24	Y	G	0.47
DRD2	16-24-175	245	24	Y	A	0.16
DRD2	16-25-286	246	24	Y	T	0.37
DRD2	16-25-279	247	24	Y		
DRD2	16-23-393	248	24	Y		
Gbeta3	16-106-364	249	24	Y	T	0.01
Gbeta3	16-16-285	250	24	Y	T	0.38
Gbeta3	16-17-121	251	24	Y	T	0.36
Gbeta3	16-84-185	252	24	Y	C	0.40
Gbeta3	16-87-74	253	24	Y	A	0.34
Gbeta3	16-91-333	254	24	Y	A	0.43
WFS1	16-128-142	255	24	Y	C	0.27
WFS1	16-133-205	256	24	Y	G	0.34
WFS1	16-135-181	257	24	Y	A	0.28
WFS1	16-145-405	258	24	Y	C	0.11
WFS1	16-177-320	259	24	Y	A	0.07
WFS1	16-4-354	260	24	Y	C	0.36



**TABLE 7C**

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO- SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY	
MAO A/B	18-473-362	261	362	Y	C	0.43
MAO A/B	99-12361-88	262	88	Y	C	0.36
MAO A/B	99-12368-335	263	335	Y	C	0.36
MAO A/B	99-12370-67	264	67	Y	A	0.29
NET	99-32148-315	265	314	Y	C	0.27
NET	19-46-322	266	322	Y	C	0.31
NET	19-47-315	267	315	Y	T	0.14
NET	19-51-347	268	346	Y		
NET	99-32052-262	269	263	Y	T	0.38
CYP3A4/7	10-213-292	270	1501	Y	G	0.11
5HTT	18-419-135	271	135	Y		
5HTT	18-424-419	272	419	Y		
5HTT	18-429-289	273	290	Y		
5HTT	18-246-256	274	256	Y	C	0.48
Gbeta3	18-355-67	275	68	Y	C	0.49
Gbeta3	18-353-267	276	266	Y	T	0.27
Gbeta3	18-338-305	277	306	Y	G	0.3
WFS1	24-243-346	278	1501	Y	T	0.3
WFS1	99-62531-351	279	1501	Y	T	0.36
WFS1	99-54279-152	280	1501	Y	G	0.44
DRD2	18-168-245	281	245	Y	A	0.45
DRD2	18-171-291	282	291	Y	C	0.37
DRD2	18-172-346	283	346	Y	T	0.45
DRD2	18-177-406	284	406	Y	T	0.37
HM74	18-298-338	285	338	Y	G	0.49
HM74	18-298-110	286	110	Y		
HM74	18-299-105	287	104	Y		
HM74	18-884-30	288	31	Y	C	0.26
HM74	18-299-343	289	342	Y		
HM74	99-61513-139	290	140	Y	A	0.26
HM74	99-61514-179	291	179	Y	G	0.27
HM74	99-61516-323	292	323	Y	C	0.33
CRHBP	18-204-70	293	70	Y	C	0.20
CRHBP	18-207-441	294	442	Y	C	0.41
CRHBP	18-210-65	295	65	Y		
CRHBP	18-212-200	296	200	Y	T	0.31
CRHBP	18-229-334	297	334	Y	T	0.33
CRHBP	18-230-332	298	332	Y	T	0.32
AVPR1A	18-966-378	299	378	Y	C	0.41
AVPR1A	18-987-308	300	307	Y	A	0.35
AVPR1A	18-1169-118	301	118	Y		
AVPR1A	18-1172-138	302	138	Y	G	0.16
AVPR1A	18-1173-92	303	92	Y	T	0.32
AVPR1A	18-1174-387	304	387	Y	C	0.21
AVPR1A	18-1175-416	305	416	Y	G	0.21
AVPR1A	18-542-146	306	146	Y	G	0.21
5HT1A	8-42-211	307	1501	Y	G	0.46
5HT1A	8-45-389	308	1501	Y	G	0.01
5HT1A	18-994-270	309	270	Y	C	0.25
5HT1A	18-912-165	310	165	Y	T	0.46
5HT1A	18-991-124	311	124	Y	T	0.45

**TABLE 7C (cont)**

5HT1A	18-920-219	312	219	Y		
5HT1A	18-911-312	313	312	Y		
5HT1A	99-65963-368	314	368	Y		
5HT1A	99-65966-225	315	225	Y		
5HT1A	99-65968-75	316	75	Y		
5HT1A	99-5069-331	317	1501	Y		
5HT1A	99-5070-176	318	175	Y	T	0.02
GABRG2	18-511-348	319	348	Y		
GABRG2	18-523-352	320	352	Y	C	0.49
GABRG2	18-545-478	321	480	Y	G	0.45
GABRG2	18-522-194	322	194	Y	G	0.32
GABRG2	18-524-284	323	284	Y	C	0.36
ADRB1R	18-626-52	324	52	Y	G	0.36
ADRB1R	18-629-189	325	189	Y	T	0.40
ADRB1R	18-1131-71	326	71	Y	T	0.41
ADRB1R	18-534-126	327	126	Y		
ADRB1R	18-596-59	328	59	Y		
ADRB1R	18-597-27	329	27	Y	A	0.20
GABRA5	18-730-203	330	203	Y	G	0.48
GABRA5	18-734-89	331	89	Y	C	0.48
GABRA5	18-895-321	332	321	Y	A	0.27
GABRA5	18-896-69	333	69	Y		
GABRA5	18-903-58	334	58	Y		
GOLF	18-590-216	335	216	Y	G	0.42
GOLF	18-817-436	336	433	Y	T	0.41
GOLF	18-829-85	337	85	Y	G	0.39
GOLF	18-832-387	338	387	Y		
GOLF	18-833-259	339	259	Y		
GOLF	18-839-271	340	271	Y	C	0.40
GOLF	18-770-194	341	194	Y	T	0.37
GOLF	18-771-302	342	302	Y	G	0.30
GOLF	18-827-53	343	53	Y	G	0.34
GOLF	18-768-318	344	318	Y	G	0.31
GOLF	18-769-26	345	26	Y	A	0.17
SLC6A3	18-709-321	346	320	Y	C	0.46
SLC6A3	18-714-280	347	281	Y	T	0.17
SLC6A3	18-843-271	348	271	Y	C	0.37
SLC6A3	18-850-265	349	265	Y	T	0.34
SLC6A3	18-853-296	350	296	Y	T	0.23
SLC6A3	18-867-331	351	332	Y	C	0.48
SLC6A3	18-877-73	352	73	Y		
SLC6A3	18-856-85	353	85	Y	C	0.42
SLC6A3	18-861-101	354	101	Y	T	0.33
PDE4b	18-635-323	355	323	Y		
PDE4b	18-636-205	356	205	Y	A	0.36
PDE4b	18-649-427	357	427	Y	C	0.46
PDE4b	18-1134-316	358	316	Y	G	0.38
PDE4b	18-633-316	359	316	Y		
COMT	18-489-425	360	425	Y		
COMT	18-492-212	361	212	Y	C	0.41
COMT	18-488-156	362	156	Y	T	0.45
COMT	18-491-266	363	266	Y	T	0.42
COMT	18-497-141	364	141	Y	T	0.43
COMT	18-503-174	365	174	Y	C	0.31
COMT	18-490-95	366	95	Y	A	0.31

**TABLE 7C (cont)**

NPY1R	18-699-115	367	114	Y		
NPY1R	18-1099-293	368	293	Y		
NPY1R	18-1105-22	369	22	Y		
SLC1	18-562-418	370	418	Y	C	0.49
SLC1	18-564-204	371	204	Y	C	0.50
SEF2-1B	18-1032-262	372	261	Y	C	0.33
SEF2-1B	18-1035-412	373	412	Y	C	0.50
SEF2-1B	18-1036-293	374	293	Y	C	0.34
SEF2-1B	18-1038-95	375	95	Y	T	0.34
SEF2-1B	18-1040-361	376	361	Y	G	0.44
SEF2-1B	18-748-356	377	356	Y	T	0.47
BDNF	18-937-181	378	179	Y	A	0.26
BDNF	18-942-175	379	175	Y	T	0.29
BDNF	18-1213-221	380	221	Y		
BDNF	18-937-147	381	145	Y		
BDNF	18-946-408	382	407	Y	C	0.20
GAP43	18-787-133	383	133	Y	A	0.39
GAP43	18-1149-239	384	239	Y	A	0.49
GAP43	18-1159-291	385	291	Y	G	0.23
GAP43	18-1135-273	386	273	Y	T	0.43
GAP43	18-1136-108	387	108	Y		
GAP43	18-1147-68	388	68	Y		
GAP43	18-1157-295	389	295	Y		
GAP43	18-802-460	390	459	Y	A	0.32
CLOCK	18-1064-110	391	109	Y	C	0.36
CLOCK	18-1068-327	392	327	Y	T	0.32
CLOCK	18-1069-365	393	365	Y	A	0.23
CLOCK	18-1073-367	394	367	Y	A	0.35
CLOCK	18-1070-272	395	272	Y	T	0.36
CLOCK	18-1057-35	396	35	Y		
CLOCK	18-1062-415	397	415	Y		
CLOCK	18-1082-165	398	165	Y		
CLOCK	18-1080-361	399	363	Y	C	0.18
HSP70	18-506-297	400	297	Y		
HSP70	18-570-38	401	38	Y		

**TABLE 7D**

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO- SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY	
MAO A/B	18-473-362	402	24	Y	C	0.43
MAO A/B	99-12361-88	403	24	Y	C	0.36
MAO A/B	99-12368-335	404	24	Y	C	0.36
MAO A/B	99-12370-67	405	24	Y	A	0.29
NET	99-32148-315	406	24	Y	C	0.27
NET	19-46-322	407	24	Y	C	0.31
NET	19-47-315	408	24	Y	T	0.14
NET	19-51-347	409	24	Y		
NET	99-32052-262	410	24	Y	T	0.38
CYP3A4/7	10-213-292	411	24	Y	G	0.11
5HTT	18-419-135	412	24	Y		
5HTT	18-424-419	413	24	Y		
5HTT	18-429-289	414	24	Y		
5HTT	18-246-256	415	24	Y	C	0.48

**TABLE 7D (cont)**

Gbeta3	18-355-67	416	24	Y	C	0.49
Gbeta3	18-353-267	417	24	Y	T	0.27
Gbeta3	18-338-305	418	24	Y	G	0.3
WFS1	24-243-346	419	24	Y	T	0.3
WFS1	99-62531-351	420	24	Y	T	0.36
WFS1	99-54279-152	421	24	Y	G	0.44
DRD2	18-168-245	422	24	Y	A	0.45
DRD2	18-171-291	423	24	Y	C	0.37
DRD2	18-172-346	424	24	Y	T	0.45
DRD2	18-177-406	425	24	Y	T	0.37
HM74	18-298-338	426	24	Y	G	0.49
HM74	18-298-110	427	24	Y		
HM74	18-299-105	428	24	Y		
HM74	18-884-30	429	24	Y	C	0.26
HM74	18-299-343	430	24	Y		
HM74	99-61513-139	431	24	Y	A	0.26
HM74	99-61514-179	432	24	Y	G	0.27
HM74	99-61516-323	433	24	Y	C	0.33
CRHBP	18-204-70	434	24	Y	C	0.20
CRHBP	18-207-441	435	24	Y	C	0.41
CRHBP	18-210-65	436	24	Y		
CRHBP	18-212-200	437	24	Y	T	0.31
CRHBP	18-229-334	438	24	Y	T	0.33
CRHBP	18-230-332	439	24	Y	T	0.32
AVPR1A	18-966-378	440	24	Y	C	0.41
AVPR1A	18-987-308	441	24	Y	A	0.35
AVPR1A	18-1169-118	442	24	Y		
AVPR1A	18-1172-138	443	24	Y	G	0.16
AVPR1A	18-1173-92	444	24	Y	T	0.32
AVPR1A	18-1174-387	445	24	Y	C	0.21
AVPR1A	18-1175-416	446	24	Y	G	0.21
AVPR1A	18-542-146	447	24	Y	G	0.21
5HT1A	8-42-211	448	24	Y	G	0.46
5HT1A	8-45-389	449	24	Y	G	0.01
5HT1A	18-994-270	450	24	Y	C	0.25
5HT1A	18-912-165	451	24	Y	T	0.46
5HT1A	18-991-124	452	24	Y	T	0.45
5HT1A	18-920-219	453	24	Y		
5HT1A	18-911-312	454	24	Y		
5HT1A	99-65963-368	455	24	Y		
5HT1A	99-65966-225	456	24	Y		
5HT1A	99-65968-75	457	24	Y		
5HT1A	99-5069-331	458	24	Y		
5HT1A	99-5070-176	459	24	Y	T	0.02
GABRG2	18-511-348	460	24	Y		
GABRG2	18-523-352	461	24	Y	C	0.49
GABRG2	18-545-478	462	24	Y	G	0.45
GABRG2	18-522-194	463	24	Y	G	0.32
GABRG2	18-524-284	464	24	Y	C	0.36
ADRB1R	18-626-52	465	24	Y	G	0.36
ADRB1R	18-629-189	466	24	Y	T	0.40
ADRB1R	18-1131-71	467	24	Y	T	0.41
ADRB1R	18-534-126	468	24	Y		
ADRB1R	18-596-59	469	24	Y		
ADRB1R	18-597-27	470	24	Y	A	0.20

**TABLE 7D (cont)**

GABRA5	18-730-203	471	24	Y	G	0.48
GABRA5	18-734-89	472	24	Y	C	0.48
GABRA5	18-895-321	473	24	Y	A	0.27
GABRA5	18-896-69	474	24	Y		
GABRA5	18-903-58	475	24	Y		
GOLF	18-590-216	476	24	Y	G	0.42
GOLF	18-817-436	477	24	Y	T	0.41
GOLF	18-829-85	478	24	Y	G	0.39
GOLF	18-832-387	479	24	Y		
GOLF	18-833-259	480	24	Y		
GOLF	18-839-271	481	24	Y	C	0.40
GOLF	18-770-194	482	24	Y	T	0.37
GOLF	18-771-302	483	24	Y	G	0.30
GOLF	18-827-53	484	24	Y	G	0.34
GOLF	18-768-318	485	24	Y	G	0.31
GOLF	18-769-26	486	24	Y	A	0.17
SLC6A3	18-709-321	487	24	Y	C	0.46
SLC6A3	18-714-280	488	24	Y	T	0.17
SLC6A3	18-843-271	489	24	Y	C	0.37
SLC6A3	18-850-265	490	24	Y	T	0.34
SLC6A3	18-853-296	491	24	Y	T	0.23
SLC6A3	18-867-331	492	24	Y	C	0.48
SLC6A3	18-877-73	493	24	Y		
SLC6A3	18-856-85	494	24	Y	C	0.42
SLC6A3	18-861-101	495	24	Y	T	0.33
PDE4b	18-635-323	496	24	Y		
PDE4b	18-636-205	497	24	Y	A	0.36
PDE4b	18-649-427	498	24	Y	C	0.46
PDE4b	18-1134-316	499	24	Y	G	0.38
PDE4b	18-633-316	500	24	Y		
COMT	18-489-425	501	24	Y		
COMT	18-492-212	502	24	Y	C	0.41
COMT	18-488-156	503	24	Y	T	0.45
COMT	18-491-266	504	24	Y	T	0.42
COMT	18-497-141	505	24	Y	T	0.43
COMT	18-503-174	506	24	Y	C	0.31
COMT	18-490-95	507	24	Y	A	0.31
NPY1R	18-699-115	508	24	Y		
NPY1R	18-1099-293	509	24	Y		
NPY1R	18-1105-22	510	24	Y		
SLC1	18-562-418	511	24	Y	C	0.49
SLC1	18-564-204	512	24	Y	C	0.496
SEF2-1B	18-1032-262	513	24	Y	C	0.33
SEF2-1B	18-1035-412	514	24	Y	C	0.50
SEF2-1B	18-1036-293	515	24	Y	C	0.34
SEF2-1B	18-1038-95	516	24	Y	T	0.34
SEF2-1B	18-1040-361	517	24	Y	G	0.44
SEF2-1B	18-748-356	518	24	Y	T	0.47
BDNF	18-937-181	519	24	Y	A	0.26
BDNF	18-942-175	520	24	Y	T	0.29
BDNF	18-1213-221	521	24	Y		
BDNF	18-937-147	522	24	Y		
BDNF	18-946-408	523	24	Y	C	0.20
GAP43	18-787-133	524	24	Y	A	0.39
GAP43	18-1149-239	525	24	Y	A	0.49

**TABLE 7D (cont)**

GAP43	18-1159-291	526	24	Y	G	0.23
GAP43	18-1135-273	527	24	Y	T	0.43
GAP43	18-1136-108	528	24	Y		
GAP43	18-1147-68	529	24	Y		
GAP43	18-1157-295	530	24	Y		
GAP43	18-802-460	531	24	Y	A	0.32
CLOCK	18-1064-110	532	24	Y	C	0.36
CLOCK	18-1068-327	533	24	Y	T	0.32
CLOCK	18-1069-365	534	24	Y	A	0.23
CLOCK	18-1073-367	535	24	Y	A	0.35
CLOCK	18-1070-272	536	24	Y	T	0.36
CLOCK	18-1057-35	537	24	Y		
CLOCK	18-1062-415	538	24	Y		
CLOCK	18-1082-165	539	24	Y		
CLOCK	18-1080-361	540	24	Y	C	0.18
HSP70	18-506-297	541	24	Y		
HSP70	18-570-38	542	24	Y		

**TABLE 8**

SEQ ID NO.	BIALLELIC MARKER ID	1 <sup>ST</sup> ALLELE	2 <sup>ND</sup> ALLELE	POSITION RANGE OF PREFERRED SEQUENCE
12	99-28149-118	C	T	[1-478]
13	99-28160-285	A	G	[1-456]
14	99-28171-458	A	G	[1-48],[141-514]
15	99-28173-395	C	T	[1-550]
16	99-32177-113	C	T	[1-466]
17	99-32181-192	C	T	[1-449]
18	99-32193-258	G	T	[1-458]
20	99-28730-351	A	G	[1-452]
21	99-32306-409	G	C	[1-455]
28	99-27097-83	C	T	[1-273]
29	99-27098-162	C	T	[226-421]
32	99-27561-106	A	G	[1-465]
33	99-27562-366	G	T	[1-470]
35	99-27110-301	G	C	[1-455]
37	99-27573-443	G	T	[1-513]
38	99-28732-133	A	G	[1-411]
40	99-28736-399	C	T	[1-453]
41	99-28738-319	C	T	[1-458]
42	99-28739-364	C	T	[1-509]
62	18-132-368	C	T	[1-480]
64	18-12-191	A	C	[1-450]
65	18-11-137	A	G	[1-157],[348-390]
66	18-93-96	G	T	[1-454]
69	18-251-176	C	T	[104-494]
72	18-393-330	G	C	[1-93],[146-479]
73	18-394-402	A	C	[1-21],[119-518]
75	18-284-139	C	T	[146-450]
76	18-285-305	A	G	[1-520]
77	18-289-239	C	T	[1-486]
78	18-291-91	C	T	[1-453]
80	18-194-130	C	T	[1-460]
81	18-198-252	A	G	[1-316],[349-459]
82	18-242-300	A	G	[224-476]
85	99-2409-298	A	G	[117-127],[160-359],[395-711]
86	99-339-54	G	C	[1-247],[293-1514],[1544-2128],[2159-3001]
98	99-32148-315	G	C	[1-24]
108	99-32077-66	A	G	[37-63]
110	99-32376-426	A	G	[235-470]

TABLE 9A

SEQ. ID NO.	BIALLELIC MARKER ID	ORIGINAL ALLELE	ALTERNATIVE ALLELE
1	99-27199-207	T	C
2	99-27207-117	C	T
3	99-27213-53	A	G
4	99-27218-333	T	G
6	99-28109-275	G	A
7	99-28110-75	C	T
8	99-28125-81	A	C
9	99-28134-215	C	T
10	99-28137-96	A	G
11	99-32204-305	G	A
19	99-28722-90	T	C
22	99-27088-246	G	A
23	99-27090-203	G	A
24	99-27091-220	G	A
25	99-27093-145	T	C
26	99-27094-406	T	C
27	99-27096-410	G	A
30	99-27550-48	A	G
31	99-27558-335	C	T
34	16-31-738	C	G
39	99-28735-56	C	T
43	99-27875-185	T	C
44	99-27880-176	T	C
46	99-28753-353	T	C
47	99-28755-206	A	G
48	99-32333-366	T	C
49	16-38-323	A	C
50	99-28484-179	A	T
51	99-30853-364	G	A
52	99-28485-198	G	T
53	99-30858-354	T	C
54	99-32002-313	G	A
55	18-15-366	C	T
56	18-20-174	G	A
59	18-2-192	G	T
60	99-26921-210	G	A
63	18-133-293	C	A
68	16-42-140	A	G
70	18-269-44	A	G
71	16-218-624	G	C
74	16-217-55	A	G
88	10-214-79	C	T
90	99-28779-168	T	C
91	99-28788-300	G	A



**TABLE 9B**

94	99-32059-169	T	C
95	99-32061-304	A	G
96	99-32065-303	T	G
97	99-32123-118	G	A
99	16-2-76	A	G
101	16-3-199	C	T
102	16-50-197	C	T
103	16-1-59	C	T
104	16-2-187	A	G
105	99-28761-311	A	G
106	99-28771-86	T	C
109	99-32078-466	C	T
111	99-32361-419	T	G
112	16-21-228	G	A
117	16-25-279	G	C
118	16-23-393	G	T
119	16-106-364	T	C
122	16-84-185	T	C
124	16-91-333	G	A
126	16-133-205	A	G
127	16-135-181	T	A
128	16-145-405	C	T
129	16-177-320	A	G

**TABLE 10**

SEQ ID NO.	BIALLELIC MARKER ID	1 <sup>ST</sup> ALLELE	2 <sup>ND</sup> ALLELE
5	99-28108-233	A	C
36	99-27563-400	A	G
45	99-28747-371	C	T
61	16-215-80	C	T
67	16-115-343	A	C
79	18-186-391	G	T
83	8-15-126	A	G
87	12-254-180	A	G
92	99-32052-262	C	T
93	99-32121-242	A	G
100	16-28-93	A	C
107	99-28791-291	A	G
113	16-22-156	C	T
114	16-23-404	A	G
115	16-24-175	A	C
116	16-25-286	C	T
120	16-16-285	C	T
121	16-17-121	C	T
123	16-87-74	A	G
125	16-128-142	C	G
130	16-4-354	C	T

**TABLE 11**

SEQ. ID NO.	POSITION RANGE OF PREFERRED SEQUENCE
1	[103-147]
7	[1-25]
8	[508-518]
9	[398-432]
10	[295-364]
11	[301-342]
23	[246-287]
25	[369-413]
30	[126-153],[182-468]
31	[271-313],[443-452]
34	[408-461]
39	[147-235],[438-457]
43	[498-549]
46	[432-448]
49	[263-320]
54	[472-489]
59	[280-321]
63	[486-505]
71	[258-437],[669-927]
74	[90-165]
79	[1-82],[150-191]
83	[1-16],[144-498],[620-800],[1300-1366], [1823-1908],[2336-2365],[2398-3001]
88	[1-1297],[1998-2689],[2895-2965]
92	[255-348],[493-499]
93	[445-467]
94	[1-16],[396-438]
96	[246-288]
97	[1-91],[420-541]
111	[443-457]
121	[130-181]
122	[160-399]
123	[144-145],[351-435]
128	[283-551]
129	[375-458]

**TABLE 12**

SEQ ID NO.	POSITION RANGE OF MICROSEQUENCING PRIMERS	COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS
1	188-206*	208-227
2	98-116*	118-136*
3	34-52*	54-73
4	314-332*	334-353
5	214-232*	234-253
6	255-274	276-295
7	54-73	75-94
8	62-80*	82-101
9	196-214*	216-235
10	77-95*	97-116
11	285-304	306-325
12	98-117	119-137*
13	266-284*	286-305
14	438-456*	458-477
15	375-394	396-414*
16	93-112	114-132*
17	172-191	193-212
18	238-256*	258-277
19	71-89*	91-110
20	332-350*	352-370*
21	387-406	408-427
22	226-245	247-266
23	185-203*	205-224
24	201-220	222-241
25	125-144	146-165
26	387-405*	407-426
27	390-409	411-430
28	63-82	84-103
29	142-161	163-182
30	28-47	49-67*
31	316-334*	336-355
32	87-105*	107-126
33	344-363	365-384
34	715-737*	739-761*
35	281-299*	301-319*
36	381-399*	401-420
37	423-442	444-462*
38	114-132*	134-153
39	36-55	57-76
40	379-398	400-418*
41	299-318	320-338*
42	345-363*	365-384
43	165-184	186-204*

**TABLE 12 (cont)**

44	156-175	177-195*
45	353-372	374-392*
46	332-351	353-371*
47	187-206	208-226*
48	346-365	367-386
49	300-322*	324-346*
50	160-178*	180-199
51	345-363*	365-384
52	179-197*	199-217*
53	334-353	355-373*
54	292-310*	312-331
55	347-365*	367-385*
56	155-173*	175-194
57	158-177	179-197*
58	375-394	396-414*
59	172-191	193-211*
60	192-210*	212-231
61	231-249*	251-270
62	348-367	369-387*
63	273-291*	293-311*
64	172-190*	192-210*
65	118-137	139-157*
66	77-95*	97-115*
67	320-342*	344-366*
68	121-139*	141-163*
69	157-175*	177-196
70	25-43*	45-64
71	601-623*	625-644
72	311-329*	331-349*
73	382-401	403-421*
74	32-54*	56-74*
75	120-138*	140-159
76	286-304*	306-325
77	219-238	240-258*
78	71-90	92-110*
79	371-390	392-410*
80	110-129	131-149*
81	233-251*	253-272
82	280-298*	300-319
83	1481-1500	1502-1520*
84	1481-1500	1502-1520*
85	408-427	429-447*
86	1482-1500*	1502-1521
87	292-310*	312-331
88	1482-1500*	1502-1521
89	1482-1500*	1502-1521
90	149-167*	169-187*

**TABLE 12 (cont.)**

91	281-299*	301-320
92	244-262*	264-282*
93	225-243*	245-264
94	149-168	170-189
95	285-303*	305-324
96	284-302*	304-322*
97	99-117*	119-138
98	294-313	315-333*
99	76-94*	96-114*
100	101-119*	121-143*
101	323-341*	343-361*
102	178-196*	198-216*
103	158-180*	182-200*
104	183-205*	207-225*
105	292-310*	312-331
106	67-85*	87-106
107	272-290*	292-311
108	47-65*	67-85*
109	448-466*	468-486*
110	407-425*	427-446
111	400-419	421-439*
112	205-227*	229-251*
113	133-155*	157-175*
114	381-403*	405-427*
115	156-174*	176-194*
116	267-285*	287-305*
117	260-278*	280-298*
118	370-392*	394-416*
119	345-363*	365-383*
120	265-284	286-304*
121	102-120*	122-140*
122	162-184*	186-208*
123	51-73*	75-97*
124	310-332*	334-356*
125	123-141*	143-161*
126	222-244*	246-268*
127	209-231*	233-251*
128	436-454*	456-474*
129	297-319*	321-343*
130	335-353*	355-373*
261	343-361*	363-382
262	68-87	89-107*
263	316-334*	336-355
264	48-66*	68-87

**TABLE 12 (cont.)**

265	295-313*	315-333*
266	302-321	323-341*
267	296-314*	316-334*
268	327-345*	347-366
269	244-262*	264-282*
270	1482-1500*	1502-1521
271	115-134	136-154*
272	400-418*	420-439
273	271-289*	291-309*
274	237-255*	257-276
275	48-67	69-87*
276	246-265	267-285*
277	287-305*	307-326
278	1482-1500*	1502-1521
279	1482-1500*	1502-1521
280	1482-1500*	1502-1521
281	225-244	246-264*
282	271-290	292-310*
283	327-345*	347-366
284	387-405*	407-426
285	319-337*	339-357*
286	91-109*	111-130
287	85-103*	105-124
288	12-30*	32-50*
289	323-341*	343-362
290	121-139*	141-160
291	160-178*	180-199
292	304-322*	324-343
293	50-69	71-89*
294	422-441	443-461*
295	46-64*	66-85
296	181-199*	201-220
297	314-333	335-353*
298	313-331*	333-352
299	358-377	379-397*
300	288-306*	308-327
301	99-117*	119-138
302	119-137*	139-158
303	72-91	93-111*
304	368-386*	388-407
305	397-415*	417-436
306	127-145*	147-165*
307	1481-1500	1482-1500*
308	1481-1500	1502-1520*
309	250-269	271-289*
310	146-164*	166-184*
311	105-123*	125-144
312	199-218	220-238*
313	293-311*	313-331*
314	349-367*	369-388
315	206-224*	226-245
316	56-74*	76-95
317	1482-1500*	1502-1521

**TABLE. 12 (cont.)**

318	156-174*	176-194*
319	328-347	349-367*
320	332-351	353-371*
321	461-479*	481-500
322	175-193*	195-214
323	265-283*	285-304
324	33-51*	53-72
325	169-188	190-208*
326	51-70	72-90*
327	106-125	127-145*
328	40-58*	60-79
329	7-26	28-46*
330	184-202*	204-223
331	70-88*	90-108*
332	302-320*	322-341
333	50-68*	70-89
334	39-57*	59-77*
335	197-215*	217-236
336	414-432*	434-452*
337	66-84*	86-105
338	368-386*	388-407
339	239-258	260-278*
340	252-270*	272-291
341	175-193*	195-213*
342	283-301*	303-321*
343	33-52	54-72*
344	299-317*	319-338
345	6-25	27-45*
346	300-319	321-339*
347	262-280*	282-300*
348	252-270*	272-290*
349	246-264*	266-284*
350	277-295*	297-315*
351	313-331*	333-352
352	54-72*	74-93
353	66-84*	86-104*
354	82-100*	102-120*
355	304-322*	324-343
356	186-204*	206-225
357	408-426*	428-447
358	297-315*	317-336
359	297-315*	317-336
360	406-424*	426-445
361	193-211*	213-231*
362	137-155*	157-175*
363	247-265*	267-285*
364	122-140*	142-160*
365	155-173*	175-194
366	75-94	96-114*
367	95-113*	115-134
368	274-292*	294-312*
369	3-21*	23-42
370	399-417*	419-438



**TABLE 12 (cont.)**

371	185-203*	205-224
372	242-260*	262-281
373	393-411*	413-431*
374	274-292*	294-313
375	75-94	96-114*
376	342-360*	362-381
377	336-355	357-375*
378	160-178*	180-198*
379	156-174*	176-195
380	202-220*	222-241
381	126-144*	146-165
382	387-406	408-426*
383	113-132	134-152*
384	220-238*	240-259
385	272-290*	292-311
386	254-272*	274-293
387	89-107*	109-128
388	49-67*	69-88
389	276-294*	296-315
390	440-458*	460-479
391	89-108	110-128*
392	307-326	328-346*
393	345-364	366-384*
394	348-366*	368-387
395	253-271*	273-292
396	16-34*	36-54*
397	396-414*	416-435
398	146-164*	166-185
399	343-362	364-382*
400	278-296*	298-317
401	19-37*	39-58

**TABLE 13**

SEQ ID NO.	POSITION RANGE OF AMPLIFICATION PRIMERS	COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS
1	1-20	431-450
2	1-21	432-452
3	1-18	446-464
4	1-20	528-546
5	1-18	394-413
6	1-18	434-454
7	1-18	530-549
8	1-18	500-518
9	1-20	453-472
10	1-18	529-546
11	1-20	384-401
12	1-19	459-478
13	1-19	439-456
14	1-18	494-514
15	1-18	532-550
16	1-19	446-466
17	1-18	432-449
18	1-19	438-458
19	1-17	429-449
20	1-18	435-451
21	1-18	437-454
22	1-19	510-527
23	1-20	431-451
24	1-20	455-473
25	1-20	453-472
26	1-20	436-455
27	1-18	432-450
28	1-18	486-504
29	1-19	404-421
30	1-19	448-468
31	1-18	432-452
32	1-19	446-465
33	1-19	450-470
34	1-25	975-1003
35	1-18	438-455
36	1-18	526-546
37	1-18	496-513
38	1-19	391-410
39	1-19	438-456
40	1-20	434-452
41	1-18	441-457
42	1-17	489-508
43	1-18	531-549

**TABLE 13 (cont)**

44	1-18	444-462
45	1-19	478-496
46	1-20	427-447
47	1-17	452-470
48	1-20	520-540
49	1-28	389-416
50	1-17	488-505
51	1-17	465-485
52	1-17	449-466
53	1-17	456-473
54	1-19	472-488
55	1-20	507-525
56	1-17	408-425
57	1-19	437-457
58	1-19	456-473
59	1-19	450-468
60	1-21	431-451
61	171-188	284-303
62	1-18	461-479
63	1-17	487-504
64	1-18	431-449
65	1-18	516-535
66	1-17	436-453
67	1-24	533-553
68	1-18	154-171
69	1-19	474-493
70	1-17	457-477
71	1-22	906-927
72	1-18	459-479
73	1-20	500-518
74	1-20	568-587
75	1-17	430-449
76	1-17	499-519
77	1-17	466-485
78	1-17	432-452
79	1-18	442-459
80	1-17	439-459
81	1-17	438-458
82	1-17	455-475
83	1376-1395	1792-1810
84	1130-1148	1534-1552
85	131-148	560-580
86	1448-1467	1883-1902
87	132-152	586-603
88	1225-1244	1747-1764
89	1414-1430	1759-1775
90	1-17	390-409

**TABLE 13 (cont)**

91	1-17	458-478
92	1-18	478-498
93	1-17	448-466
94	1-17	448-468
95	1-19	430-449
96	1-17	469-486
97	1-20	520-540
98	1-18	428-448
99	20-39	240-260
100	28-47	354-374
101	143-162	374-393
102	1-20	227-245
103	123-142	290-309
104	20-39	240-260
105	1-18	446-465
106	1-18	444-461
107	1-18	432-451
108	1-18	471-488
109	1-17	470-488
110	1-18	449-469
111	1-18	442-456
112	1-25	399-424
113	1-24	458-481
114	1-26	455-478
115	1-22	405-428
116	1-22	412-433
117	1-22	412-433
118	1-26	455-478
119	1-22	723-742
120	1-19	516-535
121	1-19	508-529
122	1-22	525-540
123	1-22	504-525
124	1-19	641-665
125	1-20	308-327
126	41-59	472-490
127	52-71	482-501
128	51-69	523-540
129	1-22	472-492
130	1-20	740-759
261	1-21	482-502
262	1-21	438-457
263	1-20	482-502
264	1-19	441-461
265	1-18	428-448
266	1-19	409-426
267	1-19	403-422
268	1-19	401-419
269	1-18	478-498

**TABLE 13(cont.)**

270	1211-1229	1588-1606
271	1-18	448-465
272	1-20	507-527
273	1-18	434-451
274	1-17	466-486
275	1-19	436-453
276	1-18	452-471
277	1-18	450-468
278	1156-1173	1652-1672
279	1149-1166	1591-1608
280	1170-1187	1635-1652
281	1-18	440-460
282	1-18	433-453
283	1-17	538-558
284	1-17	450-467
285	1-18	439-456
286	1-18	439-456
287	1-20	431-451
288	1-20	431-451
289	1-20	431-451
290	1-19	458-476
291	1-18	497-517
292	1-18	419-436
293	1-17	487-504
294	1-17	443-463
295	1-18	438-455
296	1-18	463-483
297	1-20	464-484
298	1-19	439-456
299	1-18	458-478
300	1-18	443-463
301	1-18	442-460
302	1-18	457-475
303	1-18	515-533
304	1-18	443-463
305	1-19	434-451
306	1-21	430-450
307	1263-1281	1694-1711
308	1114-1133	1516-1533
309	1-19	481-498
310	1-18	447-467
311	1-20	444-463
312	1-19	534-551
313	1-19	437-457
314	1-19	459-477
315	1-19	486-502
316	1-18	432-452
317	1171-1189	1702-1719
318	1-18	476-493
319	1-20	430-450
320	1-20	455-475
321	1-21	489-509
322	1-21	457-477

**TABLE 13 (cont.)**

323	1-19	430-450
324	1-21	485-505
325	1-20	466-486
326	1-21	437-457
327	1-19	497-517
328	1-20	495-514
329	1-20	450-470
330	1-18	456-476
331	1-20	433-453
332	1-19	435-455
333	1-19	544-561
334	1-18	442-459
335	1-20	434-453
336	1-21	514-534
337	1-20	464-483
338	1-21	580-597
339	1-18	441-461
340	1-20	430-450
341	1-18	479-496
342	1-21	461-481
343	1-21	429-449
344	1-21	409-429
345	1-21	430-450
346	1-20	433-453
347	1-19	495-514
348	1-20	433-451
349	1-20	443-460
350	1-20	440-459
351	1-18	445-463
352	1-18	432-449
353	1-19	430-450
354	1-19	462-480
355	1-21	445-465
356	1-18	473-493
357	1-18	570-589
358	1-20	412-432
359	1-20	412-432
360	1-20	515-533
361	1-20	465-485
362	1-18	550-570
363	1-20	430-450
364	1-21	416-435
365	1-20	455-475
366	1-20	481-501
367	1-21	428-448
368	1-19	459-478
369	1-18	456-476
370	1-20	475-495
371	1-18	456-476
372	1-20	447-467
373	1-21	447-466
374	1-18	467-484
375	1-18	466-484

**TABLE 13 (cont.)**

376	1-19	437-455
377	1-20	383-403
378	1-20	428-448
379	1-20	431-449
380	1-18	434-452
381	1-20	428-448
382	1-19	453-473
383	1-21	480-497
384	1-21	532-552
385	1-20	480-500
386	1-18	429-449
387	1-21	433-450
388	1-21	430-450
389	1-21	576-595
390	1-21	549-569
391	1-18	438-455
392	1-19	496-516
393	1-19	455-472
394	1-20	441-458
395	1-19	455-475
396	1-18	449-469
397	1-18	557-577
398	1-18	433-453
399	1-18	475-494
400	1-20	491-511
401	1-21	380-400

**TABLE 14**

SEQ ID NO.	POSITION RANGE OF PROBES
1	195-219
2	105-129
3	41-65
4	321-345
5	221-245
6	263-287
7	62-86
8	69-93
9	203-227
10	84-108
11	293-317
12	106-130
13	273-297
14	445-469
15	383-407
16	101-125
17	180-204
18	245-269
19	78-102
20	339-363
21	395-419
22	234-258
23	192-216
24	209-233
25	133-157
26	394-418
27	398-422
28	71-95
29	150-174
30	36-60
31	323-347
32	94-118
33	352-376
34	726-750
35	288-312
36	388-412
37	431-455
38	121-145
39	44-68
40	387-411
41	307-331
42	352-376
43	173-197
44	164-188
45	361-385



**TABLE 14 (cont.)****TABLE 14 (cont.)**

46	340-364
47	195-219
48	354-378
49	311-335
50	167-191
51	352-376
52	186-210
53	342-366
54	299-323
55	354-378
56	162-186
57	166-190
58	383-407
59	180-204
60	199-223
61	238-262
62	356-380
63	280-304
64	179-203
65	126-150
66	84-108
67	331-355
68	128-152
69	164-188
70	32-56
71	612-636
72	318-342
73	390-414
74	43-67
75	127-151
76	293-317
77	227-251
78	79-103
79	379-403
80	118-142
81	240-264
82	287-311
83	1489-1513
84	1489-1513
85	416-440
86	1489-1513
87	299-323
88	1489-1513
89	1489-1513
90	156-180
91	288-312
92	251-275
93	232-256
94	157-181
95	292-316
96	291-315
97	106-130

**TABLE 14 (cont.)**

98	302-326
99	83-107
100	108-132
101	330-354
102	185-209
103	169-193
104	194-218
105	299-323
106	74-98
107	279-303
108	54-78
109	455-479
110	414-438
111	408-432
112	216-240
113	144-168
114	392-416
115	163-187
116	274-298
117	267-291
118	381-405
119	352-376
120	273-297
121	109-133
122	173-197
123	62-86
124	321-345
125	130-154
126	233-257
127	220-244
128	443-467
129	308-332
130	342-366
261	350-374
262	76-100
263	323-347
264	55-79
265	302-326
266	310-334
267	303-327
268	334-358
269	251-275
270	1489-1513
271	123-147
272	407-431
273	278-302
274	244-268
275	56-80
276	254-278
277	294-318
278	1489-1513
279	1489-1513
280	1489-1513

**TABLE 14 (cont.)**

281	233-257
282	279-303
283	334-358
284	394-418
285	326-350
286	98-122
287	92-116
288	19-43
289	330-354
290	128-152
291	167-191
292	311-335
293	58-82
294	430-454
295	53-77
296	188-212
297	322-346
298	320-344
299	366-390
300	295-319
301	106-130
302	126-150
303	80-104
304	375-399
305	404-428
306	134-158
307	1489-1513
308	1489-1513
309	258-282
310	153-177
311	112-136
312	207-231
313	300-324
314	356-380
315	213-237
316	63-87
317	1489-1513
318	163-187
319	336-360
320	340-364
321	468-492
322	182-206
323	272-296
324	40-64
325	177-201
326	59-83
327	114-138
328	47-71
329	15-39
330	191-215
331	77-101
332	309-333
333	57-81

334	46-70
335	204-228
336	421-445
337	73-97
338	375-399
339	247-271
340	259-283
341	182-206
342	290-314
343	41-65
344	306-330
345	14-38
346	308-332
347	269-293
348	259-283
349	253-277
350	284-308
351	320-344
352	61-85
353	73-97
354	89-113
355	311-335
356	193-217
357	415-439
358	304-328
359	304-328
360	413-437
361	200-224
362	144-168
363	254-278
364	129-153
365	162-186
366	83-107
367	102-126
368	281-305
369	10-34
370	406-430
371	192-216
372	249-273
373	400-424
374	281-305
375	83-107
376	349-373
377	344-368
378	167-191
379	163-187
380	209-233
381	133-157
382	395-419
383	121-145
384	227-251
385	279-303
386	261-285

**TABLE 14 (cont.)**

387	96-120
388	56-80
389	283-307
390	447-471
391	97-121
392	315-339
393	353-377
394	355-379
395	260-284
396	23-47
397	403-427
398	153-177
399	351-375
400	285-309
401	26-50

TABLE 15

Gene	Marker	Allele 1	Allele 2	Allele 1 Frequencies		Genotype Frequencies										Numbers	
				Cases	Control s	p-value	Cases			Control s			p-value	Cases	Control s		
							11	12	22	11	12	22					
5HTR6	99-27199/207	C	T	0.72	0.70	0.71		0.51	0.41	0.08	0.48	0.45	0.07	0.83	140	94	
5HTR6	99-27207/117	C	T	0.48	0.37	0.02		0.24	0.47	0.29	0.13	0.47	0.40	0.06	139	93	
5HTR6	99-28110/75	C	T	0.64	0.52	0.01		0.41	0.45	0.14	0.27	0.51	0.22	0.05	139	90	
5HTR6	99-28134/215	C	T	0.51	0.63	0.01		0.26	0.50	0.24	0.42	0.43	0.15	0.04	138	93	
5HTR7	99-28160/285	A	G	0.49	0.51	0.73		0.27	0.44	0.29	0.24	0.53	0.23	0.37	140	91	
5HTR7	99-28171/458	A	G	0.34	0.38	0.44		0.13	0.42	0.45	0.17	0.42	0.41	0.74	136	90	
5HTR7	99-28173/395	C	T	0.51	0.55	0.33		0.27	0.47	0.26	0.27	0.57	0.16	0.18	137	94	
5HTR7	99-32181/192	C	T	0.28	0.38	0.02		0.09	0.38	0.54	0.13	0.51	0.36	0.04	136	85	
5HTR7	99-32193/258	G	T	0.70	0.65	0.26		0.53	0.34	0.12	0.41	0.48	0.11	0.12	137	85	
CHRNA7	99-28722/80	C	T	0.27	0.32	0.27		0.00	0.54	0.46	0.01	0.62	0.37	0.22	140	94	
CHRNA7	99-28730/351	A	G	0.32	0.38	0.17		0.04	0.55	0.41	0.03	0.69	0.28	0.09	139	94	
CHRNA7	99-32306/409	C	G	0.62	0.67	0.31		0.26	0.72	0.01	0.34	0.66	0.00	0.25	137	91	
CRFR1	99-27088/246	A	G	0.42	0.38	0.31		0.20	0.44	0.36	0.15	0.45	0.40	0.57	138	93	
CRFR1	99-27091/220	A	G	0.44	0.49	0.32		0.19	0.50	0.31	0.24	0.50	0.26	0.59	137	92	
CRFR1	99-27097/83	C	T	0.55	0.53	0.73		0.34	0.41	0.24	0.26	0.56	0.19	0.11	140	90	
CRFR1	99-27550/48	A	G	0.20	0.26	0.17		0.04	0.32	0.64	0.07	0.38	0.55	0.38	138	91	
MLR	19-26/204/A23	C	G	0.55	0.53	0.70		0.28	0.55	0.18	0.28	0.50	0.22	0.69	137	92	
MLR	99-27563/400	A	G	0.46	0.44	0.79		0.19	0.54	0.28	0.21	0.46	0.33	0.54	138	89	
MLR	99-28732/133	A	G	0.39	0.31	0.09		0.16	0.47	0.37	0.09	0.44	0.47	0.23	137	86	
MLR	99-28735/56	C	T	0.71	0.70	0.87		0.50	0.41	0.09	0.50	0.40	0.10	0.93	136	88	
CRFR2	99-27875/185	C	T	0.36	0.40	0.30		0.16	0.39	0.45	0.16	0.49	0.35	0.25	140	94	
CRFR2	99-27880/176	C	T	0.53	0.56	0.47		0.30	0.46	0.24	0.32	0.47	0.20	0.76	139	93	
CRFR2	99-28747/371	C	T	0.39	0.44	0.34		0.16	0.47	0.37	0.23	0.42	0.35	0.39	138	91	
CRFR2	99-28755/206	A	G	0.56	0.59	0.65		0.32	0.50	0.19	0.37	0.44	0.19	0.68	139	93	

TABLE 15 (cont.)

GRL	99-30853/364	A	G	0.56	0.58	0.62	0.35	0.41	0.24	0.39	0.39	0.23	0.87	139	93
GRL	99-30858/354	C	T	0.76	0.84	0.04	0.59	0.34	0.06	0.71	0.27	0.02	0.13	140	89
GRL	99-28485/198	G	T	0.19	0.20	0.68	0.04	0.30	0.66	0.01	0.38	0.61	0.25	134	89
GRL	99-32002/313	A	G	0.48	0.48	0.97	0.23	0.51	0.26	0.16	0.65	0.19	0.10	140	94
GRL	18-20/174	A	G	0.76	0.73	0.38	0.57	0.39	0.04	0.53	0.39	0.07	0.55	140	94
GRL	18-31/178	C	T	0.30	0.35	0.21	0.11	0.38	0.51	0.15	0.40	0.45	0.49	140	94
GRL	18-38/395	A	T	0.59	0.63	0.38	0.36	0.46	0.18	0.36	0.54	0.10	0.17	140	94
MAO A/B	18-2/192	G	T	0.70	0.68	0.66	0.56	0.26	0.17	0.56	0.24	0.20	0.78	140	93
MAO A/B	19-25/407	C	T	0.67	0.67	1.00	0.54	0.26	0.20	0.54	0.24	0.21	0.96	138	90
MAO A/B	99-28921/210	A	G	0.48	0.52	0.47	0.33	0.30	0.37	0.31	0.41	0.28	0.20	139	93
MAO A/B	18-133/293	A	C	0.30	0.27	0.46	0.16	0.29	0.55	0.14	0.26	0.60	0.77	140	92
NET	19-58/140	A	G	0.34	0.27	0.11	0.12	0.44	0.44	0.02	0.49	0.48	0.03	134	93
NET	19-14/241	C	T	0.35	0.32	0.64	0.12	0.46	0.43	0.10	0.45	0.45	0.88	136	91
NET	19-28/136	A	C	0.68	0.56	0.01	0.44	0.48	0.08	0.28	0.57	0.15	0.02	140	93
NET	19-44/251	C	T	0.24	0.21	0.40	0.09	0.31	0.60	0.02	0.38	0.60	0.11	140	93
NET	99-28788/300	A	G	0.49	0.47	0.65	0.22	0.54	0.24	0.21	0.51	0.28	0.85	140	94
NET	99-32081/304	A	G	0.41	0.39	0.71	0.16	0.51	0.34	0.14	0.51	0.35	0.92	140	94
NET	99-32121/242	A	G	0.61	0.52	0.07	0.36	0.49	0.15	0.29	0.47	0.24	0.16	140	94
TACR1	99-28761/311	A	G	0.25	0.22	0.38	0.07	0.36	0.56	0.01	0.41	0.57	0.09	140	94
TACR1	99-28771/86	C	T	0.48	0.52	0.33	0.24	0.46	0.29	0.23	0.57	0.19	0.16	140	94
TACR1	99-28791/291	A	G	0.28	0.26	0.58	0.09	0.39	0.53	0.04	0.43	0.53	0.42	140	94
TACR1	99-32361/419	G	T	0.53	0.52	0.79	0.29	0.49	0.23	0.26	0.52	0.22	0.84	140	94
DRD3	8-15/126	A	G	0.64	0.70	0.16	0.43	0.42	0.15	0.47	0.47	0.06	0.13	140	94
DRD3	8-19/372	A	G	0.23	0.28	0.22	0.09	0.29	0.62	0.03	0.50	0.47	0.004	140	94
DRD3	99-2409/298	A	G	0.36	0.40	0.30	0.14	0.44	0.42	0.11	0.60	0.30	0.07	140	94
DRD3	99-339/54	C	G	0.55	0.54	0.93	0.34	0.42	0.24	0.28	0.53	0.19	0.25	140	94
CYP3A4	12-254/180	A	G	0.43	0.54	0.02	0.19	0.47	0.34	0.32	0.45	0.23	0.06	140	94
CYP3A4	10-214/279	C	T	0.14	0.12	0.55	0.02	0.23	0.75	0.02	0.19	0.79	0.79	140	94
CYP3A4	10-217/91	C	T	0.89	0.93	0.16	0.79	0.19	0.02	0.86	0.13	0.01	0.39	140	94

TABLE 15 (cont)

5HTT	18-194/130	C	T	0.54	0.52	0.67	0.31	0.44	0.24	0.20	0.63	0.17	0.02	140	94
5HTT	18-198/252	A	G	0.52	0.49	0.57	0.29	0.47	0.24	0.20	0.59	0.21	0.20	140	94
5HTT	18-242/300	A	G	0.46	0.54	0.09	0.24	0.44	0.32	0.27	0.54	0.19	0.09	140	94
5HTT	18-186/391	G	T	0.50	0.53	0.52	0.27	0.45	0.28	0.26	0.54	0.20	0.31	140	94
DRD2	19-23/215	A	G	0.21	0.16	0.24	0.05	0.31	0.64	0.04	0.24	0.72	0.44	139	93
DRD2	19-5/377	A	G	0.55	0.53	0.76	0.30	0.50	0.20	0.26	0.55	0.19	0.78	139	93
DRD2	19-6/171	A	C	0.22	0.16	0.15	0.06	0.32	0.62	0.04	0.24	0.72	0.34	138	92
DRD2	19-7/275	C	T	0.70	0.63	0.12	0.49	0.43	0.08	0.38	0.52	0.11	0.24	135	93
DRD2	19-4/118	C	T	0.46	0.45	0.79	0.21	0.50	0.29	0.17	0.56	0.27	0.63	140	93
Gbeta3	19-58/162	C	T	0.70	0.62	0.07	0.49	0.42	0.09	0.36	0.51	0.13	0.16	139	91
Gbeta3	19-9/45	C	T	0.71	0.64	0.12	0.49	0.43	0.08	0.40	0.47	0.13	0.28	139	92
Gbeta3	19-88/185	C	T	0.43	0.40	0.50	0.24	0.38	0.38	0.25	0.29	0.46	0.41	133	82
Gbeta3	19-22/74	A	G	0.33	0.34	0.79	0.09	0.49	0.43	0.14	0.40	0.46	0.30	140	94
Gbeta3	20-205/302	C	T	0.94	0.99	0.002	0.88	0.12	0.00	0.99	0.01	0.00	0.002	140	94
WFS1	19-19/174	C	T	0.43	0.36	0.15	0.17	0.51	0.32	0.11	0.51	0.39	0.30	139	94
WFS1	19-16/127	C	G	0.33	0.27	0.19	0.09	0.49	0.43	0.05	0.44	0.51	0.38	140	94
WFS1	19-17/188	A	G	0.58	0.66	0.07	0.32	0.51	0.16	0.43	0.46	0.11	0.18	140	93
WFS1	19-18/310	A	G	0.14	0.07	0.04	0.02	0.23	0.75	0.01	0.13	0.86	0.12	140	94
TH	19-15/324	A	C	0.69	0.76	0.10	0.51	0.37	0.12	0.60	0.32	0.08	0.31	132	91
TH	18-251/176	C	T	0.58	0.57	0.87	0.36	0.44	0.20	0.29	0.57	0.14	0.11	140	94
TH	18-269/44	A	G	0.36	0.38	0.71	0.11	0.51	0.39	0.15	0.46	0.39	0.58	140	94
5HTR2c	18-12/191	A	C	0.15	0.14	0.73	0.66	0.17	0.77	0.03	0.21	0.76	0.40	137	94



**TABLE 16A**

OMNIBUS LR RANK of HAPLOTYPES

OMNIBUS LR Rank of 4-locus combinations

Gene	Cases	Controls	Marker1	Marker2	Marker3	Marker4	p-value	-log p-value
NET	Genset	Argent	19-56/140	99-28788/300	99-32061/304	99-32121/242	0.001	3.00
NET	Genset	Argent	19-28/136	99-28788/300	99-32061/304	99-32121/242	0.001	3.00
Gbeta3	Genset	Argent	19-58/162	19-9/45	19-22/74	20-205/302	0.002	2.70
NET	Genset	Argent	16-3/199	19-28/136	99-32061/304	99-32121/242	0.002	2.70
Gbeta3	Genset	Argent	19-58/162	19-9/45	19-88/185	20-205/302	0.003	2.52
NET	Genset	Argent	19-56/140	19-28/136	99-32061/304	99-32121/242	0.003	2.52
NET	Genset	Argent	19-56/140	16-3/199	99-32061/304	99-32121/242	0.005	2.30
NET	Genset	Argent	19-28/136	16-50/196	99-32061/304	99-32121/242	0.010	2.00
5HTT	Genset	Argent	18-186/391	18-194/130	18-198/252	18-242/300	0.013	1.89
NET	Genset	Argent	19-56/140	16-50/196	99-32061/304	99-32121/242	0.014	1.85

92 total combinations

**TABLE 16B**

OMNIBUS LR Rank of 3-locus combinations

Gene	Cases	Controls	Marker1	Marker2	Marker3	Marker4	p-value	-log p-value
Gbeta3	Genset	Argent	19-58/162	19-9/45	20-205/302	0	0.0001	4.00
WFS1	Genset	Argent	19-19/174	19-17/188	19-18/310	0	0.0003	3.55
NET	Genset	Argent	16-3/199	19-28/136	16-50/196	0	0.0009	3.05
NET	Genset	Argent	19-28/136	99-32061/304	99-32121/242	0	0.001	3.00
WFS1	Genset	Argent	19-19/174	19-16/127	19-17/188	0	0.001	3.00
Gbeta3	Genset	Argent	19-58/162	19-22/74	20-205/302	0	0.002	2.70
NET	Genset	Argent	99-28788/300	99-32061/304	99-32121/242	0	0.002	2.70
NET	Genset	Argent	19-56/140	99-32061/304	99-32121/242	0	0.004	2.40
NET	Genset	Argent	16-3/199	19-28/136	16-50/196	0	0.004	2.40
Gbeta3	Genset	Argent	19-9/45	19-22/74	20-205/302	0	0.006	2.22

136 total combinations

**TABLE 16 C**

OMNIBUS LR Rank of 2-locus combinations

Gene	Cases	Controls	Marker1	Marker2	Marker3	Marker4	p-value	-log p-value
Gbeta3	Genset	Argent	19-58/162	20-205/302	0	0	0.00003	4.52
WFS1	Genset	Argent	19-19/174	19-17/188	0	0	0.00021	3.68
Gbeta3	Genset	Argent	19-9/45	20-205/302	0	0	0.001	3.00
NET	Genset	Argent	99-32061/304	99-32121/242	0	0	0.003	2.52
Gbeta3	Genset	Argent	19-22/74	20-205/302	0	0	0.006	2.22
5HTR7	Genset	Argent	99-28106/185	99-32181/192	0	0	0.007	2.15
DRD3	Genset	Argent	8-15/126	99-2409/298	0	0	0.014	1.87
Gbeta3	Genset	Argent	19-88/185	20-205/302	0	0	0.014	1.85
5HTR7	Genset	Argent	99-32181/192	99-32193/258	0	0	0.015	1.82
5HTT	Genset	Argent	18-186/394	18-242/300	0	0	0.016	1.80

125 total combinations

**TABLE 17A**

Rank of Permutation Tests for Individual Haplotypes

4-Locus Combination

EM Methods										Permutation Test				Omnibus LR		
Gene	Marker1	Marker2	Marker3	Marker4	Haplo type	Case	Control	Difference	Odds Ratio	Chi-Square	number	p-value	-log p-value	LR statistic	p-value	-log p-value
NET	19-58/140	19-14/241	19-28/136	18-50/198	GTCT	0.28	0.41	-0.13	0.56	4.02	100000	0.002	2.61	19.59	0.075	1.12
GRL	18-20/174	99-32002/313	18-31/178	18-38/395	AGCA	0.06	0.17	-0.12	0.28	8.19	100000	0.003	2.57	16.09	0.360	0.44
GRL	18-20/174	18-31/178	18-38/395	99-30858/354	GTAC	0.11	0.22	-0.10	0.46	4.56	100000	0.003	2.55	25.70	0.045	1.35
GRL	18-20/174	18-38/395	99-30853/364	99-30858/354	GAAC	0.03	0.12	-0.09	0.26	6.37	1000	0.003	2.52	21.83	0.078	1.11
GRL	99-32002/313	18-31/178	18-38/395	99-30858/354	GCAC	0.06	0.14	-0.09	0.36	4.91	1000	0.003	2.52	20.00	0.159	0.80
GRL	99-32002/313	18-31/178	18-38/395	99-30858/354	GTAT	0.13	0.05	0.09	3.26	4.77	1000	0.003	2.52	20.00	0.159	0.80
5HTT	18-198/391	18-194/130	18-198/252	18-242/300	GCAA	0.02	0.08	-0.06	0.27	4.13	1000	0.003	2.52	25.66	0.013	1.89
NET	19-28/136	99-28788/300	99-32061/304	99-32121/242	AGGG	0.01	0.05	-0.04	0.14	4.28	1000	0.004	2.40	31.97	0.001	3.00
GRL	99-32002/313	18-31/178	99-30853/364	99-30858/354	GTAT	0.18	0.08	0.10	2.42	4.20	1000	0.004	2.38	16.19	0.314	0.50
5HTR7	99-28106/185	99-28171/458	99-28173/395	99-32181/192	AACC	0.27	0.38	-0.11	0.60	2.90	1000	0.005	2.30	13.67	0.034	1.47
NET	19-14/241	19-28/136	16-50/198	99-32061/304	TCTG	0.17	0.28	-0.11	0.53	3.88	1000	0.006	2.22	20.75	0.084	1.08
GRL	18-31/178	18-38/395	99-30853/364	99-30858/354	TAAT	0.14	0.05	0.09	3.06	4.68	1000	0.006	2.22	22.38	0.080	1.05
DRD3	8-15/126	8-19/372	99-2409/288	99-339/54	GCAG	0.06	0.01	0.06	9.29	4.64	1000	0.006	2.22	23.14	0.045	1.35
GRL	18-20/174	99-32002/313	18-38/395	99-30858/354	GAAC	0.08	0.15	-0.09	0.34	5.65	1000	0.007	2.15	18.83	0.175	0.76
NET	16-50/198	99-28788/300	99-32061/304	99-32121/242	TGGG	0.01	0.05	-0.05	0.10	5.15	1000	0.008	2.10	24.11	0.034	1.47
NET	19-58/140	18-50/196	99-28788/300	99-32121/242	ATAA	0.16	0.08	0.12	3.45	6.78	1000	0.009	2.05	19.07	0.240	0.62
NET	19-14/241	18-50/196	99-32061/304	99-32121/242	TTGG	0.00	0.06	-0.05	0.08	5.70	1000	0.009	2.05	27.52	0.053	1.28
5HTR7	99-28106/185	99-28173/395	99-32181/192	99-32193/258	ACCG	0.27	0.38	-0.11	0.60	2.65	1000	0.012	1.92	14.10	0.023	1.64
5HTR7	99-28171/458	99-28173/395	99-32181/192	99-32193/258	ACCG	0.27	0.38	-0.11	0.61	2.56	1000	0.012	1.92	10.14	0.067	1.17
NET	19-14/241	99-28788/300	99-32061/304	99-32121/242	TGGG	0.01	0.05	-0.04	0.15	3.82	1000	0.012	1.92	25.41	0.025	1.60

146 Total Haplotypes

846 Total Haplotypes

**TABLE 17B**

3-Locus Combination

EM Methods										Permutation Test				Omnibus LR		
Gene	Marker1	Marker2	Marker3	Marker4	Haployp e	Case	Control	differenc e	Odds Ratio	Chi- Square	Number	p-value	-log p- value	LR statistic	p-value	-log p- value
NET	99- 28788/300	99- 32061/304	99- 32121/242	0	GGG	0.01	0.07	-0.07	0.08	7.92	100000	0.0002	3.77	22.08	0.002	2.65
WFS1	19-19/174	19-17/188	19-18/310	0	CAG	0.01	0.07	-0.08	0.11	8.51	100000	0.0002	3.68	25.38	0.000	3.55
NET	16-50/196	99- 32061/304	99- 32121/242	0	TGG	0.00	0.07	-0.07	0.06	8.34	100000	0.0008	3.11	21.73	0.012	1.91
NET	19-14/241	19-28/136	16-50/196	0	TCT	0.30	0.43	-0.14	0.55	4.53	100000	0.0009	3.05	20.54	0.001	3.05
GRL	18-20/174	18-38/395	99- 30858/354	0	GAC	0.11	0.23	-0.11	0.44	5.18	100000	0.001	2.98	15.29	0.049	1.31
Gbeta3	19-58/162	19-9/45	20-205/302	0	TTC	0.21	0.35	-0.13	0.51	4.89	10000	0.001	2.96	28.52	0.000	4.00
cyp3a4	12-254/180	10-214/278	10-217/91	0	ATC	0.38	0.52	-0.14	0.57	4.41	1000	0.002	2.70	14.23	0.042	1.38
NET	19-14/241	99- 32061/304	99- 32121/242	0	TGG	0.01	0.06	-0.05	0.08	6.12	1000	0.002	2.70	20.70	0.015	1.82
GRL	99- 32002/313	18-31/178	99- 30858/354	0	GTT	0.18	0.09	0.10	0.09	4.09	1000	0.003	2.52	9.36	0.188	0.73
GRL	18-31/178	99- 30853/364	99- 30858/354	0	TAT	0.19	0.10	0.10	2.24	3.83	1000	0.003	2.52	12.79	0.109	0.96
5HTT	18-186/391	18-194/130	18-242/300	0	GCA	0.02	0.08	-0.06	0.27	4.08	1000	0.003	2.52	18.07	0.028	1.55
5HTT	18-186/391	18-198/252	18-242/300	0	GAA	0.02	0.09	-0.06	0.24	5.11	1000	0.003	2.52	17.54	0.031	1.51
DRD3	8-15/126	8-19/372	99-2409/298	0	GGA	0.11	0.04	0.08	3.28	4.31	100000	0.003	2.46	11.57	0.038	1.42
WFS1	19-19/174	19-17/188	16-145/405	0	TGT	0.01	0.06	-0.04	0.24	3.44	100000	0.004	2.41	25.29	0.001	3.27
NET	19-58/140	19-14/241	19-28/136	0	GTC	0.30	0.41	-0.11	0.61	2.92	1000	0.004	2.40	7.06	0.355	0.45
NET	19-58/140	99- 32061/304	99- 32121/242	0	GGG	0.01	0.07	-0.07	0.11	6.87	1000	0.004	2.40	24.66	0.004	2.40
5HTT6	99- 27199/207	99- 27207/117	99- 28134/215	0	CCT	0.26	0.14	0.12	2.17	4.83	1000	0.004	2.40	15.16	0.081	1.09
5HTT	18-194/130	18-198/252	18-242/300	0	CAA	0.02	0.08	-0.06	0.27	4.15	1000	0.004	2.40	16.28	0.021	1.88
WFS1	19-19/174	19-16/127	19-17/188	0	CGA	0.01	0.06	-0.05	0.21	4.02	1000	0.005	2.30	23.24	0.001	3.00
WFS1	19-19/174	19-17/188	19-18/310	0	CGA	0.12	0.08	0.08	2.16	2.32	1000	0.005	2.30	25.36	0.000	3.55

869 Total Haplotypes

**TABLE 17C**

2-Locus Combination

EM Methods														Permutation Test				Omnibus LR		
Gene	Marker1	Marker2	Marker3	Marker4	Haplotyp e	Case	Control	difference	Odds Ratio	Chi- Square	number	p-value	-log p- value	LR statistic	p-value	-log p- value				
WFS1	19-18/174	19-17/188	0	0	CA	0.02	0.08	-0.06	0.21	5.19	100000	0.0005	3.30	20.22	0.000	3.68				
Gbeta3	19-58/162	20-205/302	0	0	TC	0.25	0.38	-0.13	0.53	4.68	100000	0.0009	3.04	21.82	0.000	4.52				
DRD3	8-15/126	99-2409/298	0	0	AA	0.23	0.37	-0.13	0.52	4.95	100000	0.0012	2.93	10.17	0.014	1.87				
WFS1	19-19/174	19-17/188	0	0	CG	0.41	0.28	0.13	1.79	4.09	100000	0.0016	2.79	20.22	0.0002	3.68				
NET	19-14/241	19-28/136	0	0	TC	0.31	0.43	-0.12	0.59	3.46	1000	0.002	2.70	8.47	0.044	1.36				
NET	99-32061/304	32121/242	0	0	GG	0.01	0.09	-0.08	0.15	7.53	1000	0.002	2.70	19.47	0.003	2.52				
Gbeta3	19-9/45	20-205/302	0	0	TC	0.24	0.36	-0.12	0.58	3.58	1000	0.002	2.70	17.27	0.001	3.00				
GRL	18-31/178	99-30858/354	0	0	TT	0.20	0.10	0.10	2.31	4.19	1000	0.003	2.52	8.22	0.029	1.54				
5HTT	18-186/394	18-242/300	0	0	GA	0.03	0.11	-0.08	0.25	6.36	1000	0.003	2.52	13.34	0.016	1.80				
5HTT	18-198/252	18-242/300	0	0	AA	0.02	0.09	-0.08	0.24	4.92	1000	0.003	2.52	10.72	0.021	1.68				
CHRNA7	99-28722/190	99-32308/409	0	0	CC	0.07	0.29	-0.22	0.19	19.25	1000	0.003	2.52	9.19	0.042	1.38				
DRD3	8-15/126	99-2409/298	0	0	GA	0.13	0.04	0.09	3.58	5.16	100000	0.003	2.49	10.17	0.014	1.87				
WFS1	19-19/174	19-17/188	0	0	TG	0.01	0.06	-0.04	0.24	3.46	100000	0.004	2.45	20.22	0.000	3.68				
5HTR7	99-32181/192	99-32193/258	0	0	TG	0.42	0.28	0.14	1.87	4.16	1000	0.004	2.40	9.27	0.015	1.82				
GRL	18-38/395	99-30858/354	0	0	AC	0.44	0.58	-0.14	0.58	4.11	1000	0.004	2.40	8.98	0.023	1.64				
CRFR1	99-27091/220	99-27550/48	0	0	GG	0.36	0.25	0.11	1.72	3.20	1000	0.004	2.40	9.03	0.022	1.66				
cyp3a4	12-254/180	10-214/279	0	0	AT	0.39	0.52	-0.13	0.60	3.69	1000	0.005	2.30	7.10	0.085	1.07				
NET	19-56/140	19-14/241	0	0	GT	0.35	0.46	-0.10	0.65	2.43	1000	0.005	2.30	5.05	0.134	0.87				
CHRNA7	99-28722/190	99-28730/351	0	0	TG	0.55	0.36	0.19	2.17	8.05	1000	0.005	2.30	3.95	0.214	0.67				
cyp3a4	12-254/180	10-217/91	0	0	AC	0.41	0.53	-0.13	0.60	3.57	100000	0.006	2.26	7.40	0.084	1.08				

485 Total Haplotype

Table 18A

Gene	Marker	Allele 1	Allele 2	Allele 1 Frequencies				Genotype Frequencies								Numbers				
				Cases	Controls	Chi-square	p-value	Cases				Controls				Chi-square	p-value	Cases	Controls	
								11	12	22	11	12	22	11	12					22
5HTR6	99-27199-207	C	T	0.72	0.70	0.14	0.71	0.51	0.41	0.08	0.48	0.45	0.07	0.36	0.83	140	94			
5HTR6	99-27207-117	C	T	0.48	0.37	5.78	0.02	0.24	0.47	0.29	0.13	0.47	0.40	5.79	0.06	139	93			
5HTR6	99-28110-75	C	T	0.64	0.52	5.93	0.01	0.41	0.45	0.14	0.27	0.51	0.22	5.91	0.05	139	90			
5HTR6	99-28134-215	C	T	0.51	0.63	6.43	0.01	0.26	0.50	0.24	0.42	0.43	0.15	6.58	0.04	136	93			
5HTR7	99-28160-285	A	G	0.49	0.51	0.12	0.73	0.27	0.44	0.29	0.24	0.53	0.23	1.96	0.37	140	91			
5HTR7	99-28171-458	A	G	0.34	0.38	0.61	0.44	0.13	0.42	0.45	0.17	0.42	0.41	0.61	0.74	136	90			
5HTR7	99-28173-395	C	T	0.51	0.55	0.94	0.33	0.27	0.47	0.26	0.27	0.57	0.16	3.46	0.18	137	94			
5HTR7	99-32181-192	C	T	0.28	0.38	5.50	0.02	0.09	0.38	0.54	0.13	0.51	0.36	6.25	0.04	136	85			
5HTR7	99-32193-258	G	T	0.70	0.65	1.29	0.26	0.53	0.34	0.12	0.41	0.48	0.11	4.30	0.12	137	85			
CHRNA7	99-28722-90	C	T	0.27	0.32	1.24	0.27	0.00	0.54	0.46	0.01	0.62	0.37	2.99	0.22	140	94			
CHRNA7	99-28730-351	A	G	0.32	0.38	1.86	0.17	0.04	0.55	0.41	0.03	0.69	0.28	4.93	0.09	139	94			
CHRNA7	99-32306-409	C	G	0.62	0.67	1.02	0.31	0.26	0.72	0.01	0.34	0.66	0.00	2.77	0.25	137	91			
CRFR1	99-27088-246	A	G	0.42	0.38	1.04	0.31	0.20	0.44	0.36	0.15	0.45	0.40	1.12	0.57	138	93			
CRFR1	99-27091-220	A	G	0.44	0.49	1.00	0.32	0.19	0.50	0.31	0.24	0.50	0.26	1.04	0.59	137	92			
CRFR1	99-27097-83	C	T	0.55	0.53	0.12	0.73	0.34	0.41	0.24	0.26	0.56	0.19	4.40	0.11	140	90			
CRFR1	99-27550-48	A	G	0.20	0.26	1.93	0.17	0.04	0.32	0.64	0.07	0.38	0.55	1.92	0.38	136	91			
MLR	16-31-738-A23	C	G	0.55	0.53	0.15	0.70	0.28	0.55	0.18	0.28	0.50	0.22	0.75	0.69	137	92			
MLR	99-27563-400	A	G	0.46	0.44	0.07	0.79	0.19	0.54	0.28	0.21	0.46	0.33	1.25	0.54	138	89			
MLR	99-28732-133	A	G	0.39	0.31	2.94	0.09	0.16	0.47	0.37	0.09	0.44	0.47	2.98	0.23	137	86			
MLR	99-28735-56	C	T	0.71	0.70	0.03	0.87	0.50	0.41	0.09	0.50	0.40	0.10	0.14	0.93	136	88			
CRFR2	99-27875-185	C	T	0.36	0.40	1.06	0.30	0.16	0.39	0.45	0.16	0.49	0.35	2.76	0.25	140	94			
CRFR2	99-27880-176	C	T	0.53	0.56	0.52	0.47	0.30	0.46	0.24	0.32	0.47	0.20	0.55	0.76	139	93			
CRFR2	99-28747-371	C	T	0.39	0.44	0.90	0.34	0.16	0.47	0.37	0.23	0.42	0.35	1.88	0.39	138	91			
CRFR2	99-28755-206	A	G	0.56	0.59	0.21	0.65	0.32	0.50	0.19	0.37	0.44	0.19	0.77	0.68	139	93			

Table 18B

Gene	Marker	Allele 1	Allele 2	Allele 1 Frequencies			Genotype Frequencies								Numbers		
				Cases	Controls	Chi	p-value	Cases		Controls				Chi-square	p-value	Cases	Controls
								11	12	22	Controls						
											11	12	22				
GRL	99-30853-364	A	G	0.56	0.58	0.24	0.62	0.35	0.41	0.24	0.39	0.39	0.23	0.29	0.87	139	93
GRL	99-30858-354	C	T	0.76	0.84	4.10	0.04	0.59	0.34	0.06	0.71	0.27	0.02	4.04	0.13	140	89
GRL	99-28485-198	G	T	0.19	0.20	0.17	0.68	0.04	0.30	0.66	0.01	0.38	0.61	2.75	0.25	134	89
GRL	99-32002-313	A	G	0.48	0.48	0.00	0.97	0.23	0.51	0.26	0.16	0.65	0.19	4.61	0.10	140	94
GRL	18-20-174	A	G	0.76	0.73	0.76	0.38	0.57	0.39	0.04	0.53	0.39	0.07	1.18	0.55	140	94
GRL	18-31-178	C	T	0.30	0.35	1.55	0.21	0.11	0.38	0.51	0.15	0.40	0.45	1.41	0.49	140	94
GRL	18-38-395	A	T	0.59	0.63	0.76	0.38	0.36	0.46	0.18	0.36	0.54	0.10	3.49	0.17	140	94
MAO A-B	18-2-192	G	T	0.70	0.68	0.19	0.66	0.56	0.26	0.17	0.56	0.24	0.20	0.50	0.78	140	93
MAO A-B	18-215-80	C	T	0.67	0.67	0.00	1.00	0.54	0.26	0.20	0.54	0.24	0.21	0.08	0.96	138	90
MAO A-B	99-28921-210	A	G	0.48	0.52	0.52	0.47	0.33	0.30	0.37	0.31	0.41	0.28	3.17	0.20	139	93
MAO A-B	18-133-293	A	C	0.30	0.27	0.55	0.46	0.16	0.29	0.55	0.14	0.26	0.60	0.52	0.77	140	92
NET	99-28788-300	A	G	0.49	0.47	0.25	0.62	0.23	0.51	0.26	0.21	0.53	0.27	0.32	0.85	314	178
NET	99-32061-304	A	G	0.43	0.40	0.32	0.57	0.19	0.47	0.34	0.14	0.52	0.34	1.41	0.50	320	86
NET	99-32121-242	A	G	0.57	0.54	0.78	0.38	0.34	0.47	0.19	0.30	0.48	0.22	0.74	0.69	313	181
NET	99-32148-315	C	G	0.31	0.27	2.08	0.15	0.09	0.46	0.46	0.09	0.36	0.55	4.23	0.12	315	181
NET	19-28-136	A	C	0.68	0.61	4.35	0.04	0.44	0.47	0.09	0.37	0.49	0.14	4.77	0.09	322	183
NET	19-29-303	C	T	0.21	0.19	0.77	0.38	0.05	0.33	0.63	0.02	0.34	0.64	3.52	0.17	326	183
NET	19-46-322	C	T	0.31	0.31	0.01	0.92	0.07	0.48	0.45	0.07	0.47	0.45	0.03	0.99	317	177
NET	99-32065-303	G	T	0.42	0.43	0.04	0.85	0.18	0.49	0.34	0.14	0.57	0.29	3.02	0.22	317	182
NET	99-32131-312	C	T	0.68	0.71	0.62	0.43	0.47	0.42	0.11	0.49	0.43	0.08	1.12	0.57	315	178
TACR1	99-28761-311	A	G	0.25	0.22	0.78	0.38	0.07	0.36	0.56	0.01	0.41	0.57	4.81	0.09	140	94
TACR1	99-28771-86	C	T	0.48	0.52	0.96	0.33	0.24	0.46	0.29	0.23	0.57	0.19	3.65	0.16	140	94
TACR1	99-28791-291	A	G	0.28	0.26	0.31	0.58	0.09	0.39	0.53	0.04	0.43	0.53	1.76	0.42	140	94
TACR1	99-32361-419	G	T	0.53	0.52	0.07	0.79	0.29	0.49	0.23	0.26	0.52	0.22	0.34	0.84	140	94

Table 18B (cont)

DRD3	8-15-126	A	G	0.64	0.70	1.99	0.16	0.43	0.42	0.15	0.47	0.47	0.06	4.10	0.13	140	94
DRD3	8-19-372	A	G	0.23	0.28	1.48	0.22	0.09	0.29	0.62	0.03	0.50	0.47	11.32	0.004	140	94
DRD3	99-2409-298	A	G	0.36	0.40	1.06	0.30	0.14	0.44	0.42	0.11	0.60	0.30	5.31	0.07	140	94
DRD3	99-339-54	C	G	0.55	0.54	0.01	0.93	0.34	0.42	0.24	0.28	0.53	0.19	2.77	0.25	140	94



Table 18C

Gene	Marker	Allele 1	Allele 2	Allele 1 Frequencies			Genotype Frequencies										Numbers	
				Cases	Controls	Chi Square	p-value	Cases			Controls			Chi-square	p-value	Cases	Controls	
								11	12	22	11	12	22					
CYP3A4	12-254-180	A	G	0.43	0.54	5.86	0.02	0.19	0.47	0.34	0.32	0.45	0.23	5.73	0.06	140	94	
CYP3A4	10-214-279	C	T	0.14	0.12	0.35	0.55	0.02	0.23	0.75	0.02	0.19	0.79	0.46	0.79	140	94	
CYP3A4	10-217-91	C	T	0.89	0.93	2.01	0.16	0.79	0.19	0.02	0.86	0.13	0.01	1.88	0.39	140	94	
5HTT	18-194-130	C	T	0.54	0.52	0.18	0.67	0.31	0.44	0.24	0.20	0.63	0.17	7.73	0.02	140	94	
5HTT	18-198-252	A	G	0.52	0.49	0.32	0.57	0.29	0.47	0.24	0.20	0.59	0.21	3.19	0.20	140	94	
5HTT	18-242-300	A	G	0.46	0.54	2.89	0.09	0.24	0.44	0.32	0.27	0.54	0.19	4.89	0.09	140	94	
5HTT	18-186-391	G	T	0.50	0.53	0.41	0.52	0.27	0.45	0.28	0.26	0.54	0.20	2.37	0.31	140	94	
DRD2	16-21-228	A	G	0.21	0.16	1.40	0.24	0.05	0.31	0.64	0.04	0.24	0.72	1.65	0.44	139	93	
DRD2	16-23-404	A	G	0.55	0.53	0.09	0.76	0.30	0.50	0.20	0.26	0.55	0.19	0.50	0.78	139	93	
DRD2	16-24-175	A	C	0.22	0.16	2.07	0.15	0.06	0.32	0.62	0.04	0.24	0.72	2.19	0.34	138	92	
DRD2	16-25-286	C	T	0.70	0.63	2.41	0.12	0.49	0.43	0.08	0.38	0.52	0.11	2.87	0.24	135	93	
DRD2	16-22-156	C	T	0.46	0.45	0.07	0.79	0.21	0.50	0.29	0.17	0.56	0.27	0.94	0.63	140	93	
Gbeta3	19-58-162	C	T	0.68	0.63	2.24	0.13	0.45	0.47	0.09	0.41	0.43	0.15	4.35	0.11	229	182	
Gbeta3	19-9-45	C	T	0.69	0.66	0.60	0.44	0.45	0.48	0.07	0.45	0.42	0.12	4.45	0.11	321	185	
Gbeta3	18-355-67	C	T	0.47	0.49	0.43	0.51	0.20	0.55	0.26	0.25	0.47	0.27	2.95	0.23	311	173	
Gbeta3	18-353-267	C	T	0.78	0.73	3.58	0.06	0.60	0.37	0.03	0.54	0.38	0.08	6.14	0.05	302	180	
Gbeta3	18-388-305	A	G	0.65	0.70	2.05	0.15	0.43	0.44	0.13	0.47	0.45	0.08	2.78	0.25	319	174	

Table 18C (cont)

WFS1	19-17-188	A	G	0.57	0.66	8.62	0.003	0.32	0.50	0.18	0.43	0.47	0.10	8.92	0.01	318	180
WFS1	19-19-174	C	T	0.40	0.31	7.66	0.006	0.16	0.48	0.36	0.09	0.43	0.47	7.61	0.02	311	173
WFS1	24-243-346	C	T	0.62	0.70	5.29	0.02	0.37	0.50	0.13	0.48	0.43	0.09	5.70	0.06	321	166
WFS1	99-62531-351	C	T	0.59	0.64	2.77	0.10	0.34	0.51	0.16	0.40	0.49	0.11	2.92	0.23	316	177
WFS1	99-54279-152	C	G	0.59	0.56	0.79	0.37	0.33	0.52	0.15	0.32	0.49	0.20	1.63	0.44	306	174
TH	16-115-343	A	C	0.69	0.76	2.67	0.10	0.51	0.37	0.12	0.60	0.32	0.08	2.37	0.31	132	91
TH	18-251-176	C	T	0.58	0.57	0.02	0.87	0.36	0.44	0.20	0.29	0.57	0.14	4.43	0.11	140	94
TH	18-269-44	A	G	0.36	0.38	0.14	0.71	0.11	0.51	0.39	0.15	0.46	0.39	1.09	0.58	140	94
5HTR2c	18-12-191	A	C	0.15	0.14	0.12	0.73	0.66	0.17	0.77	0.03	0.21	0.76	1.84	0.40	137	94

**Table 19**  
OMNIBUS LR Rank of Haplotypes

	GENE	Affected	Control	Marker1	Marker2	Marker3	Marker4	p-value	-log p-value
1	WFS1	288	148	19-17-188	19-19-174	24-243-346	99-62531-351	0.003	2.49
2		277	154	19-17-188	19-19-174	24-243-346	99-54279-152	0.003	2.47
3	WFS1	274	157	19-17-188	19-19-174	99-62531-351	99-54279-152	0.007	2.17
4	SHIT	140	94	18-186-391	18-194-130	18-198-252	18-242-300	0.013	1.89
5	NET	293	79	99-32061-304	99-32121-242	19-28-136	99-32131-312	0.020	1.69
6	WFS1	283	148	19-17-188	24-243-346	99-62531-351	99-54279-152	0.023	1.65
7	NET	290	78	99-32061-304	99-32121-242	19-28-136	19-46-322	0.032	1.50
8	NET	292	73	99-32061-304	19-28-136	19-46-322	99-32131-312	0.035	1.45
9	NET	291	85	99-32061-304	99-32121-242	19-28-136	99-32065-303	0.038	1.42
10	NET	291	76	99-28788-300	99-32061-304	19-28-136	99-32131-312	0.040	1.40

  

	GENE	Affected	Control	Marker1	Marker2	Marker3	Marker4	p-value	-log p-value
1	WFS1	297	158	19-17-188	19-19-174	24-243-346		0.001	3.00
2	WFS1	282	166	19-17-188	19-19-174	99-54279-152		0.001	2.85
3	WFS1	291	156	19-17-188	24-243-346	99-54279-152		0.002	2.62
4	WFS1	293	167	19-17-188	19-19-174	99-62531-351		0.005	2.34
5	WFS1	302	150	19-17-188	24-243-346	99-62531-351		0.008	2.11
6	NET	302	79	99-32061-304	19-28-136	99-32131-312		0.017	1.76
7	NET	309	170	19-28-136	19-29-303	19-46-322		0.027	1.57
8	WFS1	287	159	19-17-188	99-62531-351	99-54279-152		0.027	1.56
9	NET	300	85	99-32061-304	99-32121-242	19-28-136		0.037	1.44
10	Gbeta3	217	167	19-58-162	19-9-45	18-355-67		0.039	1.41

Table 19 (cont)

	GENE						
1	WFS1	303	178	19-17-188	19-19-174	0.001	2.92
2	WFS1	312	160	19-17-188	24-243-346	0.001	2.92
3	5HTR7	136	82	99-28108-185	99-32181-192	0.007	2.15
4	Gbeta3	228	180	19-58-162	19-9-45	0.008	2.11
5	WFS1	307	189	19-17-188	99-62531-351	0.012	1.94
6	WFS1	298	188	19-17-188	99-54279-152	0.012	1.94
7	DRD3	140	94	8-15-126	99-2409-298	0.014	1.87
8	5HTR7	133	76	99-32181-192	99-32193-258	0.015	1.82
9	5HTT	140	94	18-186-394	18-242-300	0.016	1.80
10	Gbeta3	294	168	18-353-267	18-338-305	0.033	1.48

**Table 20A**  
**Rank of Permutation Tests for Individual Haplotypes**

Gene	Marker1	Marker2	Marker3	Marker4	Haplotype	EM methods			Chi-Square	Permutation Test			Omnibus LR
						Control	difference	number		p-value	-log p-value	p-value	
1	GRL	18-20-174	99-32002-313	18-31-178	AGCA	0.06	0.17	100000	16.39	0.003	2.57	0.360	0.44
2	GRL	18-20-174	18-31-178	99-30858-354	GTAC	0.11	0.22	100000	9.13	0.003	2.55	0.045	1.35
3	GRL	18-20-174	18-38-395	99-30853-364	GAAC	0.03	0.12	1000	12.74	0.003	2.52	0.078	1.11
4	GRL	99-32002-313	18-38-395	99-30858-354	GCAC	0.06	0.14	1000	9.82	0.003	2.52	0.159	0.80
5	GRL	99-32002-313	18-31-178	99-30858-354	GTAT	0.13	0.05	1000	9.55	0.003	2.52	0.159	0.80
6	SHIT	18-186-391	18-194-130	18-198-252	GCAA	0.02	0.08	1000	8.26	0.003	2.52	0.013	1.89
7	GRL	99-32002-313	18-31-178	99-30853-364	GTAT	0.18	0.08	1000	8.40	0.004	2.38	0.314	0.50
8	SHIT7	99-28106-185	99-28171-458	99-28173-395	AACC	0.27	0.38	1000	2.90	0.005	2.30	0.034	1.47
9	NET	99-32121-242	99-32148-315	19-46-322	AGTT	0.02	0.07	5000	13.54	0.006	2.25	0.273	0.56
10	GRL	18-31-178	99-30853-364	99-30858-354	TAAT	0.14	0.05	1000	9.35	0.006	2.22	0.090	1.05
11	DRD3	8-15-128	8-19-372	99-2409-298	GGAG	0.06	0.01	1000	9.29	0.006	2.22	0.045	1.35
12	NET	99-32061-304	19-28-136	19-46-322	GCTT	0.18	0.30	5000	11.71	0.007	2.15	0.155	0.81
13	NET	99-28788-300	99-32061-304	99-32121-242	AGAC	0.16	0.28	5000	9.89	0.007	2.14	0.073	1.14
14	GRL	18-20-174	99-32002-313	18-38-395	GAAC	0.06	0.15	1000	11.29	0.007	2.15	0.175	0.76
15	NET	99-32061-304	99-32121-242	19-28-136	GACT	0.18	0.29	5000	10.22	0.008	2.11	0.038	1.42
16	NET	99-32061-304	99-32148-315	19-29-303	ACTG	0.11	0.03	5000	9.73	0.008	2.11	0.464	0.33
17	NET	99-32061-304	19-28-136	19-46-322	GCTT	0.17	0.29	5000	11.84	0.008	2.10	0.188	0.73
18	NET	99-32061-304	99-32121-242	19-28-136	GACT	0.18	0.30	5000	11.06	0.009	2.07	0.032	1.50
19	NET	99-32061-304	99-32148-315	19-28-136	GGCT	0.11	0.22	5000	12.79	0.009	2.07	0.218	0.66
20	NET	99-28788-300	99-32061-304	99-32148-315	AGGC	0.11	0.21	5000	11.33	0.009	2.06	0.140	0.85

**Table 20B**  
**Rank of Permutation Tests for Individual Haplotypes**

Gene	Marker1	Marker2	Marker3	Haplotype	EM methods			Chi-Square			Permutation Test			Omnibus LR
					Case	Control	difference	Chi-Square	number	p-value	-log p-value	p-value	-log p-value	
1	18-20-174	18-38-395	99-30858-354	GAC	0.11	0.23	-0.11	10.35	100000	0.001	2.98	0.05	1.31	
2	WFS1 19-17-188	19-19-174	99-62531-351	ACC	0.01	0.05	-0.04	12.09	5000	0.002	2.80	0.00	2.34	
3	cyp3a4 12-254-180	10-214-279	10-217-91	ATC	0.38	0.52	-0.14	8.82	1000	0.002	2.70	0.04	1.38	
4	WFS1 19-17-188	19-19-174	24-243-346	GCT	0.34	0.24	0.10	9.80	5000	0.003	2.52	0.00	3.00	
5	GRL 99-32002-313	18-31-178	99-30858-354	GTT	0.18	0.09	0.10	8.18	1000	0.003	2.52	0.19	0.73	
6	GRL 18-31-178	99-30853-364	99-30858-354	TAT	0.19	0.10	0.10	7.65	1000	0.003	2.52	0.11	0.96	
7	5HTT 18-186-391	18-194-130	18-242-300	GCA	0.02	0.08	-0.06	8.17	1000	0.003	2.52	0.03	1.55	
8	5HTT 18-186-394	18-198-252	18-242-300	GAA	0.02	0.09	-0.06	10.22	1000	0.003	2.52	0.03	1.51	
9	DRD3 8-15-126	8-19-372	99-2409-298	GGA	0.11	0.04	0.08	8.62	100000	0.003	2.46	0.04	1.42	
10	WFS1 19-17-188	24-243-346	99-54279-152	ATG	0.01	0.04	-0.03	9.90	5000	0.004	2.36	0.00	2.62	
11	5HTR6 99-27199-207	99-27207-117	99-28134-215	CCT	0.26	0.14	0.12	9.66	1000	0.004	2.40	0.08	1.09	
12	5HTT 18-194-130	18-198-252	18-242-300	CAA	0.02	0.08	-0.06	8.29	1000	0.004	2.40	0.02	1.88	
13	NET 99-32061-304	99-32148-315	19-29-303	ACT	0.11	0.03	0.08	10.38	5000	0.006	2.25	0.38	0.42	
14	NET 99-32148-315	19-28-136	19-29-303	GCT	0.21	0.30	-0.09	9.23	5000	0.006	2.24	0.42	0.38	
15	cyp3a4 12-254-180	10-214-279	10-217-91	GTC	0.48	0.36	0.12	6.41	1000	0.006	2.22	0.04	1.38	
16	NET 99-32061-304	19-28-136	19-46-322	GCT	0.17	0.29	-0.12	11.46	5000	0.007	2.18	0.05	1.33	
17	5HTR7 99-28171-458	99-28173-395	99-32181-182	ACC	0.27	0.38	-0.11	5.71	1000	0.007	2.15	0.05	1.28	
18	GRL 99-32002-313	18-31-178	18-38-395	GCA	0.07	0.18	-0.11	14.17	1000	0.007	2.15	0.25	0.61	
19	GRL 18-31-178	18-38-395	99-30858-354	TAT	0.14	0.05	0.09	8.81	1000	0.008	2.10	0.08	1.25	
20	CHRNA7 99-28722-90	99-28730-351	99-32306-409	CAC	0.01	0.05	-0.05	10.75	1000	0.008	2.10	0.04	1.46	

**Table 20C**  
**Rank of Permutation Tests for Individual Haplotypes**

EM methods												Permutation Test				Omnibus LR	
Gene	Marker1	Marker2	Haplotype	Case	Control	difference	Chi-Square	number	p-value	-log p-value	-log p-value	-log p-value	-log p-value	-log p-value			
1	WFS1	19-17-188	24-243-346	GT	0.37	0.26	0.11	12.09	5000	0.0006	3.22	0.001	2.92	2.92			
2	WFS1	19-17-188	19-19-174	GC	0.38	0.27	0.11	11.49	5000	0.0012	2.92	0.001	2.92	2.92			
3	DRD3	8-15-126	99-2409-298	AA	0.23	0.37	-0.13	9.91	100000	0.0012	2.93	0.014	1.87	1.87			
4	WFS1	19-17-188	99-62531-351	AC	0.44	0.55	-0.11	10.05	5000	0.002	2.74	0.012	1.94	1.94			
5	WFS1	19-17-188	24-243-346	AT	0.02	0.05	-0.03	8.82	5000	0.003	2.52	0.001	2.92	2.92			
6	GRL	18-31-178	99-30858-354	TT	0.20	0.10	0.10	8.38	1000	0.003	2.52	0.029	1.54	1.54			
7	5HTT	18-186-394	18-242-300	GA	0.03	0.11	-0.08	12.72	1000	0.003	2.52	0.016	1.80	1.80			
8	5HTT	18-198-252	18-242-300	AA	0.02	0.09	-0.06	9.84	1000	0.003	2.52	0.021	1.68	1.68			
9	CHRNA7	99-28722-90	99-32306-409	CC	0.07	0.29	-0.22	19.25	1000	0.003	2.52	0.042	1.38	1.38			
10	Gbeta3	19-58-162	19-9-45	CT	0.06	0.01	0.04	10.37	5000	0.003	2.49	0.008	2.11	2.11			
11	DRD3	8-15-126	99-2409-298	GA	0.13	0.04	0.09	10.32	100000	0.003	2.49	0.014	1.87	1.87			
12	5HTR7	99-32181-192	99-32193-258	TG	0.42	0.28	0.14	8.33	1000	0.004	2.40	0.015	1.82	1.82			
13	GRL	18-38-395	99-30858-354	AC	0.44	0.58	-0.14	8.22	1000	0.004	2.40	0.023	1.64	1.64			
14	CRFR1	99-27091-220	99-27550-48	GG	0.36	0.25	0.11	6.39	1000	0.004	2.40	0.022	1.66	1.66			
15	cyp3a4	12-254-180	10-214-279	AT	0.39	0.52	-0.13	7.37	1000	0.005	2.30	0.085	1.07	1.07			
16	CHRNA7	99-28722-90	99-28730-351	TG	0.55	0.36	0.19	8.05	1000	0.005	2.30	0.214	0.67	0.67			
17	cyp3a4	12-254-180	10-217-91	AC	0.41	0.53	-0.13	7.14	100000	0.006	2.26	0.084	1.08	1.08			
18	NET	99-32061-304	19-28-136	GC	0.17	0.27	-0.11	9.91	5000	0.006	2.22	0.039	1.41	1.41			
19	5HTT	18-194-133	18-242-300	CA	0.02	0.08	-0.06	9.41	1000	0.006	2.22	0.03	1.51	1.51			
20	5HTR6	99-27207-117	99-28110-75	TT	0.32	0.44	-0.12	6.64	1000	0.006	2.22	0.06	1.22	1.22			

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Table 7 and the complements thereof.

2. The polynucleotide according to claim 1, wherein said span includes a CNS disorder-related biallelic marker in said sequence.

3. An isolated polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Table 9 and the complements thereof, wherein said span includes a CNS disorder-related biallelic marker in said sequence with the alternative allele present at said biallelic marker.

4. An isolated polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Table 9 and the complements thereof, wherein said span includes a CNS disorder-related biallelic marker in said sequence with the original allele present at said biallelic marker.

5. An isolated polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Table 10 and the complements thereof, wherein said span includes a CNS disorder-related biallelic marker in said sequence.

6. The polynucleotide according to any one of claims 2 to 5, wherein said contiguous span is 18 to 35 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.

7. The polynucleotide according to claim 6, wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

8. A polynucleotide for use in a hybridization assay for determining the identity of a nucleotide at a CNS disorder-related biallelic marker.

9. A polynucleotide for use in a sequencing assay for determining the identity of a nucleotide at a CNS disorder-related biallelic marker.



10. A polynucleotide for use in an allele specific amplification assay for determining the identity of a CNS disorder-related biallelic marker.

5 11. A polynucleotide for use in amplifying a segment of nucleotides comprising a CNS disorder-related biallelic marker.

12. A use according to any one of claims 8 to 11, wherein said polynucleotide is selected from the sequences described in Table 7.

10

13. A method of genotyping an individual comprising: (a) obtaining a biological sample comprising a nucleic acid from said individual; (b) determining the identity of a polymorphic base at a biallelic marker from said nucleic acid; wherein said biallelic marker is selected from any one biallelic marker of Table 7; wherein the identity of the polymorphic base  
15 determines the genotype of the individual at said position.

14. A method according to claim 13, wherein said CNS disorder-related biallelic marker is selected from the biallelic markers described in Table 7.

20 15. The method according to claim 14, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252,  
25 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409.

30

16. The method according to claim 14, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174.

35

17. The method according to claim 13, wherein said biological sample is derived from a single subject.

18. The method according to claim 17, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said subject's genome.
19. The method according claim 13, wherein said biological sample is derived from multiple subjects.
20. The method according to claim 13, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.
21. A method of determining the frequency in a population of an allele of a CNS disorder-related biallelic marker, comprising:
- a) genotyping individuals from said population for said biallelic marker according to the method of claim 13; and
  - b) determining the proportional representation of said biallelic marker in said population.
22. The method according to claim 21, wherein said CNS disorder-related biallelic marker is selected from the biallelic markers described in Table 7.
23. The method according to claim 22, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409.
24. The method according to claim 22, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174.

25. The method of detecting an association between an allele and a phenotype, comprising the steps of:

- a) determining the frequency of at least one CNS disorder-related biallelic marker allele in a trait positive population according to the method of claim 21;
- b) determining the frequency of said CNS disorder-related biallelic marker allele in a control population according to the method of claim 21; and
- c) determining whether a statistically significant association exists between said allele and said phenotype.

26. The method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:

- a) genotyping each individual in said population for at least one CNS disorder-related biallelic marker according to claim 13;
- b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and
- c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

27. The method according to claim 26, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, or an expectation maximization algorithm.

28. The method according to claim 26, wherein said CNS disorder-related biallelic marker is selected from the biallelic markers described in Table 7.

29. The method according to claim 28, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, 19-16-127, 99-32148-315, 19-46-322, 99-32131-312, 99-32065-303, 19-44-251, 19-29-303, 18-355-67, 18-353-267, 18-338-305, 16-88-185, 24-243-346, 99-62531-351, 99-54279-152, 99-28171-458, 99-28173-395, 18-186-394, 8-15-126, 99-2409-298, 99-28722-90 and 99-32306-409.

30. The method according to claim 28, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, 20-205-302, 24-243-346, 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 19-17-188 and 19-19-174.

5

31. The method according to claim 28, wherein said haplotype comprises one of the following sets of biallelic markers:

- 99-28106-185, and 99-32181-192;
- 18-20-174, 99-32002-313, 18-31-178, and 18-38-395;
- 10 18-20-174, 18-31-178, 18-38-395, and 99-30858-354;
- 18-20-174, 18-38-395, 99-30853-364, and 99-30858-354;
- 99-32002-313, 18-31-178, 18-38-395, and 99-30858-354;
- 18-20-174, 18-38-395, and 99-30858-354;
- 99-32002-313, 18-31-178, and 99-30858-354;
- 15 18-31-178, 99-30853-364, and 99-30858-354;
- 19-56-140, 99-28788-300, 99-32061-304, and 99-32121-242;
- 19-28-136, 99-28788-300, 99-32061-304, and 99-32121-242;
- 19-14-241, 19-28-136, 99-32061-304, and 99-32121-242;
- 19-56-140, 19-28-136, 99-32061-304, and 99-32121-242;
- 20 19-14-241, 19-28-136, and 16-50-196;
- 19-28-136, 99-32061-304, and 99-32121-242;
- 99-28788-300, 99-32061-304, and 99-32121-242;
- 99-32061-304, and 99-32121-242;
- 19-56-140, 19-14-241, 19-28-136, and 16-50-196;
- 25 99-28788-300, 99-32061-304, and 99-32121-242;
- 16-50-196, 99-32061-304, and 99-32121-242;
- 19-14-241, 19-28-136, and 16-50-196;
- 19-14-241, 99-32061-304, and 99-32121-242;
- 19-14-241, and 19-28-136;
- 30 99-32061-304, and 99-32121-242;
- 8-15/126, and 99-2409/298;
- 12-254/180, 10-214/279, and 10-217/91;
- 18-186/391, 18-194/130, and 18-242/300;
- 18-186/394, 18-198/252, and 18-242/300;
- 35 19-58-162, 19-9-45, 19-22-74, and 20-205-302;
- 19-58-162, 19-9-45, 19-88-185, and 20-205-302;
- 19-58-162, 19-9-45, and 20-205-302;

- 19-58-162, 19-22-74, and 20-205-302;  
 19-58-162, and 20-205-302;  
 19-9-45, and 20-205-302;  
 19-22-74, and 20-205-302;  
 5 19-19-174, 19-17-188, and 19-18-310;  
 19-19-174, 19-16-127, and 19-17-188;  
 19-19-174, and 19-17-188; and  
 19-17-188, 19-19-174, 24-243-346, and 99-62531-351;  
 19-17-188, 19-19-174, 24-243-346, and 99-54279-152;  
 10 19-17-188, 19-19-174, 99-62531-351, and 99-54279-152;  
 99-32002-313, 18-31-178, 99-30853-364, and 99-30858-354;  
 99-32121-242, 99-32148-315, 19-46-322, and 99-32131-312;  
 99-28106-185, 99-28171-458, 99-28173-395, and 99-32181-192;  
 18-186-391, 18-194-130, 18-198-252, and 18-242-300.  
 15 19-17-188, 19-19-174, and 24-243-346;  
 19-17-188, 19-19-174, and 99-54279-152;  
 19-17-188, 24-243-346, and 99-54279-152;  
 19-17-188, 19-19-174, and 99-62531-351;  
 19-17-188, 24-243-346, and 99-62531-351;  
 20 99-32061-304, 19-28-136, and 99-32131-312;  
 12-254-180, 10-214-279, and 10-217-91;  
 18-186-391, 18-194-130, and 18-242-300;  
 18-186-394, 18-198-252, and 18-242-300;  
 8-15-126, 8-19-372, and 99-2409-298.  
 25 19-17-188, and 19-19-174;  
 19-17-188, and 24-243-346;  
 19-17-188, and 99-62531-351;  
 19-17-188, and 99-54279-152;  
 19-58-162, and 19-9-45;  
 30 8-15-126, and 99-2409-298;  
 18-31-178, and 99-30858-354;  
 18-186-394, and 18-242-300;  
 18-198-252, and 18-242-300; and  
 99-28722-90, and 99-32306-409.  
 35

32. The method according to claim 28, wherein said CNS disorder-related biallelic marker comprises one of the following sets of biallelic markers:

99-28788-300, 99-32061-304, and 99-32121-242;  
19-14-241, 19-28-136, and 16-50-196;  
19-17-188, 19-19-174, and 24-243-176; and  
19-58-162, 19-9-45, and 20-205-302.

5

33. The method of detecting an association between a haplotype and a phenotype, comprising the steps of:

- a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 26;
- 10 b) estimating the frequency of said haplotype in a control population according to the method of claim 26; and
- c) determining whether a statistically significant association exists between said haplotype and said phenotype.

15 34. The method according to either claim 25 or 33, wherein said control population is a trait negative population.

35. The method according to either claim 25 or 33, wherein said case control population is a random population.

20

36. The method according to claim 56, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-27207-117, 99-28110-75, 99-28134-215, 99-32181-192, 99-28106-185, 99-30858-354, 18-20-174, 99-32002-313, 18-31-178, 18-38-395, 99-30853-364, 19-56-140, 19-28-136, 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 16-50-196, 8-19-372, 12-254-180, 10-214-279, 10-217-91, 18-194-130, 18-186-391, 18-198-252, 25 18-242-300, 20-205-302, 19-58-162, 19-9-45, 19-22-74, 19-88-185, 19-18-310, 19-19-174, 19-17-188, and 19-16-127.

37. The method according to claim 33, wherein said CNS disorder-related biallelic marker is selected from the group consisting of 99-28788-300, 99-32061-304, 99-32121-242, 19-14-241, 19-28-136, 16-50-196, 19-58-162, 19-9-45, and 20-205-302.

38. The method according to claim 33, wherein said haplotype comprises one of the following sets of biallelic markers:

- 35 99-28106-185, and 99-32181-192;
- 18-20-174, 99-32002-313, 18-31-178, and 18-38-395;
- 18-20-174, 18-31-178, 18-38-395, and 99-30858-354;

- 18-20-174, 18-38-395, 99-30853-364, and 99-30858-354;  
 99-32002-313, 18-31-178, 18-38-395, and 99-30858-354;  
 18-20-174, 18-38-395, and 99-30858-354;  
 99-32002-313, 18-31-178, and 99-30858-354;  
 5 18-31-178, 99-30853-364, and 99-30858-354;  
 19-56-140, 99-28788-300, 99-32061-304, and 99-32121-242;  
 19-28-136, 99-28788-300, 99-32061-304, and 99-32121-242;  
 19-14-241, 19-28-136, 99-32061-304, and 99-32121-242;  
 19-56-140, 19-28-136, 99-32061-304, and 99-32121-242;  
 10 19-14-241, 19-28-136, and 16-50-196;  
 19-28-136, 99-32061-304, and 99-32121-242;  
 99-28788-300, 99-32061-304, and 99-32121-242;  
 99-32061-304, and 99-32121-242;  
 15 19-56-140, 19-14-241, 19-28-136, and 16-50-196;  
 99-28788-300, 99-32061-304, and 99-32121-242;  
 16-50-196, 99-32061-304, and 99-32121-242;  
 19-14-241, 19-28-136, and 16-50-196;  
 19-14-241, 99-32061-304, and 99-32121-242;  
 19-14-241, and 19-28-136;  
 20 99-32061-304, and 99-32121-242;  
 8-15/126, and 99-2409/298;  
 12-254/180, 10-214/279, and 10-217/91;  
 18-186/391, 18-194/130, and 18-242/300;  
 18-186/394, 18-198/252, and 18-242/300;  
 25 19-58-162, 19-9-45, 19-22-74, and 20-205-302;  
 19-58-162, 19-9-45, 19-88-185, and 20-205-302;  
 19-58-162, 19-9-45, and 20-205-302;  
 19-58-162, 19-22-74, and 20-205-302;  
 19-58-162, and 20-205-302;  
 30 19-9-45, and 20-205-302;  
 19-22-74, and 20-205-302;  
 19-19-174, 19-17-188, and 19-18-310;  
 19-19-174, 19-16-127, and 19-17-188;  
 19-19-174, and 19-17-188; and  
 35 19-17-188, 19-19-174, 24-243-346, and 99-62531-351;  
 19-17-188, 19-19-174, 24-243-346, and 99-54279-152;  
 19-17-188, 19-19-174, 99-62531-351, and 99-54279-152;

99-32002-313, 18-31-178, 99-30853-364, and 99-30858-354;  
 99-32121-242, 99-32148-315, 19-46-322, and 99-32131-312;  
 99-28106-185, 99-28171-458, 99-28173-395, and 99-32181-192;  
 18-186-391, 18-194-130, 18-198-252, and 18-242-300.  
 19-17-188, 19-19-174, and 24-243-346;  
 19-17-188, 19-19-174, and 99-54279-152;  
 19-17-188, 24-243-346, and 99-54279-152;  
 19-17-188, 19-19-174, and 99-62531-351;  
 19-17-188, 24-243-346, and 99-62531-351;  
 99-32061-304, 19-28-136, and 99-32131-312;  
 12-254-180, 10-214-279, and 10-217-91;  
 18-186-391, 18-194-130, and 18-242-300;  
 18-186-394, 18-198-252, and 18-242-300;  
 8-15-126, 8-19-372, and 99-2409-298.  
 19-17-188, and 19-19-174;  
 19-17-188, and 24-243-346;  
 19-17-188, and 99-62531-351;  
 19-17-188, and 99-54279-152;  
 19-58-162, and 19-9-45;  
 8-15-126, and 99-2409-298;  
 18-31-178, and 99-30858-354;  
 18-186-394, and 18-242-300;  
 18-198-252, and 18-242-300; and  
 99-28722-90, and 99-32306-409.

39. The method according to claim 33, wherein said haplotype comprises one of the following sets of biallelic markers:

99-28788-300, 99-32061-304, and 99-32121-242;  
 19-14-241, 19-28-136, and 16-50-196;  
 19-17-188, 19-19-174, and 24-243-176; and  
 19-58-162, 19-9-45, and 20-205-302.

40. The method according to either claim 25 or 33, wherein said phenotype is a CNS disorder.

41. The method according to either claim 25 or 33, wherein said phenotype is a response to an agent acting on a CNS disorder.



42. The method according to either claim 25 or 33, wherein said phenotype is a side effect to an agent acting on a CNS disorder.

5 43. The method according to claim 25, wherein the identity of the nucleotides at all of the biallelic markers described in Table 7 is determined in steps a) and b).

44. The method of administering a drug or treatment comprising:  
a) obtaining a nucleic acid sample from an individual;  
10 b) determining the identity of the polymorphic base of at least one CNS disorder-related biallelic marker according to the method of claim 13 which is associated with a positive response to said drug or treatment, or at least one CNS disorder-related marker which is associated with a negative response to said drug or treatment; and  
c) administering said drug or treatment to said individual if said nucleic acid  
15 sample contains at least one biallelic marker associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

45. The method of selecting an individual for inclusion in a clinical trial of a drug or  
20 treatment comprising:  
a) obtaining a nucleic acid sample from an individual;  
b) determining the identity of the polymorphic base of at least one CNS disorder-related biallelic marker according to the method of claim 13 which is associated with a  
25 positive response to said drug or treatment, or at least one biallelic marker associated with a negative response to said drug or treatment in said nucleic acid sample; and  
c) including said individual in said clinical trial if said nucleic acid sample contains at least one biallelic marker which is associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

30 46. The diagnostic kit comprising a polynucleotide according to any one of claims 2, 3, 4 and 5.

47. The use of a polynucleotide in a hybridization assay for determining the identity  
35 of a nucleotide at a CNS disorder-related biallelic marker.

48. The use of a polynucleotide in a sequencing assay for determining the identity of a nucleotide at a CNS disorder-related biallelic marker.
49. The use of a polynucleotide in an allele specific amplification assay for  
5 determining the identity of a CNS disorder-related biallelic marker.
50. The use of a polynucleotide in amplifying a segment of nucleotides comprising a CNS disorder-related biallelic marker.

## SEQUENCE LISTING

&lt;110&gt; GENSET

<120> BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
GENES INVOLVED IN CENTRAL NERVOUS SYSTEM DISORDERS.

&lt;130&gt; 75.W01

&lt;150&gt; 60/175,854

&lt;151&gt; 2000-01-13

&lt;160&gt; 544

&lt;170&gt; Patent.pm

&lt;210&gt; 1

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 207

&lt;223&gt; 99-27199-207 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 188..206

&lt;223&gt; 99-27199-207.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 208..227

&lt;223&gt; 99-27199-207.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..20

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 431..450

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 195..219

&lt;223&gt; 99-27199-207 potential probe

&lt;400&gt; 1

tataagaggc	ttgattcagg	ttctggaact	cagtaggtag	aagcctccat	gcctatccat	60
gcattgtttgc	gtgtttgcat	gtgtgtacat	gcacatttgc	acatgattgt	ccacgttcac	120
gtgtgtgcat	gtgtatgtgt	gtgacattca	tctcctccac	tgctgttgga	gtccctccca	180
gcacccaatg	tggccaggga	cactgayggc	cttttctggg	gtcttttgcc	agattgccaa	240
ggaatcatcg	aggacgtcat	cctgctgggt	gcgcctgtgg	agggagaagc	caagcattgg	300
gagcctttcc	ggaagggtgg	gtccggggagg	atcatcaacg	gctactgcag	gtctgtccaa	360
acctcgtgcc	agcgggggaag	tgacaatgct	tacggagcac	ttagtatgcc	caggctctgt	420
gttgggggaca	catatttgag	acctaattccc				450

&lt;210&gt; 2

&lt;211&gt; 452

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 117  
<223> 99-27207-117 : polymorphic base C or T

<220>  
<221> misc\_binding  
<222> 98..116  
<223> 99-27207-117.mis1

<220>  
<221> misc\_binding  
<222> 118..136  
<223> 99-27207-117.mis2, complement

<220>  
<221> primer\_bind  
<222> 1..21  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 432..452  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 105..129  
<223> 99-27207-117 potential probe

<400> 2  
ccaaaaagaa atcacagcaa cgtgaagggtt aaggctaact tttcaaacat cagaatcctg 60  
acaatgggtg cagtagcttt caaggagaca tgggtgtgtg ccagcccctc cagggcygtg 120  
tggacagctt tttgtgtatt ttcttgggtg actcacagca tcaaagggag aaaggaggta 180  
gtaattgttc agcacttgac atgtgcttga acacttcgta atcgcaatct gtgccaggca 240  
gtggcaccat ctcccccttt tagatgaaga aaccgaggca ccgagataaa aagtaacttg 300  
ctcaaggcaa ttttaggaagt tgtaaaacca accaacacat atggaatgtg tattatctgc 360  
taggctcatt taatatctca tctgaccttc cagataccca totgatgtag gtaccactcc 420  
cagctccaat tgtgagattc agaggggaga aa 452

<210> 3  
<211> 464  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 53  
<223> 99-27213-53 : polymorphic base A or G

<220>  
<221> misc\_binding  
<222> 34..52  
<223> 99-27213-53.mis1

<220>  
<221> misc\_binding  
<222> 54..73  
<223> 99-27213-53.mis2, potential complement

```

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 446..464
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 41..65
<223> 99-27213-53 potential probe

<400> 3
tatgtagact ctttccccag gaaaaggctt cacacatgta attgtttatg carcgttagg      60
gactctcaga ttctgtggtc tctggaagga tctgagaccc agggaagcca tagcaactgt      120
tcagccagga gacctggctc tcagtttgat tctgctacta accctctgtg tggccttggg      180
cacgtgtctt tccctccctg gacaccagca cacatTTTct ttttttacct atacaattaa      240
gggattgaat gatacgtaaa tttctcttga ctgtaagggt ttgtgtttct gggagggtgag      300
ttcatcactg ggccgaccaa ggtgactctt tgcagctgag gtctagagtg tgacgtacca      360
cccctctgct cctgggtccc tgtctgagcc ctaaggccac cgggcttccc tcacttggtt      420
agtgacttca cctctcctct ctgtgcctca tttcttcate tctc                        464

<210> 4
<211> 546
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 333
<223> 99-27218-333 : polymorphic base G or T

<220>
<221> misc_binding
<222> 314..332
<223> 99-27218-333.mis1

<220>
<221> misc_binding
<222> 334..353
<223> 99-27218-333.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 528..546
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 321..345
<223> 99-27218-333 potential probe

<400> 4
gaagagtaga ggtaaaagag ttaaaatgat taacacattt accctgatct tggctattgt      60
gggtcgtagg tgggtcttat tgtgggtcgt ggctattgta ggtctgataa tcaatattca      120

```

tgtttatata	tgtaatagta	atcattaatg	tgtactttctt	gaaacaattt	agtaccaggt	180
attgtggtaa	gccttggcag	ggggtggcac	acagggtgaat	aggcactggc	cctaccctcg	240
aggggcttac	tgccctgagg	aatgtgaaaa	ggatgaggga	catttgaccc	ccattttgga	300
aaatatgcag	atattttaata	gggtggaccag	gtkggggagt	gtgtttcact	ccttgaaggt	360
gtcccaaagg	agaggggatac	tttggttcct	tctgggaatg	atgagaatga	ccatcactta	420
ttgagcactt	aaccgcatgc	caggcacggg	gctgagcatg	ttatatttta	catcattatc	480
tcatatcctt	gtaagatatt	tctccatttt	tacaatggaa	gctcatgggtg	gcagaatccc	540
tccttt						546

&lt;210&gt; 5

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 233

&lt;223&gt; 99-28108-233 : polymorphic base A or C

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 214..232

&lt;223&gt; 99-28108-233.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 234..253

&lt;223&gt; 99-28108-233.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..18

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 394..413

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 221..245

&lt;223&gt; 99-28108-233 potential probe

&lt;400&gt; 5

catgcctgtt	cttccatcca	cactccaggg	ctgcccacca	gctgacaggc	accatcaact	60
ggcagcaaca	gagcaggcgc	aggtacaaag	aaggcagctc	actcctgctc	ttaggagatc	120
caatcagatc	tgccctgtac	agccatgtag	gctgtgcgct	gcataactcc	agggacatga	180
gtcacacaga	cacaatgtga	gtgtgctccc	ccgtcatgca	acatctggac	acmactaaca	240
gagcatgggtg	aatacatgct	gaattgcatt	cagtatgggt	gtgaactagg	cctgggggaca	300
agaatgaatt	ttacatggaa	agaatttctt	gtagcaggaa	cagaggggat	aacaacagca	360
ataaataata	ataagaagaa	gctaccactt	cttgagcatg	taccacatac	caa	413

&lt;210&gt; 6

&lt;211&gt; 454

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 275

&lt;223&gt; 99-28109-275 : polymorphic base A or G

```

<220>
<221> misc_binding
<222> 255..274
<223> 99-28109-275.mis1, potential

<220>
<221> misc_binding
<222> 276..295
<223> 99-28109-275.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 434..454
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 263..287
<223> 99-28109-275 potential probe

<400> 6
caatgtcatc gacaaccctt ggggggtgtg tctccatcga tcagcagagg ttggcaagca      60
cctggccac atcctgctct cccggcagca ggtacctggg aatggctgtg tgggcgtggc      120
attgagcaag aggggaagtc aggtgctgac ttgttcacag atatcagcct tagaggcaag      180
gctacttgga gataactcaa tggttttggg ggtgtgggca gtccttgctg cctctccagt      240
tcaagtaatg aatgtgtcct aggatgaaca gtaaraatta tagactctgc agctctagca      300
gggtatttagg taaggactga ataacagggc atctgcaggt aggaacaagt ctgggggact      360
ctggcagaag caaaagtggc tcctatgtat cagctcttca ttcaagtgtt taggataatc      420
actgggctca tttgggtgat atttcagtgg aaac                                     454

<210> 7
<211> 549
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 74
<223> 99-28110-75 : polymorphic base C or T

<220>
<221> misc_binding
<222> 54..73
<223> 99-28110-75.mis1, potential

<220>
<221> misc_binding
<222> 75..94
<223> 99-28110-75.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 530..549

```

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 62..86

<223> 99-28110-75 potential probe

<400> 7

aaccacttct	cactcacctc	tgtgcccaca	gccagccccg	cacatcgtgg	ggtttccgtg	60
ggaaccagat	cccygcaggt	acaaatgggg	cccagccctt	cctgtttcct	gcctcaaaag	120
acaccccaac	ttacccaaac	agaggetgcc	atcacccacc	tccatctgcc	ccagtgactc	180
cttccaagcc	catcaggccc	ctttgggttc	tttcacttct	tggacctcaa	tttcctcatg	240
tataaaatga	ggctaataaa	gagacctata	ccacgtgggc	tggctgtgtg	gctttgataa	300
tacatgtaac	aggcttattg	gcacagggtt	agaggccact	accagaagct	acagagatgt	360
gtgaatgcag	gcagtactga	agcagtgggt	aacagcccag	gttcatccgg	ctctaccact	420
cacatgccgt	ggcaccgcct	gcagcctcag	ttttcacacc	tgtacaacgg	gttactacca	480
ctatgcagga	cctctatgag	gatcaaata	cttaccgccg	aaaacatgtg	agttgttggc	540
tactgcggt						549

<210> 8

<211> 518

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 81

<223> 99-28125-81 : polymorphic base A or C

<220>

<221> misc\_binding

<222> 62..80

<223> 99-28125-81.mis1

<220>

<221> misc\_binding

<222> 82..101

<223> 99-28125-81.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 500..518

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 69..93

<223> 99-28125-81 potential probe

<400> 8

ggggagtgtt	gttaaaagta	cagattcyta	agccctaccc	cagatctcct	gcatgtggga	60
ccgaggaagc	tgtaattcca	maagctctct	gggaccttga	tgttccctaa	actctaagaa	120
ccactgtccc	gctgtgactg	tcaagtctcc	acatgacctt	ggtgctgttg	ggctgtttca	180
agttcatttg	accttgggct	ttaaagggtc	ctccttgtga	ggaggaacag	gtaccctgag	240
gctgaccctc	agatctctga	gctggaaagg	acctctggat	accagctcct	ttggtccttc	300
cggcaggatc	caaaagtctg	ggcctgggca	ctggactgga	atctgcacat	ctatcaggag	360
caatgggggg	atggtgcagc	acccattgat	catgggctga	tttagaagga	ggccgtgagg	420
aaggggtgca	ggctggaagc	atgggcgggc	ttcggggaga	ggtgtgtggc	tggaagacag	480



tggttctgcta gctcgtgccc tccttccac ttcatggt

518

<210> 9  
 <211> 472  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 215  
 <223> 99-28134-215 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 196..214  
 <223> 99-28134-215.mis1

<220>  
 <221> misc\_binding  
 <222> 216..235  
 <223> 99-28134-215.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 453..472  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 203..227  
 <223> 99-28134-215 potential probe

<400> 9	
tggatggatg gggcttctac tcaggccagt cttagagggc tcagttttgg gtttaatctt	60
ccctcctgcc ccaaagtctg agtcacagct ttggctgaaa ccccgaggt cctccttctc	120
aaaccccaaa ggggtgcttc ctttctagcc ctgcagccgc cagccttcac gggccccctc	180
ctctggctgg agggctctgc accctgtttg ggtayaggct cctgcacgt ggcggcctcc	240
tgttctagca ccctgccctg tctccaaggc agcactcaga aagctcagcc taggcccctc	300
cagccccctc ctccaccacc aaagactaac acagaagcct ctcagacctt gttcaaagac	360
ctccctgtgg yccwatcttt gtttttcagt ctgtgtccac tcgcccattg cccttcccc	420
agctccaacc agccaagccg cccagcctc tcctgtcatc ctgctgctct ca	472

<210> 10  
 <211> 546  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 96  
 <223> 99-28137-96 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 77..95  
 <223> 99-28137-96.mis1

<220>

<221> misc\_binding  
 <222> 97..116  
 <223> 99-28137-96.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 529..546  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 84..108  
 <223> 99-28137-96 potential probe

<400> 10	
caggaatgct gctattacca ccgctggcca caaggggtcc cagccctgca ggcagccgca	60
ccaaggctcg aaaagcagtc ccagctctta gcaggrcaga ctctgccagg cagagaaggc	120
gccctgaatg gccggccccc agagaaagct gctgagctca tggttatccc tgggtccaca	180
accatttggc actgtaggag caacgataac ccgcatatga tctactgtgca cgttgttatt	240
gcagacagca gagagaaagg ccccagggac cagcagctct gcgtgcagtc tgcgttctgc	300
tcccaggctt attctcattg gctgtgtgac cttgggcaag ccccatcccc tctctgacct	360
tgtttctctg tcttccaagg gaaatcgctg tgatctctaa gggccttttc agcaacagcc	420
ttgccaacaa caaaagcacc tgaagtagcc tttatgttgg agggatatct gagccatcct	480
tgctattcac cacaaactgt cagcttactg aagttttaaa ttcttctgcc agattgtcat	540
tgctcct	546

<210> 11  
 <211> 401  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 305  
 <223> 99-32204-305 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 285..304  
 <223> 99-32204-305.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 306..325  
 <223> 99-32204-305.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 384..401  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding

&lt;222&gt; 293..317

&lt;223&gt; 99-32204-305 potential probe

&lt;400&gt; 11

gtttgggttta	cttagccatc	ccctcccca	atacatacct	cattaccacc	ccaaggtaat	60
cccagtaaat	tgcaagtggg	caaattataa	tcactgtggt	agcagtagct	aacattttatc	120
cagggttcac	tggtgccaga	cagtgttacc	atgccattta	acctgcccac	ctcacctgtg	180
aggcagggtcc	tggtattatc	cacatgttat	ctcagaggga	aatgaagctg	agaggtaaag	240
tgaggacaca	aagccaattt	ccagggggaa	caggactccc	ccagggtggt	ggacttcaga	300
gtccractct	taaccccatc	ctccactgcc	tccctctgcc	accttgtaaa	tcaaaataac	360
gatactagct	aacatcggtt	ttagtctcat	gtagttgagc	c		401

&lt;210&gt; 12

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 118

&lt;223&gt; 99-28149-118 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 98..117

&lt;223&gt; 99-28149-118.mis1, potential

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 119..137

&lt;223&gt; 99-28149-118.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..19

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 459..478

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 106..130

&lt;223&gt; 99-28149-118 potential probe

&lt;400&gt; 12

cagcaaattg	ctagtgaact	tgcaactttt	tcacctttt	cttcatctta	atgaactagg	60
aaggtcattt	tctagatggc	tttgctgaa	taagcccaca	tacgatactg	tgaccttyga	120
tgggaggagc	tagcatgtga	tgtaaggcc	aagtccatgg	aatggacagc	aatgcacaac	180
agataattcc	tcatgtctca	cgacagtgg	aagattccca	gtggctgctt	tggtgagagc	240
ttttaattgg	ggttcttagg	aacttgtatt	attatttaaa	ccagagtgtg	agctcctaga	300
gaacaccggc	tgctcatggtc	cttttttaag	tactccacta	tcttgcgat	aatgagtcct	360
ccttacagtt	tggtgagtc	ataagtacat	ggtgaactta	gcatatcagg	gtacagcata	420
ggggacctgg	ccaaattctg	ctcgttgtta	gtcaccagct	ggatgtccac	attcatca	478

&lt;210&gt; 13

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

<221> allele  
 <222> 285  
 <223> 99-28160-285 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 266..284  
 <223> 99-28160-285.mis1

<220>  
 <221> misc\_binding  
 <222> 286..305  
 <223> 99-28160-285.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 439..456  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 273..297  
 <223> 99-28160-285 potential probe

<400> 13  
 caaaagagtc aaagcagagg ccttgagaat tgcttgagaa tttatgctac tttcaggagc 60  
 tttttgtggt ataacaatgc agagcataga aggaggaagg aaatgggtatt tgtttcaaag 120  
 gatcattatt tactttctggt ttcagtagtc agttagccag tagatatact gagaaactta 180  
 agaaagtccc catcatctct gttgaagaag gataagttgg tgcacgatga caatataaca 240  
 ttatatgtga tcatagtgtt atggatcaag tgctagggga tcgcrataat gggagtaagt 300  
 agctggggtg ggggtgcagat aggaaggacc ttacagtaga ggtgacactt gagcaaggtc 360  
 ttaagggata aataggagtt tgctaggcta tgaagtgggg actagaagtg cagacacttt 420  
 ctgtcttctc cactttggcc tgttactcta tttccc 456

<210> 14  
 <211> 514  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 457  
 <223> 99-28171-458 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 438..456  
 <223> 99-28171-458.mis1

<220>  
 <221> misc\_binding  
 <222> 458..477  
 <223> 99-28171-458.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 494..514  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 445..469  
 <223> 99-28171-458 potential probe

<400> 14  
 ggaagggttg ggattgtgaa rgagggccca ggagctctat agcataccaa acactccatt 60  
 tgtgtacttt gcagctcttt tcccttttgt catcttcact gtatgcttag ggcaccataa 120  
 tttcaattat gcaatttcct ctaaaatctc ccacaaacct cttctggagt ctaagtaact 180  
 tgtcatcgca tttctgtcat gtgatagatg tgtttctaaa aaattggatt ccactccttt 240  
 tcttgaataa tcacatgact tcagattatt tagcatttta tgacataagc agtttgatac 300  
 ctgctttggc ccagcagttt tgggatgggg tagatgttaa ttatctccat atgcaggtaa 360  
 tacagtagaa tcttaggtag ttcatgggtc acacagttaa atgactctct caaggggttg 420  
 acaagggatt tgtactcaag ctttgattcc aaatctctctg ttatttctca ctgggaaatg 480  
 ctttttaaag ttactttaca gcagaactct ttgt 514

<210> 15  
 <211> 550  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 395  
 <223> 99-28173-395 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 375..394  
 <223> 99-28173-395.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 396..414  
 <223> 99-28173-395.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 532..550  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 383..407  
 <223> 99-28173-395 potential probe

<400> 15  
 agagccaatg agatacacgt tcaactagga cagaaatact atcttaacaa atgtcattcc 60  
 cagaaataat caacacaggt gaaagaatta gagatgggga aaagtcaaaa aatgagagag 120  
 ggaaagggtg cagtgtggaa aatagcattt aaattctaac caaactagaa tcagacatat 180  
 aggaaaaatc aaaataaaat ctgggagcct tgaagccgga ggaagaatta aggaaatctg 240  
 tgttcgggag ggaaaagcag aaggggcctt caagtacaac tgaattaaat caagatggac 300

tgccagttct	agaaaaagac	aagttttctcc	attccccgta	aatgctcagg	agtaaacc	360
agtagtcaca	gctgggccag	tcccaactta	tactytgggc	aatcgaaact	catttgccaa	420
gcagagactt	ggaccatact	gcctagaaca	tgcctaccat	tctttcttta	ttcttttgaa	480
agagtactgc	cactcaagtg	acttttgcaa	ttgagagtct	gattatcatc	tctatgctga	540
aaatccttca						550

&lt;210&gt; 16

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 113

&lt;223&gt; 99-32177-113 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 93..112

&lt;223&gt; 99-32177-113.mis1, potential

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 114..132

&lt;223&gt; 99-32177-113.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..19

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 446..466

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 101..125

&lt;223&gt; 99-32177-113 potential probe

&lt;400&gt; 16

cccagaaata	gaaaccaact	atcaggcaaa	gccttcgtga	ggcaatttgg	ggttgtaaca	60
ctacattacc	tacaaatcaa	tggatatatt	aggagaaatt	aaaaagggat	gaygtactct	120
gttcaaaaaa	aaggtttgaa	accagcaga	ttcctgtggg	ctttgcatcc	ccagccctag	180
gcattctctgt	ttaaagaggc	agcttagtga	taaggaggga	ggagagaatt	tctaagaagg	240
ggtagaagtg	tagacttata	tttatatata	tttttaaaaa	gtttttattg	tttagcagct	300
tcagtaaggt	ataatttcaa	gatcataaaa	ttaccaggga	taagtgggta	tagataagta	360
tataggtcat	ttattttgag	tgaattttta	gagttttgta	tctatcaaca	caattcagtt	420
ttagaacatt	ttttaatatc	tcttacttca	ttttgggttg	ctgtaa		466

&lt;210&gt; 17

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 192

&lt;223&gt; 99-32181-192 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

```

<222> 172..191
<223> 99-32181-192.mis1, potential

<220>
<221> misc_binding
<222> 193..212
<223> 99-32181-192.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 432..449
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 180..204
<223> 99-32181-192 potential probe

<400> 17
gtcagacatt cctcatggsc aaacctgata ccactccttt cttgctgtgt actcctaacc      60
tctatcagcc tccctgtcct catcaccag gagtaggggt gggggtgtga gtgtgcccac      120
agagtgggtca tggggattaa atgagatgaa tcatgcatag cccttggcac ccaacaatgg      180
gattgtctact gycagttcct atgctcctct acttgggtat tgccttcatt gctgacaccc      240
atggcttttct ttctgggatg tgtggccttc atcaaaaatg tgtttattta gtgaaaaaaa      300
aaaaaaggac cctgagattt tcatttaatt ttgcctatgt tctcacactg ctccatagca      360
cagcactgat gatactaaaa agctaactcc tggatctaag ctgctaagac cttcacatca      420
ctggcagttt gctaattgtc gtgttctgc                                     449

<210> 18
<211> 458
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 257
<223> 99-32193-258 : polymorphic base G or T

<220>
<221> misc_binding
<222> 238..256
<223> 99-32193-258.mis1

<220>
<221> misc_binding
<222> 258..277
<223> 99-32193-258.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 438..458
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 245..269
<223> 99-32193-258 potential probe

<400> 18
gaaggagatg agattagaga agtggtgcaa attatattgg gattcagacc aggtaaagag      60
tttggacttt attctaagtg cggcagaacc actggagact ttgaaacata gggtgaaatg      120
gtctggcttt taattttaat gggtcattgt gggtactttg tggagaatga aatggaggag      180
ggtgagaatg aaaacttgga gaccaatggg aaggcttcta cgtagtcaa ggcaagaggt      240
aatcgtagct tggactkggt tggagtagtg gagacagaga caactggaga aattccggat      300
ctgtcttgga ggtgtatcgg caggccttgc tgatggactg gatgtaggcg ctgagggaga      360
caggcatgaa ggatgactct tgtgcttttg gctcaagcaa ttcagtagat ggtgatactg      420
tttaccaaga catgatgga gtagaattgg tggtaaaa      458

<210> 19
<211> 450
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 90
<223> 99-28722-90 : polymorphic base C or T

<220>
<221> misc_binding
<222> 71..89
<223> 99-28722-90.mis1

<220>
<221> misc_binding
<222> 91..110
<223> 99-28722-90.mis2, potential complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..449
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 78..102
<223> 99-28722-90 potential probe

<400> 19
atacgataca ctctgccaag tccattttga attccatggc ctgaatcatt aactttcaaa      60
gccaaagcat ttaaaagata aaattatccy cttggcactc ctcaaactgt gctcttgacc      120
tcttctgtta ggctacagtt ttgtttctgg ctgtgcaaat gtcacataat gccactgcac      180
ccggcagtat cttcttcata gcaacagatc ataataaaag tccctcggag gctgtttgtg      240
tttcacatac acatggaatg aaagaaaaat gcagtgtgct atataaagcg agagaaatgc      300
ataagcttca tctttcattt gcagccaatt ggttttaata agcttttatg ctgagaggtg      360
aataattagc atatgttctt aattaagatt gttctagagc agtagagtgc tccaggtcgt      420
taaaaatggg tttgtgtctc aatgtcttaa      450

<210> 20
<211> 452
<212> DNA

```



<213> Homo Sapiens

<220>

<221> allele

<222> 351

<223> 99-28730-351 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 332..350

<223> 99-28730-351.mis1

<220>

<221> misc\_binding

<222> 352..370

<223> 99-28730-351.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 435..451

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 339..363

<223> 99-28730-351 potential probe

<400> 20

attcttggta	tcctacacga	aatctattta	tatccaacat	aactaatgtt	ctgaggaacc	60
cactttatga	aacaggattt	tgtactgcta	ttagtggtga	gtcacaataa	gaagggaaag	120
atacccaagc	tcgcattgtg	agaggtcata	cagagatggg	tccaaatgga	atcaggagtt	180
gaaaggcata	gagatgtccc	tagaaactgg	aggagaccac	caagttgttc	taaagccagg	240
agaagaatct	aacattggcc	tgaaagctaa	agcctacctg	tgggtacaaa	ttggacaaag	300
gatactttgc	tggacagtca	gaaattcagc	tgtggagcac	caggctggca	rtgagctctg	360
ccctcaggca	cgccacatag	gcagcaccag	gactgaggac	atctgaggct	gagaacggat	420
gtaagaacca	tcttggtggt	gtgagatgaa	tt			452

<210> 21

<211> 455

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 407

<223> 99-32306-409 : polymorphic base G or C

<220>

<221> misc\_binding

<222> 387..406

<223> 99-32306-409.mis1, potential

<220>

<221> misc\_binding

<222> 408..427

<223> 99-32306-409.mis2, potential complement

<220>

```

<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 437..454
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 395..419
<223> 99-32306-409 potential probe

<220>
<221> misc_feature
<222> 162
<223> n=a, g, c or t

<400> 21
catttgcacc tgcactcccc tgaccttgca ctgtggtaga ccagttgctc tctaagtctg      60
ctgctcagtt gtcactctgag atagtccttt attgtcttga ggtggggcta tgtctccttt    120
tgtctaggat ttttattggt tttactgcag aatatcatca angatttata tttttcactg    180
aagatgcata aagggtaaac attctgaggg ctaggatgac tgaaaatgtg tttatttggc    240
atcgacactc agtataattt ttttttacca ggtgtagaat tctaagttta waataatttc    300
ctctgtggac tttgaagtta ctgcctcatt gtttccagtg ttactaatga gaaatctsat    360
gcgagtttga ctgtgatttc tttacagatg ccctgttttg ttcttstct tctaaaacat    420
cacaatgatg catttagggg tgggtgattt tttta                                455

<210> 22
<211> 527
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 246
<223> 99-27088-246 : polymorphic base A or G

<220>
<221> misc_binding
<222> 226..245
<223> 99-27088-246.mis1, potential

<220>
<221> misc_binding
<222> 247..266
<223> 99-27088-246.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 510..527
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 234..258
<223> 99-27088-246 potential probe

```

```

<400> 22
gtttttctta gcttgctggt gtttttaact caataaaatg tcaattaact tcgtgagctt      60
tcctttaact ctatataatc tttgcgtttg aatggctgcc aatcaaacgc aaagatagat      120
gttttctttg aatatgggcc aatttccgtg tatgcacctt gttgtcagga tcagctagat      180
tatggtgtag taacaatgtc gatattctcaa tggcttgaca aaagtttggg ttccgctcat      240
gctacrtggt ctgtgagatc agtggggagc tcggagtttc cacagttacc agcaaacgga      300
gagaattctg gagggcctcg aacaggcaag caaatgatct agcccggaag tgatgtttgt      360
cactttcctt cacatctcat tggctgaac tggtcacatg accccaggca accccagagg      420
gccaggaaat tcgggctcct tgtgcttgcc aggaaaggag agtggccctg ttgaaaccgc      480
ctgtgactga gacagtgaag gaaatttgac ctaaccaact ccatctt                    527

```

```

<210> 23
<211> 451
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 204
<223> 99-27090-203 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 185..203
<223> 99-27090-203.mis1

```

```

<220>
<221> misc_binding
<222> 205..224
<223> 99-27090-203.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 431..451
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 192..216
<223> 99-27090-203 potential probe

```

```

<400> 23
gaactctcct ctaatagaac ttccaagttg gccccgcagg cactatcttg gtgcagagga      60
accgctcaag cttgacttta aatctggctc tgccactaaa tcaccaggg cctttcctct      120
ttgggccccg gtttccctgt ctgtaaaatg agaggattga acagggcagt ccctagagtc      180
tggtcagaag ttctcagact gggrettggt ttcttgact tttcattttg tcaactgtga      240
tgtcatcaca cacacacca cgcacagagt ggagtgagga tttcggctgc acagcaggat      300
ggccagatg ataggaggag gcagggggcg atcactggct gggaggatgg ctgggaaaag      360
aggaggaagg ggaaaggcac gcgaggtcac aaatgcacca aaaggcattt cctggcmtag      420
ccctgtgcct cccttctaaa gagccatcac a                                     451

```

```

<210> 24
<211> 473
<212> DNA
<213> Homo Sapiens

```

```

<220>

```

```

<221> allele
<222> 221
<223> 99-27091-220 : polymorphic base A or G

<220>
<221> misc_binding
<222> 201..220
<223> 99-27091-220.mis1, potential

<220>
<221> misc_binding
<222> 222..241
<223> 99-27091-220.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 455..473
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 209..233
<223> 99-27091-220 potential probe

<400> 24
atcagcggat ggtgaagagg agatcagcgg atggtgggag gaaaaatgca ggaaatctct      60
ggacttttca tggaagtatg attcaggaat aaggcagaag ccctcacaaa cttccacag      120
agcaagagggt ggcacaggca cagattctgc tacagagcag acctttccag agaggaaagg      180
ttgggttggg aattttaaga agcatttttc ttgcataac rcaacaccag tcctctgtgt      240
ttagaaaatg cctgtgtgaa ccatcacatt caagagaggg acacaagtgt cagggttcta      300
ggcagccaag ggaagactag ccctttgcct ggaatttggc ttcattttct gacgaatcaa      360
gatttgctct gtcctctgt gcacgccagg acattaagat gcgagaataa gaacttatag      420
cctgtatatt tgccatctaa ttagtgtctt gggtcctaag tgctttgtgc cga          473

<210> 25
<211> 472
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 145
<223> 99-27093-145 : polymorphic base C or T

<220>
<221> misc_binding
<222> 125..144
<223> 99-27093-145.mis1, potential

<220>
<221> misc_binding
<222> 146..165
<223> 99-27093-145.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 453..472
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 133..157
<223> 99-27093-145 potential probe

<400> 25
aggctaggag atgaggagtg gggctgggct gcctctgcac atcatcaaag ccaacactca      60
gtctaattcca aatcttgcta gagcatagaa cataaggtag aatgagtctt taagcaactg      120
ggagtcattct cgaggtaaac agaaytccaa gagtaacgaa ggcccagagt gaatttattt      180
tgagagagtt tcctgttgga gtagcagaca ctctgcagta gtgtttttct ctctcctggg      240
tgggactgcc ctgcctatat gcacttaagg catagagttt cctgttcttg cctcttctca      300
gagccttgca ttgaaactca aatgtattct cagaaatttc tctccacaca atgacatatc      360
gcctctgtgc ttttactctc tttgtctttc tctttctctc aaccattgtt ttccacccat      420
cctctttttc ctaaacttct taagattgtt ggccatttcc ctttctccct cc              472

<210> 26
<211> 455
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 406
<223> 99-27094-406 : polymorphic base C or T

<220>
<221> misc_binding
<222> 387..405
<223> 99-27094-406.mis1

<220>
<221> misc_binding
<222> 407..426
<223> 99-27094-406.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 436..455
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 394..418
<223> 99-27094-406 potential probe

<400> 26
ttatagggtcc caagaagcag ggcctagaaa ccaagagctt gacacgcagt caaactccaa      60
agcagtgtgt gagtgaagga aggaaagacg ggtgttgaaa agcaggtgac tttgagaagg      120
gaggggtccc tggcagcacc tcccttcctc ccggtttcta ggctctaggg tggggctgaa      180
tgatcatgag gcacaaaggt gggtgacatg caagtgtctga gaagcactga gctcacaacg      240
gccctcatca tcttctcaga gccaccaagg agctactggc caccaaggag ctactccata      300
ggccttcctg ttggaattac agaaccactc tgaaccaga gatcaagtcc agccctatcc      360

```

accaggcatc ccaggagaag ccaagaccct atgcccagtt ccgccyggcc accaaggccc 420  
 ttctgaagga gcaccctcat tggggaacct ctcca 455

<210> 27  
 <211> 450  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 410  
 <223> 99-27096-410 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 390..409  
 <223> 99-27096-410.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 411..430  
 <223> 99-27096-410.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 432..450  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 398..422  
 <223> 99-27096-410 potential probe

<400> 27  
 gagtggagag atttgtagct cagctgcaag ttttatttgg agccttgggg ctgccaggct 60  
 gtgcacggaa gtgaggcatt agccagttag tgaacctcgt gctctgccag cttcagcttc 120  
 agtgccgttt tgattttctc tactagttag aagatagtaa atcacatgaa gtcttgaaaa 180  
 cttgggtctg aaaggagcgc cagtggctgg gactgggtgat ggagtggagg agcaagagggc 240  
 atctgagaaa ggccaaaagc actttggttt gatttcagag aagatgacat gttcagttca 300  
 cccattttac catatgcttc gactgtagtt ccactgttt cagggtgcta gttgttggtg 360  
 agaagtggag gaagccaaga accctccccg ggaaaatggt tttcatcacr cacaccaact 420  
 gcattttattt gcaaattctc acactgcccc 450

<210> 28  
 <211> 504  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 83  
 <223> 99-27097-83 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 63..82  
 <223> 99-27097-83.mis1, potential

```

<220>
<221> misc_binding
<222> 84..103
<223> 99-27097-83.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 486..504
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 71..95
<223> 99-27097-83 potential probe

<220>
<221> misc_feature
<222> 213
<223> n=a, g, c or t

<400> 28
gttctttttca ctacctcctg cttaattttt aatttctaag attagaccct tcatctatcc      60
atgacacctg cctgtcatcc ccygaaaaaa ggtgaacgcc gttcagaaat ttttctagcc      120
tgagctcact cccagttcac ttatttttgc tttgtcatgg ctgcccagtc cccacttgta      180
gaccaggaat aggtcatggc tgcggggact acnacctgtc gctgctgcaa gggccggcct      240
ctgtttccgg ggctgagtgg gggccagacc tgccaggagc accatcttct gtgggtcctg      300
cctggatgtc acatcccggc cccaagaagt cactgcaaac cttcgtatta ttgagcttca      360
catcctagaa tttgctgtca ctgtggctgc tgcattgaagt tgcctgaga gaaacgggca      420
ttgtcattaa cagggaattt gatggtctgg gggaaaagtc atcctcattc tcttgcagat      480
ctatgggtga ttgagactgg ctga                                           504

<210> 29
<211> 421
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 162
<223> 99-27098-162 : polymorphic base C or T

<220>
<221> misc_binding
<222> 142..161
<223> 99-27098-162.mis1, potential

<220>
<221> misc_binding
<222> 163..182
<223> 99-27098-162.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind

```

<222> 404..421  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 150..174  
 <223> 99-27098-162 potential probe

<400> 29  
 acttctgccc agtttggtgc aggggagctg ggtagttgcc gacttttcct atcttgatcc 60  
 ctactcagtg taacaattta tctgtacaac tgattccatc accaggatct ttagaccct 120  
 ctggtcattc agccaatcac aagcactcat ccacaggaca cygccgatga tgccatttac 180  
 tgagcagtta ctatgtgctt ggccctagtg agtaccgggt tagcttgtgt gaaccccatg 240  
 gcaaccctg agacaggtag catcatactc caagttgtgg atgacaaaaa actctccaag 300  
 cagctaaaca atatggctta ggtctcacag tgagcagggg gctgggattt gtgccagga 360  
 ggcccgatca ggcctacct ccttaaccat tagggcaaac tgcctccaca tgcagaacac 420  
 t 421

<210> 30  
 <211> 468  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 48  
 <223> 99-27550-48 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 28..47  
 <223> 99-27550-48.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 49..67  
 <223> 99-27550-48.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 448..468  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 36..60  
 <223> 99-27550-48 potential probe

<400> 30  
 tgtgtgtgtg gggatatgtg gaacattttt catgcttgat gtgagccrga agaaaaatga 60  
 gcttctctat ttgataagtg tggacctgcc cacagcacta aatttggttc tgccgtcacc 120  
 ggcgccatga agcagcagcc tggtttagag gcttgctttt ggtttcaaata aatttctcca 180  
 ggctcatgtt acatatgacc cattcacaga ggctggaggg catggcttct ccagtcctta 240  
 gcactaaaga cgtgtctttt ggctcctgca cgactagcac aggcagtaga accagatggg 300  
 ggatgctctg aggttcgaga ggcaggaagg caagcgggag agagcttggg cctggacaga 360  
 gggatgagct ggctccctcc ccagctgtga aatctctgag tctcagttg cttctctgca 420  
 aaatgaggat aataatcccc acctcgggac tgaggattaa cgaggcaa 468



<210> 31  
 <211> 452  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 335  
 <223> 99-27558-335 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 316..334  
 <223> 99-27558-335.mis1

<220>  
 <221> misc\_binding  
 <222> 336..355  
 <223> 99-27558-335.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 432..452  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 323..347  
 <223> 99-27558-335 potential probe

<400> 31  
 gtcaaatcaa cactcgtcta cattcaaatt tcacattttt cccctcttaa gataacagta 60  
 taattgagaa ctgacagga cctaatgaca gtatgggtccc ctacactga atgggtcacat 120  
 ttgcctaaat tgaaataacg tatgctagaa acaatcttaa gcagatctgt cattttaact 180  
 atatgtgatg tagagttgaa tgttcattcc agataattta gtcaatgtag gtaactaatg 240  
 gctcacacta attcaggcca agaaaatgca ttccctctct ttcttctctg ccctttctct 300  
 tgctgaaaga gaaatctcat ggccgcatat gttayacaat catgcccact tatgtaggat 360  
 cacagaaggc agaatagcag agaagaaaga aaactggaga gttgggtcct gacctagcc 420  
 atcttgtatg accttagaca attcattacc tt 452

<210> 32  
 <211> 465  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 106  
 <223> 99-27561-106 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 87..105  
 <223> 99-27561-106.mis1

<220>  
 <221> misc\_binding  
 <222> 107..126

<223> 99-27561-106.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 446..465

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 94..118

<223> 99-27561-106 potential probe

<400> 32

cagtcactca	aacaatgtca	caaagaaccc	tttgacagga	atgtatcctg	tggtgactct	60
actttgctct	gagtagtctt	tccccagggtg	atgataaaaa	tggtortcat	cgccagggtt	120
gtgtcctggt	tagtaggaat	atacaagaag	agctcagtaa	atgctggccc	caccactaag	180
caaaaacaaa	acttttggtg	ttgttattgt	tgttttaaat	aacagcttag	acctttcttc	240
tttccttggt	attctctttc	atctgtaatc	cagttttcta	cttctgaagt	atagaatggt	300
ctgatgattt	attcttcatt	acccacaact	tgcacatggt	tatttaaaaa	tgccaggatt	360
gcctggccgt	tgtgtgctgt	taacctttgt	ttgctgtag	tggatccctg	aagttcaggc	420
tcccagggga	gcagataatg	ggtatccagt	tctgcaata	tccac		465

<210> 33

<211> 470

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 364

<223> 99-27562-366 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 344..363

<223> 99-27562-366.misl, potential

<220>

<221> misc\_binding

<222> 365..384

<223> 99-27562-366.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 450..470

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 352..376

<223> 99-27562-366 potential probe

<400> 33

tccctccacc	accactttcc	tcatacccg	gttcagagac	ccccaagsc	ccctyamamt	60
cccagaaaca	ccccctggc	cactcctaac	ttgccatgcc	caggagttag	gtgcttccac	120
tagtgacatg	gagctggcgt	ttggggggca	cctcagcagg	tgacgggaag	agaagacccc	180
agcctcacca	gctgggctgc	agcaggggaga	ggagtcctca	tggtccagca	gggactctca	240
gctgtttttcc	tgtaaaacca	tggttctcaa	ctggggggcca	ctgagatgtc	tagagagatg	300
tttttgtttt	cacaactcgg	ggagggtgct	actgacatct	tgtgggtaga	ggccaggaat	360
gctkttaaag	atcctacaag	gaaggcacag	gacagtctcc	tacatcaaaa	tatgacccag	420
ccccaatgtc	accactgctg	gggttgacac	tggcactgct	atcttaatta		470

&lt;210&gt; 34

&lt;211&gt; 1003

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 738

&lt;223&gt; 16-31-738 : polymorphic base C or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 715..737

&lt;223&gt; 16-31-738.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 739..761

&lt;223&gt; 16-31-738.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..25

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 975..1003

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 726..750

&lt;223&gt; 16-31-738 potential probe

&lt;400&gt; 34

ccactttgga	taaagtccct	ctaactagca	gcttttaact	gcctttgcga	tgaggaggtct	60
accacccttc	ctttacccaa	agatgaattt	cggatcattt	tctgtacaat	ttttaaagga	120
cgtttgaata	atatttcttt	ctttatcatt	gcggacgctc	ccaaatctca	gcggaggtgt	180
agcgcataag	ggcagttgaa	ggagatatag	atcctataga	tcctgtataa	aagggggtct	240
ggaattctgc	atttcccgtt	cgctagcatt	cgcgaaactc	ttgagacagc	gtacgcttcc	300
tatggcatca	gttggaattt	aagggcaagg	gagaagggtg	ctcggcgtgc	ggccgcggcg	360
taccggagct	gcactttgca	gggagaagtg	gctgcgtaat	ccggagcaca	gtcagtatgg	420
tgctgtgtgc	ttgttgtttt	gttttgtttt	ccacttttct	cccccttttc	ccgccacacc	480
actattttgg	aaagtgttggc	cactttggat	aaatgccctc	taactagcag	cttttaactg	540
cctttgcgat	gggaggtcta	ccacccttcc	tttaccctaa	gatgaatttc	ggatcatttt	600
ctgtacaatt	tttaaaggac	gtttgaataa	tatttctttc	tttatcattg	cggacgctcc	660
caaatctcag	ccggaggtgt	agcgcataag	ggcagttgaa	ggagatatag	atcctaataag	720
atcctgtata	aaaggggstc	tggaatttcg	tcagtttgaa	gttcgctagc	attcgcgaaa	780
ctcttgagac	aggctacgct	tcctatggca	tcagtttgaa	ttttaagggc	aagggagaag	840
gggacgaagc	ttcttttggg	ggcatcctta	ctctgctact	gaattttagg	tgctgggctt	900
tgccactca	atttaaaaag	accaggttta	aataataatg	gtttatggca	ccatcagttt	960
taattattta	ttatgacata	ggagtttaga	aaacttttga	tag		1003

<210> 35  
 <211> 455  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 300  
 <223> 99-27110-301 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 281..299  
 <223> 99-27110-301.mis1

<220>  
 <221> misc\_binding  
 <222> 301..319  
 <223> 99-27110-301.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 438..455  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 288..312  
 <223> 99-27110-301 potential probe

<400> 35  
 ttcacattgg gtggcagctg gtcgaaacat tcctgtcagt gactgcagga cagtaacctt 60  
 cagacctcga atgcccccta attttctgaa atgaagttac agttcctttt ctgttcaact 120  
 agcaagctaa agttcagccc tcttacctga ttccacactg atcatctgga aggaaggtag 180  
 gattcaagga gaactctttg agtgggaagag cagtcagaga tgtaattctg cgcctgttct 240  
 cttacagcaa aaccaagaac ttttgctcta agagagtgga ctttgggagt gaactttgts 300  
 agatgattag atggtgatgt cctttcttgt taaaggagga aatccatgta ggagcctcag 360  
 gatcgcacag gctgaggact gagtgtaaa catggcaggc cttccttcat ggggcttgag 420  
 ggatttctctg cagtgccctt cctcctctcc ctgac 455

<210> 36  
 <211> 546  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 400  
 <223> 99-27563-400 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 381..399  
 <223> 99-27563-400.mis1

<220>  
 <221> misc\_binding  
 <222> 401..420

<223> 99-27563-400.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 526..546

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 388..412

<223> 99-27563-400 potential probe

<400> 36

taaccacact gaaacctctt cggttgtctt gaaacctttc tactttttct gtactttttg	60
ttttgttctt ggtctcccgc ttggggcatt tgtgggactc cagcacgttt tctggcttct	120
gcttcacact gctccatcgg ggaatgacac actgcggtgt ctgcagctcc tggaagggtg	180
catttgacaa cacatgtggg agaggaggtc cttggagtgc tgcagctttg ggaaagctgc	240
ctcgtttccc ttttctctta gaagcagaac cagctctacg agagtgagac tgggaacttg	300
atggctcaga gagcatcttt tctctccatt ttagaaaatc agattttctc ctgtgggaaa	360
aaaaaattcc atgcactctc tctctgttaa agatcagctr ttcccttctg atcttggaag	420
gaggttctgc actcctggaa ccggtcacag gaacgcacag atcatggcag gatgcgctgg	480
gacggcccat cttggcaagg ttcagtctga atggcatgga gaccgggaga tagaggggtt	540
ttagat	546

<210> 37

<211> 513

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 443

<223> 99-27573-443 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 423..442

<223> 99-27573-443.mis1, potential

<220>

<221> misc\_binding

<222> 444..462

<223> 99-27573-443.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 496..513

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 431..455

<223> 99-27573-443 potential probe

```

<400> 37
gtctcgtttc attcagtgac attttgaaca cacacgtggt ccctgtctgc agcaccagg 60
tgctcttcac ctaagatacc cgtcttctg ctaaaccagt acaccagttt ccacgagcag 120
tttcccagg cttctgact cctcagcatg ctctcagatt gtttcccctg cgggagaact 180
agcaccgtgt tcttcagtac cagcatggc tcctggccag cccctagggtg caatcctcca 240
acacggtgac actcagcaac ctaggggcaa gtttaccac ttgtctccct atacacaatg 300
ctcctgcacc tgctcaccta ccaggggccc tcccggccca gcagcctacc ctgtctgcca 360
cagctctgct tcctggcatt cccacctctg cctcaagctt tgcctttcct ctcaagctcc 420
ccgccctgct ctaatcttgc ccktcttggt ctcagctcca gttccacctc cccaatact 480
ccccctgtgg cctctctaac ccatacacct tcc 513

```

```

<210> 38
<211> 411
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 133
<223> 99-28732-133 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 114..132
<223> 99-28732-133.mis1

```

```

<220>
<221> misc_binding
<222> 134..153
<223> 99-28732-133.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 391..410
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 121..145
<223> 99-28732-133 potential probe

```

```

<400> 38
ctgttggtgt tccccctca cagcataaa ccagtgtacg tgaatcctaa cttgccaata 60
cctcagagat aggaaaatat attttgatgt acagacgctt tatgggcttg tgctggaagg 120
tcacgtgcct tartggatcat gagatcctgg tgcaaagtgg atagaaagtg cttctttgta 180
tgacgcgtcc tccccttcgt agatggccag tcccccgaa tgtctttaat atctgaactt 240
gagaatgagg atgttgattt ctaattctag cccaacctt gattgtctat ggctcttcag 300
ttatcctgga aaatcaaaat atattttact atcttgaagt attggcaagt taggattcat 360
aaacacttgg atgaccagcc acaaggcaat gtggcattgt ggttaagagg c 411

```

```

<210> 39
<211> 457
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele

```

```

<222> 56
<223> 99-28735-56 : polymorphic base C or T

<220>
<221> misc_binding
<222> 36..55
<223> 99-28735-56.mis1, potential

<220>
<221> misc_binding
<222> 57..76
<223> 99-28735-56.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 438..456
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 44..68
<223> 99-28735-56 potential probe

<400> 39
ttgtcctgat taccatttct aagactaaag aatctttacg tggtgaaagt cctagycagc      60
catcattcgg cacaacagtg gcttgtcaaa agggatgtga gcaggtcata ccagcctcag      120
gagggtagag caaagcaaaa aaggaaatct tgccatgtca tgtttcaaag ctcttggtgaa      180
tcttgagatc tcattagaaa tctgtcacag ttttaataga gtcccaccaa gatgtgctct      240
gcctgctctt ttgcaggttg gtcaggatag gaagcagggc ctcccagtg ccagttcctc      300
ggggaacaat tcacgagaat ctaaggagtt gtctcccagc agtgccagga aagagtggct      360
gccaaaatgt tactagtaat taaggactag gcacctgagg gcagcaacta agcacatact      420
agttattata acatccagta gaacaaatga aactcct                                457

<210> 40
<211> 453
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 399
<223> 99-28736-399 : polymorphic base C or T

<220>
<221> misc_binding
<222> 379..398
<223> 99-28736-399.mis1, potential

<220>
<221> misc_binding
<222> 400..418
<223> 99-28736-399.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

```

<220>  
 <221> primer\_bind  
 <222> 434..452  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 387..411  
 <223> 99-28736-399 potential probe

<400> 40  
 gtttcttatt actgattctg aacatctgtc acaaagcaga ttttggtcag gacattatga 60  
 acaactgcat cattcattac cgggtgaaat aagtgttaaca ccaccaggcc actataccac 120  
 cagtgcatt catttcccac aaaacatcaa cactgaaaca tacactacac atgcacacaa 180  
 aatggcatga atacaatgat tattcaatgt atagtctaaa ttttcttat ccttttaatc 240  
 cacttgtag aaattccttt tctcaagata gatgaggggt aaaagtgaca ttttctaacc 300  
 ttctcctcta cttcgaaatt ctgtgaactt cctctaata gaactaagta gcggtgcagt 360  
 ttctctttaa tgataaatga tttgttggtt ttttgtgtgc attgcttaga agcagtgcagt 420  
 gttaaggaca acaccttaaa agtgtagct ccc 453

<210> 41  
 <211> 458  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 319  
 <223> 99-28738-319 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 299..318  
 <223> 99-28738-319.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 320..338  
 <223> 99-28738-319.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 441..457  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 307..331  
 <223> 99-28738-319 potential probe

<400> 41  
 ggagagacac actgagacat tctcttctag tccagactat gagagcatgt aacacatata 60  
 acatgagacc cagcacctag caccgtgtca gacacatgat tatctgtgta atgactgagt 120  
 aagcaaattc agagatgtgc tctcaaagcg atctggcagc aagttacttc ctcatgcct 180  
 tcactgacct tgactctgac attgttcttc ataccaggat ttttagagac ttctcacttc 240  
 atccaaacac cccagctggc agtgctacta gtgtgcagcc accatcaggg aaaagctttg 300  
 gattctatgc aaaacaggyt ctcagggttg taacaatgtg ggggcctgag tggcaagggg 360  
 cccagggtcg aagtcagagc cctagaggag actcctggtc acctagatgc atctgggaaa 420



ttaacccctg ggccttgctc gctgtwacct gcaatacg

458

<210> 42

<211> 509

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 364

<223> 99-28739-364 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 345..363

<223> 99-28739-364.mis1

<220>

<221> misc\_binding

<222> 365..384

<223> 99-28739-364.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..17

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 489..508

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 352..376

<223> 99-28739-364 potential probe

<400> 42

ctcctcctcc	aaaacacacg	gagacactgg	tatttggtg	cacatgtgtg	tacatatgta	60
caaatgtgtg	actatgtatg	tgtacgtgtg	tacacgcaca	ctttcttttt	aggaagactc	120
caaatcatct	cgggacttta	gacctggaga	acgtaagtct	cctgggtcag	acgcctacca	180
ggctgtcctc	ttttatccaa	actggcagat	ctgcattggc	tttaggcact	gaccctcatt	240
cacatggctg	tgtgcccaga	gcaggatatcc	tatacccgt	gtgattctca	ttgggtctaaa	300
tccttgcaaa	tgatggatgt	agggtaagca	tgtgactcag	ttctgcatac	tgggatgtga	360
ggaygggtaa	actaggaaga	aattcctgga	aaagttttct	cattcttaaa	ggaacacaag	420
gatgagacac	ctccttccgc	cagagtgtgg	ccatgataca	tgggaactgtg	gtagtcatct	480
cgtcccgcga	gggaaacaag	acagaggcc				509

<210> 43

<211> 549

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 185

<223> 99-27875-185 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 165..184

<223> 99-27875-185.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 186..204  
 <223> 99-27875-185.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 531..549  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 173..197  
 <223> 99-27875-185 potential probe

<400> 43  
 taagggtaaa ggagagagat ttaagattaa tataagtaaaa accctataaaa cctaacttta 60  
 agttaactat taagtatcta tattaactca tgaaaagttt atctttttaa aaatatcaac 120  
 ttcctagctc agatcactga caaggtttat aattagtgt caataccatc cccactaata 180  
 agtaycaagt accagggtc cttggagaaa tgtctgattc caagtctggg acaggaaatg 240  
 tataagatga gatggcaata tcttgtcata ttaaaggaag ttttcagaga ctacaagggc 300  
 tgtgtcaaaa ggactcagca gagaactcct agtcaccaa gactggacaa tttaaccacc 360  
 aataagataa ctgcaactga ctgaatatca aatatttgaa tctaaagttc acaacagtag 420  
 gagggaaaaa cgaaaaggca ggcaggaact cgtgcatttc tgaaggatgt tagggaacca 480  
 actaatggaa aacaggttta aaaagacaag ggggtgggaga atggatgaag macttattct 540  
 cacctttct 549

<210> 44  
 <211> 462  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 176  
 <223> 99-27880-176 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 156..175  
 <223> 99-27880-176.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 177..195  
 <223> 99-27880-176.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 444..462  
 <223> downstream amplification primer, complement

<220>

<221> misc\_binding  
 <222> 164..188  
 <223> 99-27880-176 potential probe

<400> 44  
 gtaggggtgaa agttgtggca ggaggattgt tctagatata tagggcagac aacattgctg 60  
 aagttggggt gaggatgtat cagtaaccaa ctggagttct ggaaacaacc tccgtccagg 120  
 tatttggggg gcctatatga cagaaaggcc agcaagcaag cttaccctca tcactyactt 180  
 ggcctctatt caaatagcct acttttgtct gatctatcca gggatgtgtg ggaaggcata 240  
 ttggggctgg tgagttctat atttcttttag aaatttatta tgactcagct gtttatgact 300  
 taagtttttt gtgatttcta tacgtttattc ctgggtatcat ctcttagagt aatacattcc 360  
 atataaaata cgaggtgtag ctaaacataa ctttctaagg ccccaaagtg ttttcccagg 420  
 cccagcgccc acccatttcc tgtcttctct tcttactcac tg 462

<210> 45  
 <211> 497  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 373  
 <223> 99-28747-371 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 353..372  
 <223> 99-28747-371.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 374..392  
 <223> 99-28747-371.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 478..496  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 361..385  
 <223> 99-28747-371 potential probe

<400> 45  
 agcaacactc agtgggctcg tcgccatgac gccagcctgt ggaggaaagt ggggagggga 60  
 ccaacacagg acccctgtgg cagaagctgc cttggaactg agaaacatca ctagaactca 120  
 tcaagccctc caccacctg gtgcagatga actgaggtct gaagagggga gaccacctgc 180  
 ccaaagggag aaaagcagtc agtaggatgg ccgggattag atctggctct cagttcctag 240  
 ttcctatgaa gtaatgcagg gagaagacag ctggctggca ggatgccagc agcatccctc 300  
 caggggggca aggggtgcc tttctctaca ggcttttagg gaccagacct tctcaatcta 360  
 gatagacaga atyctccctc ccaggacatc cccagaagcc acagagttct gggggctctc 420  
 agagatagca ggagaccacc accccagaat gaggatagcc attcttggtg tgagcrggat 480  
 ttcccctacc caaggac 497

<210> 46  
 <211> 448  
 <212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 352

<223> 99-28753-353 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 332..351

<223> 99-28753-353.mis1, potential

<220>

<221> misc\_binding

<222> 353..371

<223> 99-28753-353.mis2, complement

<220>

<221> primer\_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 427..447

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 340..364

<223> 99-28753-353 potential probe

<400> 46

ccacagccct	cgctattaac	catggggcag	tactccctcc	acaagaggca	ttcggtttgc	60
gaggagagct	tagaggtttg	gaaagaagac	tcatacctcc	ggcctggagg	atcagggagg	120
acttagccct	ctgagctgga	cttctgggga	caggttggat	tttagcaggt	gagtgttaata	180
ggcacaggag	aggccctcta	ggctgagggg	actgagcaaa	ggcaaggaga	caggctgggc	240
tttgtgcctt	gggaggagtg	tggtgtatgg	agaacaggga	gtaggagaaa	gaaacaatga	300
ggctggggag	gggcatggag	gtcaggtgat	gcagggcatt	ctacagggct	tyaccatctg	360
gagaggggagc	ctgggtgagc	ttgtgagcag	agaagctcaa	ttttggggagc	acactgtcct	420
ctggagggaaa	ggagaagtaa	ggggattt				448

<210> 47

<211> 471

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 207

<223> 99-28755-206 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 187..206

<223> 99-28755-206.mis1, potential

<220>

<221> misc\_binding

<222> 208..226

<223> 99-28755-206.mis2, complement

<220>

<221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 452..470  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 195..219  
 <223> 99-28755-206 potential probe

<400> 47  
 tcttgaggga tatgaggcat tataaaaatt cctgggttgt gggagaatga gtacttatca 60  
 tcttctcctt tgagttaaat ttttttgtgc ccaattttat agaaatcatg tggatccctt 120  
 ttgcaaatgg atgaatgctg ttagaagctg aacaggcaag gctgtatgtt tggagaagct 180  
 gggaccctat ccgctgcact cagagcrggg accatccgcc aaggagagaca gggaagggtc 240  
 tgtgccacct gctggaggga gggcagagga aggcaggag aaggctatgg gtctgctgac 300  
 aaaccacgc tgctctgag ggtgaggga ggttgggctt tcctgaaggg aggggcctcc 360  
 atttctgtc tgatgctggc atggcctgtg ctaggtgtcc ccgtgggctc tcattcagcc 420  
 ttcactgtga gcctccgagg tggacttaga tccattgcta aacagatgag g 471

<210> 48  
 <211> 541  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 366  
 <223> 99-32333-366 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 346..365  
 <223> 99-32333-366.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 367..386  
 <223> 99-32333-366.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 520..540  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 354..378  
 <223> 99-32333-366 potential probe

<400> 48  
 acttagttca ttctttgagg ttaaattgtcc tagaaagaac yayacggttg atgtctaaca 60  
 ttacgtacac tcaagcttta gaatggccaa gtggatgacg ctgtttcttt caattaacct 120  
 gacatataca acctctcctt tctagccatt cttctgggtg gctttcctag taatctgccc 180

```

aggagtgtaa cttctgcagg cagaggtgag gtaaaaatgg tgaagtaagg caaggagata 240
aagaggaaga aggcaaggag cagtgtattca gaagcatcag accgaaaaga aaatttgtgg 300
gagctgatga agacttctta taaacttcta tcttcagcaa tacttgaatg ctaggaaagg 360
ctatayccca gacaactatt atccccattta tgatctgtca agctttcaca gtgaaatcac 420
tcaggattct tattttttttt aaaaaaaccc cagatccctg ggtctcagac ctagtgaatc 480
agcatctcca gagtagaacc taggaattca catctttacc ccaaaagtac ccagacaat 540
t

```

<210> 49

<211> 416

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 323

<223> 16-38-323 : polymorphic base A or C

<220>

<221> misc\_binding

<222> 300..322

<223> 16-38-323.mis1

<220>

<221> misc\_binding

<222> 324..346

<223> 16-38-323.mis2, complement

<220>

<221> primer\_bind

<222> 1..28

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 389..416

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 311..335

<223> 16-38-323 potential probe

<400> 49

```

agttgtcttt ttatgttttg catcttacct ggtattgcct ttgccattt cactgctgca 60
atcacttgcc gccctcctaa catgttgagc gtatgcatga tcctccaagt tgagtctgga 120
acagagctat catatcctgc atataacact tcagggtcaa taacctccaa cagtgcacc 180
agggtagggg tgagttgtgg taacgttgca ggaactattg ttttgttacc aggattttca 240
gaggtttctt gtgagactcc tgtagtgcc tgctgaattc cttttatttt tttctttggt 300
tttcgagctg tgggtattta aamaaataca tagaaatgaa ctgtaatggg aaggtctgcg 360
ctacacagtt tattcaagaa gtattttttac tttctaaaac tattaagatg ggagaa 416

```

<210> 50

<211> 506

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 179

<223> 99-28484-179 : polymorphic base A or T

<220>

<221> misc\_binding  
 <222> 160..178  
 <223> 99-28484-179.mis1

<220>  
 <221> misc\_binding  
 <222> 180..199  
 <223> 99-28484-179.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 488..505  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 167..191  
 <223> 99-28484-179 potential probe

<400> 50  
 ggggctacaa aatattctgg tactccatcc tagaccagag tttcaagggt cggtatcatt 60  
 tgtagcatga tactggatcc tcacagtgtc tgcctttcat tcagggtgcc ggaaacgtct 120  
 gcctgaatga atgggtgtaa tttacctgca cattttacat gcttctctag gtgtgtgawt 180  
 aactcataat ccatccatga ctttcaccca taatcctcct tgtagcaatt gctttgcttg 240  
 caacaaaact aagtagacat atctagcttt atgcatgggt ttctctctct gaactctaac 300  
 ataaactcag cctcaggaat tattcggttt ctactacatt tgccattctg attgggaacc 360  
 accagcattc aggtattcac ctggaacaag gcattttgtt ccaagggttc ctcaactaaa 420  
 agcaagcacc ctagcaatag ttcataatgg aacttcctaa cattctcaga atgtttggca 480  
 cagctgtgag tgaacacaca ttgagc 506

<210> 51  
 <211> 486  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 364  
 <223> 99-30853-364 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 345..363  
 <223> 99-30853-364.mis1

<220>  
 <221> misc\_binding  
 <222> 365..384  
 <223> 99-30853-364.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 465..485

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 352..376

<223> 99-30853-364 potential probe

<400> 51

tggttctcaag	caaggtcggc	aaactatgac	ctgcccgtca	aatccaacct	gccacctgtc	60
acctaacaat	tctgtaactg	ctcccacata	caacatgggc	gtcatcataa	atcctatagg	120
tattgttgag	agcaggagga	aagtttggtt	gagtgaagtga	gagaccttac	ccaagccttc	180
ctgtggtctc	taggagtcac	ggcagagtcc	gctgacactg	gtctgctttt	aaccagcctt	240
gccagtgaac	tttcaaattc	cctgaggagc	aaaaggccaa	attgaacctg	aaagaaaaca	300
cctctcagtg	ttgactgagt	tgtagtagaa	aatggacctg	acaaaacgtt	agtacacttt	360
ctcrattggg	ttagctcaaa	atatgttatt	aggtcttttt	tccagaggaa	aatgcttaca	420
cagaccctct	tcctccccac	tccttcacct	ctacaggaga	aaatgaggmw	wyacagaaca	480
ctatta						486

<210> 52

<211> 467

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 198

<223> 99-28485-198 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 179..197

<223> 99-28485-198.mis1

<220>

<221> misc\_binding

<222> 199..217

<223> 99-28485-198.mis2, complement

<220>

<221> primer\_bind

<222> 1..17

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 449..466

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 186..210

<223> 99-28485-198 potential probe

<400> 52

gcattataag	gcaacacctg	gatctgaatt	cagctctgcc	taattccaaa	atctatgcac	60
ctcataacct	tgtgactgtt	gcctggcagg	ggcctgcaga	gtagcatcca	ttaagcttga	120
cagagttttt	taagattatg	tgggtcactt	aacagacagt	cttaaggtaa	gggttaaacat	180
caaaagttaat	ttctgttktc	tatctatcct	gcccccttcta	tccttcatat	cacaatggag	240
cacaaattat	aattaagaga	tacaaaagca	ttcagtcact	tccatttttt	tcttttagata	300
cttactatat	taagtcttaa	atgaacatat	tggcattcca	aattattaag	ataatgtcat	360
gctgggtcatt	gaaatgctaa	attaacatga	agactacatt	tcaaaaatac	aaaagtataa	420
ataggagtgt	tttgtatatt	cataccacga	tttttgcctt	tagagga		467



<210> 53  
 <211> 474  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 354  
 <223> 99-30858-354 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 334..353  
 <223> 99-30858-354.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 355..373  
 <223> 99-30858-354.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 456..473  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 342..366  
 <223> 99-30858-354 potential probe

<400> 53  
 aatctactgg gaaactgtcc atttcaacaa gagcacctca gacagtaact ggaaagagaa 60  
 atagctcata ttctcaggaa cgtagtcat cttgaagcag catgattcgt gataacctgga 120  
 aaatgcacat ggcagtcact aaaattgggt tctagggata cttttaataa gatttgagag 180  
 gagctggatc cattcattcc catggtacct aacacagcac cactacacag caggcctgtc 240  
 ccaaatttcc tttgctgctg gagaacatcc tcatggggga gcccccaagc tgcctaggaa 300  
 atgggttaac aggagggcac tcagggatct ccttcagttt ctccagccat cttygctgcc 360  
 acgcccagc ccaggccacc ttcacctctc acctgggcgc ttccactggc cgcctgacac 420  
 atcttgctac tggcttccac tcttgctccc agaaccctt cttcacatag cagc 474

<210> 54  
 <211> 489  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 311  
 <223> 99-32002-313 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 292..310  
 <223> 99-32002-313.mis1

<220>  
 <221> misc\_binding  
 <222> 312..331

<223> 99-32002-313.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 472..488

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 299..323

<223> 99-32002-313 potential probe

<400> 54

aagaccacat ttcagcaagg actggctctg aatgacacct ggattctatg gcctttccct	60
ccactttggg aagctcttta gttagacagg tactgtaggc ggcaggagaa aaaaagctaa	120
ttattacttg ttggagtctt gtctcaggca tgctgtggg ctgtgcaaga ttcgctgctc	180
tgctgctgtt gtcattttga tgctacaatt acagagaggc gggttcagcac ccagccgac	240
gggtgtggctg ccaaacacat ttgagcatga caagataaat ttgttagaca ccagcacagg	300
gtgggtgaga rgacatcctg ctgactttat aaagtgatgt ggggcagggt tgctgaggta	360
agtgatgatt gtcaagtttg ccagagatga tagataactc ctttggcaga acacctagg	420
cattcctttt aaagtcagggt agctaagagg ctgtttggtt tctgcagcgc tgctacctac	480
ttggggaac	489

<210> 55

<211> 526

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 366

<223> 18-15-366 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 347..365

<223> 18-15-366.mis1

<220>

<221> misc\_binding

<222> 367..385

<223> 18-15-366.mis2, complement

<220>

<221> primer\_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 507..525

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 354..378

<223> 18-15-366 potential probe

```

<400> 55
atgaaattag aatgacctac atcaaagagc taggaaaagc cattgtcaag agggaaggaa      60
actccagcca gaactggcag cggttttatc aactgacaaa actcttggat tctatgcatg      120
aagtaagtgt caaacataaa gccaaatata agagttttct gggacaaagt atgttttgat      180
tagtgaatat aattatatac cagcagcgcc cccacccccg ccccagttt gtggatgttg      240
gtgatagctt gagttcaact tatgaacttc agttttgtag acatttttcc taaggccaat      300
tatgaaatat cctttcacct agtcatgtgt atataaaatc accatgttat tacagaattt      360
agtaayactg tttttaaaaa gtatgattaa tccattaaat tagaataatg cacccttcat      420
atattatggg actacagtga ttcatgaaat aattctatat aattctacat acaatcaaag      480
aaatataaaa tgtgttttgt acggaagtgc ttatttttca tctggg      526

```

```

<210> 56
<211> 426
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 174
<223> 18-20-174 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 155..173
<223> 18-20-174.mis1

```

```

<220>
<221> misc_binding
<222> 175..194
<223> 18-20-174.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 408..425
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 162..186
<223> 18-20-174 potential probe

```

```

<400> 56
ttctctcttc agtgttcatg aaccacagat aagttccttt cccacatttt cacagtcata      60
ggatccagta aggaaggccc gagtgatact tgctgggtca ctgagctggg gatgcctggg      120
ctcagctcca gacatgctgg gtcccaggcc tgagcttggt tcttcaaact aggratacat      180
caattactta attattgctg gtacaaaaca gggctaaagg aaggccaggc tcaagagcac      240
agttaaaaaa gaaatccctt ccacagctgc ccttgccctg gttgggggtg aggccagcag      300
gcccctcatt gccaggtagg aagcattaga tacgcctgat gagctagaag ctttcttttt      360
tadacaatga agtagaggca aggtgttcta actccccgtc cagagaagag smaggaaagc      420
tagaac      426

```

```

<210> 57
<211> 458
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele

```

```

<222> 178
<223> 18-31-178 : polymorphic base C or T

<220>
<221> misc_binding
<222> 158..177
<223> 18-31-178.mis1, potential

<220>
<221> misc_binding
<222> 179..197
<223> 18-31-178.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 437..457
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 166..190
<223> 18-31-178 potential probe

<400> 57
gtttttgtat gattcagtgt gaattaaatc ccacagtgt aaggacttta ctttcttaat      60
gtagattttc aaatacacaa ttactgatgt ttataagtag atttattaca ccaaagcacc      120
tagcaaattc ttgaatggat caggtcttat ttttcagtct tactttgcaa atttaagyca      180
aataattaag gatttggttaa atatttgtct taatatcaag cttttgcata tcggggccct      240
cttttataag ctttataagc aatcttttgt tttctctgct tgctcaaagt agctatgttt      300
gttgatatctg ttagtatttg ctctataaca aacatactgg gtgccttccc acttagattt      360
ggcaattatc actcctgtaa atgagatatt acataagata ggaaaaagaa cagtatcttt      420
ccaagaagaa tagtatcctt ccatattaac agtttaga                               458

<210> 58
<211> 474
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 395
<223> 18-38-395 : polymorphic base A or T

<220>
<221> misc_binding
<222> 375..394
<223> 18-38-395.mis1, potential

<220>
<221> misc_binding
<222> 396..414
<223> 18-38-395.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

```

<220>  
 <221> primer\_bind  
 <222> 456..473  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 383..407  
 <223> 18-38-395 potential probe

<400> 58  
 actgtaattg tatggtaaca tttaactgta caggacttgg gaagttaggt ctagctgtga 60  
 gtccaagaaa aggaaatgat ttgtttcatc agccaacaat ttttgctata aaagcaaagc 120  
 aatgtgagtg gggggccctaa aaatccccac tgttttcgcc attctgacta ccaccactc 180  
 cccaccaaag gtccctgggg cacaccctgc agaccttatt actttagggc acacattttg 240  
 aaaagggctg actttgctaa ttgacttgg cattttgatt aaagttactt tcatattttg 300  
 attaaagtta taactgcatg atacaggcat actcttatca ccagtgtttt aagaacatga 360  
 aacgggaagc tgatgacttc taaaccattt cacawtgagt ctaaattcac tgcttaataa 420  
 taaataacaa tgataataat agtaacagat gtgtaccact cacatatacc acca 474

<210> 59  
 <211> 469  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 192  
 <223> 18-2-192 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 172..191  
 <223> 18-2-192.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 193..211  
 <223> 18-2-192.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 450..468  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 180..204  
 <223> 18-2-192 potential probe

<400> 59  
 catcaaaata tcccaaaaga tgtttgga aa atagtgtttt ataagaccta tagattgtga 60  
 ttgagtaggt ttgaggtggg gcctgtgtat ttgtattttt caacaagctt ttcagggtgat 120  
 tatgataagc aaccagattt agaaaccagt gaataagttc aacgagatga tttgcacagt 180  
 ggctcttttt akctcatcact taggttctgt tttttttaga gccaaattaa tcaatcagt 240  
 cattgtttta acatccttgc cttacatatc ttttccaaaa atttttaatt ttaaaggga 300  
 gaagggaaag ggaaagataa tttcctatgt ttgtgtgaac acatccttgg ctcttcta 360  
 aatatgaaat acagtaaata atgacttgta actattataa ttgtttttta cattcatgaa 420

tgaaaactaa ctacaatgtg gggtgattgg attccaggtt tcactctgc

469

<210> 60

<211> 451

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 211

<223> 99-26921-210 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 192..210

<223> 99-26921-210.mis1

<220>

<221> misc\_binding

<222> 212..231

<223> 99-26921-210.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 431..451

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 199..223

<223> 99-26921-210 potential probe

<400> 60

gaggaagatg gggtacttat ccatcaaatac atgttagtca cagactcatg gctgcttttc	60
ggggggcatt agccccaccc gcactgctca cctgcctggg tttagagcaa gaggagctcc	120
agtggccaga gaaagcctgc aggcaaaaac ttgcatcaga cagaggcctt aagttcatgt	180
gtatgaaaaa aagtgccaaag gagatttggg rggatccctg caatgtctgc tacaaatgtc	240
aagactcttg gctggaaaacc tggccagaat atgggtccac ttcctgaaac cggaaacatt	300
ggtggccaaa gaagaaggag caggcaaaagg aaggagctg gcaaaggaga ctggtggagc	360
actagcgatt taggagggaa gcaggaaatt gtactatcat gggagtgatg agaagtgacg	420
ttttagaatg cccakttaat acatagccca a	451

<210> 61

<211> 327

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 250

<223> 16-215-80 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 231..249

<223> 16-215-80.mis1

<220>

<221> misc\_binding  
 <222> 251..270  
 <223> 16-215-80.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 171..188  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 284..303  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 238..262  
 <223> 16-215-80 potential probe

<220>  
 <221> misc\_feature  
 <222> 29  
 <223> n=a, g, c or t

<400> 61	
ccctgcccac cttccaagta actctgtgna acctcttggt tcccttgaag ggtgattcgt	60
caacccgtgg gcaggatttt ctttgcgggc acagagactg ccacaaagtg gagcggctac	120
atggaagggg cagttgaggc tggagaacga gcagctaggg aggtaagcag gaaagcccag	180
gctctctccc tcccccatgg tgactttctt tcaggtctta aatggtctcg ggaaggtgac	240
cgagaaagay atctgggtac aagaacctga atcaaaggta agtttggtga ctctgggcac	300
tatctctcct tagaccaatc atggaac	327

<210> 62  
 <211> 480  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 368  
 <223> 18-132-368 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 348..367  
 <223> 18-132-368.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 369..387  
 <223> 18-132-368.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 461..479  
 <223> downstream amplification primer, complement

<220>

<221> misc\_binding  
 <222> 356..380  
 <223> 18-132-368 potential probe

<400> 62  
 ccccaactaa ttctcccctg ttgttcagaa tgaaattcag aatatagtgt catggaaatt 60  
 gaactggcct ttttaactgt atcaaaccatg gtagaaagat tggtagcat gagaaaacac 120  
 caaaagattt atcgaagtac acagtgtcct ctggctgttg gcccctgtgc cttgtctgca 180  
 gattggggaa tcaccccagg tcgggcaatg cttgtctctc attggcctcc catgtattcg 240  
 aattagcatt gagagcaaga gagaggcagg aacgagaaac agggctcctg aaatttgttc 300  
 tcttggggca agtgcattgg cactgatgcc tgaagatttg gatgcagacc agacaacctc 360  
 ttggggtyct tttctgcatt gaggtttgat ttttattgag ttaaaatctt aacaataaag 420  
 atatttttagg atggggccag actgcaaagt acataaaagt caggaaggag aacacaaaga 480

<210> 63  
 <211> 505  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 292  
 <223> 18-133-293 : polymorphic base A or C

<220>  
 <221> misc\_binding  
 <222> 273..291  
 <223> 18-133-293.mis1

<220>  
 <221> misc\_binding  
 <222> 293..311  
 <223> 18-133-293.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 487..504  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 280..304  
 <223> 18-133-293 potential probe

<400> 63  
 agatgtgaga agtgtggcta gctgacagcc ccttgctgtg attttcttca ggatctgcct 60  
 cagcttttagt gttaacttca caatattctt ggggaaacac aagccaatga ctaaacaaaa 120  
 cagtcttcat agggaaaccc gcagtgaatg actaagcaag gcagtggat ggagctagac 180  
 atttattcca gttgagtaac tccgggcttc tctgagaagt atctttcact gggaactccc 240  
 acttggctgg cagagacttt ccagatctgc atctggatag ccctcttctg amgtttcctt 300  
 tcagaaagag agataaagtt tattttttgt ttgtatgaag atgaatttct tttgccttca 360  
 caattgaata acaacttacc ttggtaaagg atttttggct caaaataact tttcctctga 420  
 accgtttctc ccagtgccct aatattgagc aaatgtcaag cctagagAAC agttaaaga 480  
 atatttgacc aacaccaaca tagtc 505

<210> 64  
 <211> 450  
 <212> DNA



<213> Homo Sapiens

<220>

<221> allele

<222> 191

<223> 18-12-191 : polymorphic base A or C

<220>

<221> misc\_binding

<222> 172..190

<223> 18-12-191.mis1

<220>

<221> misc\_binding

<222> 192..210

<223> 18-12-191.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 431..449

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 179..203

<223> 18-12-191 potential probe

<400> 64

tttgccctagt	tttgactggt	ggagcatcat	attaaagttt	tacatatataa	aaaataaagt	60
caacaagggt	ggggaatata	tgcaaaaaca	aaacaaaatc	cctaaatgtg	aacaattggt	120
atcagaacca	cagagaaaaa	aaattcaaac	taatcctagc	attttgaaga	caatgctttg	180
actatatgcc	mttggtggaa	aacattctaa	agataaaatt	gcaatgaaat	tttaaacatt	240
gcatttcatt	tattggtagt	ggtatgggta	tagaaattct	gaaattaatt	tcttgtatgg	300
taggatatag	aaaatataaa	taataaatat	atcaatgggt	tggggacaaa	gttactcact	360
gtgagaaaaa	tgaggaaaaa	taaagaattg	gaaagtagca	agagtcctgt	gttcgtgaat	420
tgggattaaa	ggtattgata	tataggagca				450

<210> 65

<211> 536

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 138

<223> 18-11-137 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 118..137

<223> 18-11-137.mis1, potential

<220>

<221> misc\_binding

<222> 139..157

<223> 18-11-137.mis2, complement

<220>

```

<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 516..535
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 126..150
<223> 18-11-137 potential probe

<400> 65
tttctcaagt ggctctggca tctgttaaaa tgccaaactc gtggtcctta acaccttggt      60
atgctggcac ctctctgcag acttttctca atgtaacctc agaagttggg gaggactggg      120
gagaagggag gtcttgcrgg gaggagaaaa gggaaagtgg gcaactccac tgaaggctgt      180
cacacatttg ggggctgttc cgcacagttt taccttctctc tttgggcccc tcctttctct      240
tccctctcag tccccttgtc agatggttga tggggatcac tgggagttgg ggtgactgtc      300
aggaaggcag agaggggggt tgggcagcag gtgggaagtg gggccaggtg gcctctcggg      360
gttctcccac ctacagttc tggggagttc agggttctgc aagcagagtg atccttaatt      420
aataaacagc ggggcaggct cgggctccac gtcaggaaaa ctgcagtcag ccacgtggg      480
ccaccgccc tctgcagagc acacgcaaca gcgcagtcac taaagctgaa ctgagc      536

<210> 66
<211> 454
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 96
<223> 18-93-96 : polymorphic base G or T

<220>
<221> misc_binding
<222> 77..95
<223> 18-93-96.mis1

<220>
<221> misc_binding
<222> 97..115
<223> 18-93-96.mis2, complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 436..453
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 84..108
<223> 18-93-96 potential probe

<400> 66
caaatgccaa agggttcaca atgctgagat ttatcttact gttattttat aattttgagc      60
agcatttggt tttagtgggt tgtggcagaa attgtktctc tacagaatat tatcttaaga      120

```

gaacatattg	aacataaagt	taaaagtttt	ccatcccttg	aaattcacta	gtggtaactt	180
tgaacttcaa	gaaaatgtca	tttgagtttg	ataatgtctc	aataaagcct	ctctctgatg	240
actaattctt	agtcattctt	cccttctctt	acttcataatg	gcacttatta	tagctttgtc	300
acttgatcta	gactactctg	cattgctttt	tatttttttt	tctggaaaca	tcaagggttag	360
gaatcatgtg	ttatggttct	gtgtcactcg	tacctggggc	acctaagtgt	acatatatat	420
gtgtgtgtgt	gcgctctggg	ctgtttaacc	ttat			454

&lt;210&gt; 67

&lt;211&gt; 553

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 343

&lt;223&gt; 16-115-343 : polymorphic base A or C

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 320..342

&lt;223&gt; 16-115-343.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 344..366

&lt;223&gt; 16-115-343.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..24

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 533..553

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 331..355

&lt;223&gt; 16-115-343 potential probe

&lt;400&gt; 67

caccgtcaca	ataaaagaaa	ctgtgggtctc	tacacctgcc	tggccccaca	tctgtgccac	60
agagacagac	cctgggatcc	tcagactccc	acacccccac	cccagcctca	ctcagagggt	120
tcgccctggc	ctccttctct	ctctgggaga	tggttgcccg	ccctggccag	gcagctggcc	180
cctccggggc	tggtttcccc	gtcacccctg	aggccccgcc	cagctctgag	ccccaaagcag	240
ctccagaggc	tcgggcaccc	tggccgagct	gccccatctc	cgtgggggtgc	cctcccaagg	300
tggggagcca	cgtgacagtg	ggagggcctc	tctcaggcct	ggmagggagc	aggggtcaca	360
aactgtgctg	gctgggggtg	gtctcagagg	tgggcctgca	ggcctaacc	tccctgctga	420
cagggctccc	agcccttgag	agaaacaggg	atggaggaac	agctgccctg	atgccctcac	480
ccaccggag	caggccctgc	gaaccaaggg	gaacctcagt	gtggccccc	gcattgtgtgc	540
tgatggggag	ggt					553

&lt;210&gt; 68

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 140

&lt;223&gt; 16-42-140 : polymorphic base A or G

```

<220>
<221> misc_binding
<222> 121..139
<223> 16-42-140.mis1

<220>
<221> misc_binding
<222> 141..163
<223> 16-42-140.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 154..171
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 128..152
<223> 16-42-140 potential probe

<400> 68
cattggggcgc aggcagagcc tcatcgagga cgcccgcaag gagcgggagg cggcgggtggc      60
agcagcggcc gctgcagtc cctcggagcc cggggacccc ctggaggctg tggcctttga      120
ggagaaggag gggaaggccr tgctaaacct gctcttctcc ccgagggcca c              171

<210> 69
<211> 494
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 176
<223> 18-251-176 : polymorphic base C or T

<220>
<221> misc_binding
<222> 157..175
<223> 18-251-176.mis1

<220>
<221> misc_binding
<222> 177..196
<223> 18-251-176.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 474..493
<223> downstream amplification primer, complement

<220>
<221> misc_binding

```

&lt;222&gt; 164..188

&lt;223&gt; 18-251-176 potential probe

&lt;400&gt; 69

gaaacccct	cacacatcct	ggcctctact	cgtacacaat	atttctcttt	ttttaacttg	60
gctgcagtga	aaaagaatat	ttttagtaag	ctacttggtg	tttacctaaa	gcagccttaa	120
gaagccaga	gcaggggatc	tgtaagtga	acgtagaagt	ggaagacaga	tttgcytctc	180
tcaggcacta	gggcacttgg	ctgtagagg	gtgagtatgg	caaacatcat	gggaattatg	240
agtagtgccg	ccacatccaa	agctgcacgt	gggttttcct	gggcaaagaa	actcaatgac	300
tgtgcatcaa	gagtgtaccc	agtctgacag	caggaaattg	acagaaacga	acagcccaa	360
gccccagggc	acatggaggc	actcacctca	ggcacracat	ttcagcagga	gccaaaatca	420
aaataaataa	tattttatta	caatttttta	aaagacagga	tctaacaggg	ccagatgagg	480
gtaaagcgag	tgaa					494

&lt;210&gt; 70

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 44

&lt;223&gt; 18-269-44 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 25..43

&lt;223&gt; 18-269-44.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 45..64

&lt;223&gt; 18-269-44.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..17

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 457..477

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 32..56

&lt;223&gt; 18-269-44 potential probe

&lt;400&gt; 70

ctcatgggtc	gttgctcctg	gcttggcmag	atggatggtc	aggracttga	aaggaacaca	60
tttgggaaaa	cggtagcagg	aggtgtgggg	aagtgtgttg	tggttagagg	tctctgaaag	120
ggcagagcgt	gaagatcctc	gcagcccatg	tgacatttgc	caaagggcaa	ccgcctcagc	180
cgaggagaag	ctcagtgacc	aggtagacaa	gatggccctt	tctttgggca	tcagtcaggc	240
tccttcccca	gccaccctgt	cattgtcagc	aggctggtga	agatagagac	tgtggtagca	300
gggatggagg	tcacacatgg	gatcggcaca	ggggctccac	tcaccaaggc	ccatccacta	360
agtgcgccgc	tgccccagtg	ttgcagggga	tctgccagcc	tccagggtga	gtggatgata	420
tgagacagct	gccggcatgg	aactggcacc	gctgcgcttt	caccaggata	gaggcttg	478

&lt;210&gt; 71

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

<220>  
 <221> allele  
 <222> 624  
 <223> 16-218-624 : polymorphic base C or G

<220>  
 <221> misc\_binding  
 <222> 601..623  
 <223> 16-218-624.mis1

<220>  
 <221> misc\_binding  
 <222> 625..644  
 <223> 16-218-624.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..22  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 906..927  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 612..636  
 <223> 16-218-624 potential probe

<400> 71  
 gaatcccttt caccctccat actgtatcca aagatcactt ttttcaaagg tcacctaggc 60  
 agaataatca aattaatgct ttttaatttg taataactgaa aagtaaattg caatgtatgc 120  
 acacacagat tgaaaatcag gtgccacaga catgagcatg cacagagaat ttctgcatc 180  
 tcatgcctta gtttatcaaa taaggaaaat gtataaaaag ctactccaca attggtgtgt 240  
 gaatatatta ctttatctaa atgcatcttc tcaggccagg catggtgatt gatgcctata 300  
 attccaactg ctcaggagtc tgaggatcgc ttgagtcctg gagttctagg ctgcagttag 360  
 tatcacagt ccttcagcct gggcaagaaa gtgagattct agctctaaaa tattttaaaa 420  
 ttcatctttt caccctcagtt tgtgtgcctc tgctggaaaa gaaagtccaa aggttattgt 480  
 tacattatgc aaataatatg ggcttgcaat caaaagagct gggtccctaat tctcacttta 540  
 ccactaactt gctgagtgac ttcaggtaag tcacttaact tctctgggtc tcatttaaac 600  
 caagtgatct ctttaagtca tttstaagt gtgaaactgc tgatttaattg agatatacat 660  
 tttggataat gatatgggta gattgtgtcc ccacccaaat ctcatcttga attgtagccc 720  
 ccataattcc cacgtgttgt gggagagacc tgggtggagg taactgaatc ataagggtagg 780  
 gttgttccca tgctgttctt gtgatagtaa ataagtctca tcagatctga tggttttaga 840  
 aaggggagtt ctctttcaca tgctctctct tgctgccac catgtaagac gtgtctttgc 900  
 ttctccattg ccttctgcca tgattgt 927

<210> 72  
 <211> 479  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 330  
 <223> 18-393-330 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 311..329  
 <223> 18-393-330.mis1

```

<220>
<221> misc_binding
<222> 331..349
<223> 18-393-330.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 459..479
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 318..342
<223> 18-393-330 potential probe

<220>
<221> misc_feature
<222> 457
<223> n=a, g, c or t

<400> 72
agtgtacttc gtgattgggg caaactctgg gccagatctt gtggtctgaa attcagactc      60
tgcagtttac taactgtgtg attttgagtg actgcttaat ctctctgggc cccttttctt      120
catctgtaaa gtgggggtaa taatggcatc cacttcttag ggtagttgta accaataaat      180
gagttaatac aggaaaggcc ctttaataac tatgccataa tgtttttgct attattttta      240
ttctgtgaag aaaaggagcc aaagagtggg ataagatgag tttatattga gatcctaaaa      300
gacagaaagc tagtcctgt ttctcaatcs tccttctaaa gtcactttaa ccatcagctc      360
ccatctatgc agacagcaaa ctcagcaaca agaaagagcc cttaataact catctcaagt      420
caccagaaac tcataggaag gcacagaaga ccaagtnaca aactactcct ttcattcct      479

<210> 73
<211> 518
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 402
<223> 18-394-402 : polymorphic base A or C

<220>
<221> misc_binding
<222> 382..401
<223> 18-394-402.mis1, potential

<220>
<221> misc_binding
<222> 403..421
<223> 18-394-402.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind

```

<222> 500..518  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 390..414  
 <223> 18-394-402 potential probe

<400> 73  
 cttctgagga taacaaacac cmatgggaaa ggcaacttat taaggtagcat attacagtct 60  
 tctaattgtct aaagccagct agacatacat ttaaattcca gcagaaattc tctgaaagggt 120  
 ttgcctccac ctaggtctt ccaacattag aagaacttca gagagaaagt aggacatttt 180  
 gtctctcttg ggtatttggg aatcaagggtg cagacttggg gtagcattgg gggccccatg 240  
 aagaattgaa tacctaggct tatatcaaag ccgccccctac ctatacatgc tccccagtg 300  
 cccctgtggc ccaatattcc aagaatggct cggggaatgg ccagctcccc cacagtcatt 360  
 tcagattgga gcaggctcct tagaagtcct tgggtgtccga gmcttagtcc cacaatggat 420  
 gctggatatg ggtcaacatc ctggattcat ggagagagga gggcatgtgg caaaatatag 480  
 ttaacttaca ttatttcttc ctcattatcc cctcaatt 518

<210> 74  
 <211> 587  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 55  
 <223> 16-217-55 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 32..54  
 <223> 16-217-55.mis1

<220>  
 <221> misc\_binding  
 <222> 56..74  
 <223> 16-217-55.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 568..587  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 43..67  
 <223> 16-217-55 potential probe

<400> 74  
 aacaggcgac tttgtcaagc ccagtcccct ccgtagctgg atttcacctc caggrcagcc 60  
 agctggacag acaggcagat gcaggctcag cccctgggt gccgtgggac acacacacac 120  
 aactgcccac agccactgcc caccacacac acctagtgc gatgctggca cccccccaga 180  
 aggaggctca cagctcgcag gggagacctg ggctggacaa aaccagggg aggggagggt 240  
 gtgtggggac caggccccctg ctgagaaccc tggggggaag cctgaggggg aattggggga 300  
 tggagccac actccacacc aggtctggcc ctcgagtggg tcggccttgg tgccagcccc 360  
 tctgcggcca gagaaaagca gcttagggct gagctggaga cgcgggtgtcc ccgactgtgg 420  
 gggaggggga ctcgagggtt ccccttgatg gacacagtga atccaggcgg ctggggcaga 480



gaccagcagc acgggacacg cgtgacctgt gctcctttcg agccgcagac gtcacagtga 540  
cgacgtttta gtcctaatc tccccaaatc ggcgggaagg attagag 587

<210> 75

<211> 450

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 139

<223> 18-284-139 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 120..138

<223> 18-284-139.mis1

<220>

<221> misc\_binding

<222> 140..159

<223> 18-284-139.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..17

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 430..449

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 127..151

<223> 18-284-139 potential probe

<400> 75

gactcctagc ctcattgaag gatgggttaga gaggcacggg gagctatcta gtggcaggcc 60  
cacgggtatat gtttgctgct ttctacaaat acgagatcaa aggaaaataa agcaggggtg 120  
gttcctgtca gtgtggagy agacccggga aagcatcctg gtggctgtca ggccttgctc 180  
acggccccctt tctctttcag ggagaggatc ctccacagtg gtatcctgct gcgtgccctc 240  
ccaggacagc acccagaggc ccgaattgct gctgcacaga gagcactcgg cctcaccoca 300  
cgttttccct aagttctgtc tagtaattcc actttggaga ggggggtgtt ccttgacaga 360  
tttagagagt tgatgtaact tcctcggatc agttctgctg gctccatccc ctacctgctc 420  
agccctgcac aaagtggcta agcacgccac 450

<210> 76

<211> 520

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 305

<223> 18-285-305 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 286..304

<223> 18-285-305.mis1

```

<220>
<221> misc_binding
<222> 306..325
<223> 18-285-305.mis2, potential complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 499..519
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 293..317
<223> 18-285-305 potential probe

<400> 76
gaggtgggag aaattacagc tgaggtagaa gctgcctcgg aaggccaggt gaagagccac      60
acctgtcaga tgggcttgtg gcctgcgttg ggcagggact cccagcaggc tgctgtccgg      120
ccacagttca gcctctgccy gagggccggc cctgcctgtg ctccttatcc tatagctgca      180
gggccagctg aaagaagcaa ggcgtttccc tccccatat cctgttctcg tagcatttat      240
ggtgcagtct cccacgcctg actgctgtct acttagaaaa ctgctgaaag ccagttgcat      300
ttcaratagt gtctgtgcca ccttcagagc ccttttgtga tcatgtttta tcagcttatt      360
ttatgtttta tgtgtgggct tcggcgatct ggggacatct ggtcaaccag ggcaggcaac      420
cttggtttcca agtggcagat gccaggggtg gtccagtctc cagaaaggga tttccctgg      480
gaccattggc acctgttact tgtagtcttt tcagccttgg      520

<210> 77
<211> 486
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 239
<223> 18-289-239 : polymorphic base C or T

<220>
<221> misc_binding
<222> 219..238
<223> 18-289-239.mis1, potential

<220>
<221> misc_binding
<222> 240..258
<223> 18-289-239.mis2, complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 466..485
<223> downstream amplification primer, complement

<220>
<221> misc_binding

```

<222> 227..251  
 <223> 18-289-239 potential probe

<220>  
 <221> misc\_feature  
 <222> 154,156  
 <223> n=a, g, c or t

<400> 77  
 taaaaagcag ccggtgtccca cagcaaggct gccctgtgtc ccacagcaag gctgcctctc 60  
 cagctcaaaa aaaaatcctg ggcacagatc ttgagactct gctgctgtgg gactcttctc 120  
 gcacccacca cccagggcct caggaaggag ctgnancagg gtgtttttaga aagaccttac 180  
 tctataaatg caaaaaccca gacttagtta acaaaagcct attacaaaga cattttctyc 240  
 tattgctacc tctccccatt taaatcctgt ctgtacaaaa aaataaaaac attagctggg 300  
 catggtggca cgtgcctgtg gtcccagcta cttgggaggc tgagggtgaga gcagtgcctg 360  
 agcctgggag gccgaggctg cagcgagccg ggatcctgac gccgccctcc agcccggcca 420  
 cagagaaaga cccacagagc ttskccgcag ccctcgtcca gcgcactgag atccctcacc 480  
 aaggac 486

<210> 78  
 <211> 453  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 91  
 <223> 18-291-91 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 71..90  
 <223> 18-291-91.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 92..110  
 <223> 18-291-91.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 432..452  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 79..103  
 <223> 18-291-91 potential probe

<400> 78  
 cctccatgca ggaacagcct accctggact ggatccagct ctctcccagg cccaggttgt 60  
 gggagaaatg ggggacctcc gcctcccaat ygtgctggct ggaactttcc tgtgctgggg 120  
 attcggcggt tgccagccagg gtggccagtc aggggtgccag gctcccatct gaacactgac 180  
 agactgtggg ctgtgcagtc tacagcattg ggcacaacct cagcttgcta aaatactcag 240  
 tgcaggctgg gtgtgggtgt cagcctgta atcccagcta ctcgaggaggc tgaggcagga 300  
 ggatccctta aagctaggga gtcaaagctg cagttagccg agatcgtgcc actgcactcc 360  
 ggcctgggtg acggagaccc tgtctcaaaa aagaaaagaa aacgagtatt ggggtggagag 420  
 aggaccaagc ccaattacta ctttagtgcg gct 453

<210> 79  
 <211> 460  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 391  
 <223> 18-186-391 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 371..390  
 <223> 18-186-391.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 392..410  
 <223> 18-186-391.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 442..459  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 379..403  
 <223> 18-186-391 potential probe

<400> 79  
 taggggtcaa ataaatgcat actatgcgga cagacagaga ttttcgattt ttttttttta 60  
 gtttaataaa gtttgaaaac tttcaaagct cctgtacaat tccattaata ccagacttgg 120  
 caaaacgcta attctgtttg aaaaggtgtt tttttaaaag tagtatattt gaacaatgtc 180  
 taagtatgtg ggggtggggag aatccatata cgaatatctt cataaagcaa gttcttaaaa 240  
 tttgcaaaagc tattaggtta gtgcaaaaag aatcatgggt tttcttttgc accaactaat 300  
 atttaccact gaacacgctg gcatttagat cacttccttc tttcagcatg ctagacagta 360  
 aagagaatgg gcatgaggtg gcaggaagaa kgaaagagtg aagataatgg agttaggtca 420  
 gtgagggata tttcctaaat tccccacttc ttttcctcta 460

<210> 80  
 <211> 460  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 130  
 <223> 18-194-130 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 110..129  
 <223> 18-194-130.mis1, potential

<220>  
 <221> misc\_binding

```

<222> 131..149
<223> 18-194-130.mis2, complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..459
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 118..142
<223> 18-194-130 potential probe

<400> 80
agctggaagc ctgtttggct tactattggt aagaaaaagt taaaatttta atctgtctga      60
acattatagt acatccaaat caataaaatg ttttagttgt gggttttcat cagttttaat      120
cagataatgy cttacttctg tagatatagt ctagtatagt tcaaataaaa agacagttgt      180
acatagataa gacaaagcat attgtgaaaa tggtgggaaa tttaggttat tttaatgatg      240
gctgagaatt tgtgaacttt tctcatatgc tattaaactg aattactagt aaatttatgg      300
taccgagtat atcaaacagt gagggattta aagtaatttt gcaatttgct aaaatttcat      360
ccttaacata ctggctaaga gtgaaaaagc aagaagagag aaaaggaaaa ggatggaact      420
aagacaattc tattagaagt ggggagatgg caagaaaatt      460

<210> 81
<211> 459
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 252
<223> 18-198-252 : polymorphic base A or G

<220>
<221> misc_binding
<222> 233..251
<223> 18-198-252.mis1

<220>
<221> misc_binding
<222> 253..272
<223> 18-198-252.mis2, potential complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 438..458
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 240..264
<223> 18-198-252 potential probe

```

```

<400> 81
ctgaaaaaag agctgacaaa attcaatccc taattaaaat gtttagcaac taaagttatt    60
ggttaatttt gagaattgat cctgtgttaa caaacatcac caaagtctca aggcttaca    120
tacaaagggt tatttctcgc tcatgttaca tgtccattgt ggacggctgt ggctcctcac    180
tgtcttcatt ctaggactga agctgaaggc acagtaccta tatgcaacat attgttcata    240
tggcagaggg grgaaaagca atgacttaat caagcaatga ctctgaagt tttgctcaga    300
tacagcatac atcacttcca ctggctaaag caagcctcat ggctaagcct gatatcaaga    360
aggtaggaag tatactctct cacagggagg tgcacctggt agaaggactc tattatagag    420
ataaactcag tagagaggat tgccgaatag ttgtaaata    459

```

<210> 82

<211> 476

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 299

<223> 18-242-300 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 280..298

<223> 18-242-300.mis1

<220>

<221> misc\_binding

<222> 300..319

<223> 18-242-300.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..17

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 455..475

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 287..311

<223> 18-242-300 potential probe

<400> 82

```

acctgacatt aagagacaag cagccgggat ggctcctaac cagatcttct ttccctgttc    60
ccaaaccatc tttcttcata gccggctctg gggatgagga gcctgggtta ggaggaaggt    120
ttgcaattga ccagggttcct gttttgaagg cttccacctt gacttaagat agcaccgctc    180
agaagatgga tgtgtgttta gcaatttccc attttattac ctgcagacaa agaaaaaaaa    240
agatataaat agatgtttta ccacacaaat aattcacatt actgtcttct ttatgactrt    300
gaaataataa aataaaatta aatcaacagc aataacaatt tcggcacagt ggttactagg    360
caaatctgga aaaccaaatt gaaataagaa aactcataaa ctgggtgttg ggagcacact    420
gtggaatttt tcttggtcaa aattctcaca gagtgttcaa gtgaaagggtg tatta    476

```

<210> 83

<211> 3001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1501

<223> 8-15-126 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 1481..1500

<223> 8-15-126.mis1, potential

<220>

<221> misc\_binding

<222> 1502..1520

<223> 8-15-126.mis2, complement

<220>

<221> primer\_bind

<222> 1376..1395

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 1792..1810

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 1489..1513

<223> 8-15-126 potential probe

<220>

<221> misc\_feature

<222> 15,619,631,646,2196,2462

<223> n=a, g, c or t

<400> 83

ttggaaacag	gctcntgagc	agttgggtag	agaattccct	gagtgtgggc	tagacagggt	60
tgtaaacctta	gtggaccttc	tccttggcac	tgtgggaggt	tacaacatca	ttctatagag	120
gttagaggca	taaccagtag	agggtgcctt	agtccttttg	ggctgctatc	acaaaatacc	180
ataaactgag	tagtttataa	acaacagata	tctatttttg	acagttctga	aggctgggaa	240
gtccaagatc	aaggcaccag	aagattcagt	gtctgggtgag	ggcctgcttt	ctgggtcata	300
gatggctgtc	ttttcactat	gtcttcccat	ggtgaaagag	attagctagc	tctctgggtc	360
tcttttataa	aagcactaat	cttattcatg	agggtctctgc	cctcataacc	taatcacctc	420
tcaaagaccc	ccacctccta	ataccatcat	attgggaatt	aggatttcta	catatgaatt	480
tagggagaca	caaacaccga	gaccacagca	gaagaccaga	gtggactcct	ctatagcacc	540
tcctctagag	cttggggcaa	gagtcacttt	tgcttgggtt	tcagggttac	tccttaagtc	600
acaggcctta	tgtcttcnc	ctagccttca	ngaactgtga	gacaantaaa	tttctgctct	660
ttataaatta	cccagactca	ggtgttctgt	tatagcaacc	caaaatggac	taagatagat	720
gggttttcatt	attcccacat	tttacctggg	aagaatctgg	agctcagaga	ggtaaagtaa	780
tatgcataag	gtcccagagt	taggaagcag	cagagctggg	attgtaatcc	tgcaacagct	840
tcccatctca	ctcagagtcc	aagcatggta	ctttcaatag	ccctgcacaa	tctgtctacc	900
tcacaccctc	ctattctact	cctgcctcac	ttggctccag	cctcaccaga	ctccctccta	960
tgacttctat	gtgctagccc	ttcctgctgg	cccggttgt	tctcactgct	cagactgcta	1020
tcacatctga	taactgcatg	gtctgcttcc	tgatctcttc	cagggtcaaga	ctcaattgct	1080
gattttctcca	tgaggagtcc	ctgattatac	tcagatactc	actcacatac	gcacaatctt	1140
caccogttac	ttacctgcct	ctctgatttg	tctccaatat	acgtatcatt	attgaacaca	1200
ccacatcttt	tatttatctt	gtttattatc	tgtcttctcc	tctagaatgg	gagcttcaaa	1260
gggaaggaat	taaaatttta	tctgttttgt	tcattgctct	atctccaact	ctcacaacag	1320
tgcctactat	atagaaaatg	ctcaataaat	atttgctgat	gcaataaata	aaaaaatgta	1380
actaagcaac	caagcccca	agagtctgat	tttattaata	ttgttttctg	tctcctcaca	1440
ggaagccctt	tggcatcacg	cacctccctc	tgggctatgg	catctctgag	ccagctgagt	1500
rgccacctga	actacacctg	tggggcagag	aactccacag	gtgccagcca	ggcccgcaca	1560
catgcctact	atgccctctc	ctactgcgag	ctcatcctgg	ccatcgctct	gggcaatggc	1620
ctgggtgtgca	tggctgtgct	gaaggagcgg	gccctgcaga	ctaccaccaa	ctacttagta	1680
gtgagcctgg	ctgtggcaga	cttgctgggtg	gccaccttgg	tgatgccctg	gggtgtatatac	1740
ctggagggtga	gtagacttca	ggtgcatgtt	gtctctatga	ctgtgctagt	acttgtcttc	1800

```

cctgagttct ggcctttggg gctcaaaaga ctccccagac agtcaggaac tgaggaagga 1860
aggagagctc tcattctccc tgtaatgaga gagttaaac tctggaaaac agtcaccatc 1920
ctgtccctca tccacatcag aaccaaggag ctgagaatga ttctgttcat gggctctccag 1980
tgttcaggtg actggatttg agtgacggga ctcttcctaa tatggcctag agttttattct 2040
ctgtgccaga catgtctcaa tgacatgggtg ggctgggtga agcagtccag aagacctctt 2100
caccagtgtt taatgtatat gagggtgagg gtgtgcagga gggatgtgag gccaggagga 2160
aaaagggaatt atagaaaaaa aaaattagtg aatgtnaagg gaagatagaa agaataacca 2220
gcgaacagat cagacttctt tcgatggctc agtccctctt tgctctttcc tcctgggtac 2280
cagttctcca tagactctgc taccaaagga acagacaaaa ccctcaaatg tatattttcc 2340
atgtgtccat gaatagtaca gagcctttgc cagagagata gtgcagcaga tcctgggtgaa 2400
ttcttttggg gagaaacatt tattaaattt gaaagtattt tcaattggga gtgcaaaaca 2460
gnagccaggg ggtggtcaag acaaaacacc catttgctaa caaagaaatc aggggtgacca 2520
tatctgttca agaaacagat attcttacca ggaaaacatg caattactta agatatgttt 2580
ttttaaaaaa acctgagtat actattaata tttctcctct gcactgtgtg tcatttttaa 2640
gaggtatcca atgaaggatc aaaatgatgc tatgattaag agaaattaag attcatcaaa 2700
ttaatatctc agttaatatt gatagtaaaa gtgacagtta attaagtatg acatatcacg 2760
ggagagcaaa aacctgtac atagactgcc tgtgctaata cctttgttaa agaattggctg 2820
ggaactaaaa ttagacttat gatctcaagg gggagacata aagagagaaa aaaagaaaac 2880
agagaaataa aaggaaaaga agaaaaacaa ctaggctgtg tagatctaaa ggctaaggga 2940
atacttgagg aaaaaatatg cattttattct tcccagttag gataatccta gttgggaggg 3000
t 3001

```

```

<210> 84
<211> 2684
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 1501
<223> 8-19-372 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 1481..1500
<223> 8-19-372.mis1, potential

```

```

<220>
<221> misc_binding
<222> 1502..1520
<223> 8-19-372.mis2, complement

```

```

<220>
<221> primer_bind
<222> 1130..1148
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 1534..1552
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 1489..1513
<223> 8-19-372 potential probe

```

```

<220>
<221> misc_feature
<222> 240
<223> n=a, g, c or t

```

```

<400> 84

```



aaggccaact	ttgagggttg	agaatcccca	accctttatg	aagactggcc	gggtgtacca	60
acagttgttg	ctcacagtgc	tggatgaagc	acagatgttc	catgtcacia	tggtaaagag	120
ggatggggag	ttaaaaattat	agaaagaaca	ttggcttggt	cataaaactg	gctgcaagaa	180
catatttttc	agggtgcagcc	ttgggtact	tactgaacct	ctctgagctt	taatctgctn	240
catccgaaaa	gagagacagt	aataatggca	cctgtctcat	ataacgttgc	cataattatt	300
agggtgggata	aggggtacaa	agctcttggc	tcacgcctg	gcagatatta	gtttgttttt	360
cttttctttt	tcaagatggg	gcacgtttca	ggcccatctt	gggccttgga	ggaatctcag	420
catctgctat	gaagaaggca	aagctagagg	gacctcccaa	ggagaaatgg	caggaaacatt	480
tcaggatata	aagcagggac	aaggaccctt	ctaagtgcac	attctccatg	tcacaatatc	540
attacctgcc	tttttcccat	cccacctctg	acaagtgtct	ggattccctg	aaaaatcaaa	600
tctctgtctt	gtattcagcc	gccatctgcc	ctccatccca	gattcaaaat	tggaagaactg	660
gcattctcag	caaataaggc	ttcttctctt	cattgcattc	aaacaattct	ccaatgcctc	720
cgcaccagca	ggcccttttc	tgagggtctg	atccctctct	ggagcctctg	cctgtgtgcc	780
ctgtaatgct	ctcccagacc	tcccaggctg	catgtctctg	tgtgacactt	gtgacatcct	840
atgaaaggga	tcactgtgtt	atctagactg	tttgtccctt	tgagagaaga	catgggtgtt	900
cattcatctt	tgtagcccca	gtgtctggcg	tatgattgtt	ggtaactttt	tatttttaagc	960
aagctgtaag	aaactcaaag	atgaattaga	ccttctaccc	tcaaggacct	gacagtatac	1020
gtatctgaga	ctgcatcctt	cccacccctt	gtgcagcaga	aagtgcaggc	accacacgtg	1080
acatggagcc	gtgttttatg	ctccttactg	agttctgata	cttgctaact	gctttacctt	1140
cccccttctc	atccacaggg	gacccactgt	tctgtcccat	ctccaaccct	gattttgtca	1200
tctactcttc	agtgggtgtc	ttctacctgc	cctttggagt	gactgtcctt	gtctatgcca	1260
gaatctatgt	ggtgctgaaa	caaaggagac	ggaaaaggat	cctcactcga	cagaacagtc	1320
agtgcaacag	tgtcaggcct	ggcttcccc	aacaagtaag	taccctggag	ggggtagagg	1380
gaagacaaca	cccaatctcc	tgacttccca	gcctgtgtcc	agcagtgcac	gattttgccc	1440
tttagctaaa	ttggagacac	aaatctgaca	ccgactttgg	aatctgctaa	ttttggctgc	1500
rttttgaagg	taggaaatcc	aatctcaaga	aaacattgat	agttgcctct	agagcctgcc	1560
ttacctggca	aagtgattgg	agagctcctg	ggcttgttct	gcttcccttc	aaagtctttc	1620
attttcccca	aatgggcagc	agctcagatg	tcccacagg	tttgaagttt	aagtgcagca	1680
gttgtacctt	gcactgctgg	tgggttccca	gaactgaact	tttgtctaaa	ccactcatgc	1740
caagaatcac	tgggggtccat	caaagccttt	tttcttact	ggatctgtcc	gtgtgtcaag	1800
gaactgacaa	gctgggtggga	taggggtgctg	ataaagcatt	ttattggatc	tttctaggct	1860
ctgaaaagaa	atgtcattgc	ctctgcaatg	atcttcta	tgtaggggt	ttaatctctc	1920
cttaccat	tgctgtgcac	ttagtagttt	tcccacgatg	tacttgaagc	atgaatggat	1980
atataccgat	cacttgaaat	ctactaggga	agggacagtg	gtaacattaa	acagcatctg	2040
ccttcatgga	gcttagaatc	tagaaaagca	aataaagcac	ccctccactc	aatgttaatg	2100
aagatcccag	agctgaatag	gatgtttgcc	aaatgtgagg	tgaagacaat	taagcactca	2160
attatgaagt	gctctggagg	ttatagaaga	gaaaacccaa	tatgtctcagt	gatattggtt	2220
ggctgtgtcc	ccacccaaat	ctcatcttga	attgtagctc	ccacaattcc	catgtgtcat	2280
gggaggggac	cagtgggagc	taactgaatg	atgggggtgg	gtctttccct	tgtgtttctc	2340
atgatagtga	ataagtctca	cgagatctga	tggttttatg	agggggagtt	tccctgcaca	2400
aattttctct	tgtctgtctg	catgcaagac	gtgcctttca	ccttccacca	tgattgtgag	2460
gcctccccag	ccacatggaa	ctgtgaatcc	attaaacttc	tttttcttta	taaattaccc	2520
agtctcaggt	atgtctttat	tagcagcatg	aaaacaggct	aatacactca	ggaaagggtc	2580
ccatagacag	agtaagaatt	gagtttgatc	ttgaagacag	atccaatttg	ggtgtctaga	2640
ttaatctttg	atgacctaga	taatcttttt	tttttttttt	tttt		2684

&lt;210&gt; 85

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 428

&lt;223&gt; 99-2409-298 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 408..427

&lt;223&gt; 99-2409-298.mis1, potential

&lt;220&gt;

&lt;221&gt; misc\_binding

```

<222> 429..447
<223> 99-2409-298.mis2, complement

<220>
<221> primer_bind
<222> 131..148
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 560..580
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 416..440
<223> 99-2409-298 potential probe

<220>
<221> misc_feature
<222> 27,108,118
<223> n=a, g, c or t

<400> 85
ctcaaagatg tcgttgacga aggagtncat gatcccatg gccttagagg agatgccggt      60
gtcagagtgg acctgcttca gcaccttggt caagtacacg gagtagcntc cettgcgntg      120
cgcttggttt cttgccgtac ttcttctgcg ccgtagtcac ccacctcttg gaagccctaa      180
ttgggatcag gagcggactt tgttggtctt ggcattgtcg gggcgacta caggctgagg      240
tgaactaaca gcagctcgag aaaacgggaa ttaatttaat gtttgtcttt actaccaaac      300
tgtaagtttc gtgagattag gaccatattt gcatcattca ttattatgtc tctgggaccc      360
agcacaatgc ctagtacata ttaggacttc aataaacaaa tgcaaagtag cgcattggggc      420
tgcagccrca gatctcctgg gatctgggtc tgggagcagg cagtggcatc tgacacttca      480
tatcccttaa agaagacaaa atgtattcta tgacagatag ggaaccagag ccagggacta      540
gagtgtgact ccctgacttg ttagaggagg ttgggaaaaa tggccttgac tatcttccta      600
ggcagaggcg ggcaactat gcacccacgc ccaaatccag ccctctgcct gttttggtaa      660
ataaagtttt attggaacac agttacatac tttttttttt tttttttttt t              711

<210> 86
<211> 3001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1501
<223> 99-339-54 : polymorphic base G or C

<220>
<221> misc_binding
<222> 1482..1500
<223> 99-339-54.mis1

<220>
<221> misc_binding
<222> 1502..1521
<223> 99-339-54.mis2, potential complement

<220>
<221> primer_bind
<222> 1448..1467
<223> upstream amplification primer

<220>

```

<221> primer\_bind  
 <222> 1883..1902  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 1489..1513  
 <223> 99-339-54 potential probe

<220>  
 <221> misc\_feature  
 <222> 120,890,929,2457  
 <223> n=a, g, c or t

<400> 86  
 atactataaa gattcagaga ctttccacat tagtaaaatt tttagaggct cagtaggctg 60  
 gggaatgctg agacatgcac ttcaaagtaa aggacaaatt attgtaactt gcatttcccn 120  
 ataactaaga aggaaaccca gcaccaataa gcgctctctg gttctgaaag cagcacattt 180  
 cacactcaga gacactactc tagcacatac gccagctgaa acatgagtct accagatttg 240  
 gagagagccc agagcaggaa agggctctgc agcaggacca ggcagtagtg caagctgctc 300  
 tgtcatatga tgattttggt cacatgatgt ggtagagcct acagtatagg aggtatcatt 360  
 gatagaaaaa ggctgtgtac attttatggc aggcctcaat aggcaaacac aaatagaccc 420  
 ctaggattca gaagcaagac aagcaatttg cagcagagaa ctatacgttt agataaatat 480  
 tcctgggtgcc ctactggttc ctagtaggaa cacagcacc aactatggga tgccaagggt 540  
 ccacacagca aggactgccc attgccaatt ctgacagacc cccaaatcat gaaggcaggc 600  
 aggcctacca acaattgtaa ggaaggaaat gatacgtttg ggatcaggca ttagcagagc 660  
 cagagagcac aaataagttg cacgcataat tggcccagac tactagggtc atccatcaca 720  
 tttgcaactga tgcctcacc ttagctcaca cttacggcag cataaagtga gggcaaaagc 780  
 tgagtttgat ttatgtacgg gtaagatttg aatgtagtag caagctaaaa atagactatt 840  
 gctatataac aggaccacat ccttagcggtg tcccagaaaa ttagggatgn agagaaattc 900  
 ttccaatgg ataaagcatc agatgggtgnc ctttgcagag agaaatactc tgagataaga 960  
 tatgtatcac ttataggcag tagtgaatta tttggacagt tgactctata caacctggga 1020  
 agtagaatgt cttagccagt tgatgtcagc cagctcctat cagtgcctggc acaataggca 1080  
 cattaatgga ccatgggtta ggaatggaga caccatccta acaagactaa ctgactttat 1140  
 ttttattttt tttgagacgg agtttcactc ttgtcaccca ggctggagtg caatgggtacc 1200  
 atctcggctc actgcaacct ctgcctccca gggtcaagtg attctcctct gtcagcctcc 1260  
 caagtagctg ggattacagg cacctgccac caagcctctg taatttttgt attttttagta 1320  
 gacatggggg ttccacatgt tggccaggct ggtctctaac tcctgacctc aggtgatctg 1380  
 ctggcctcgg cctccaaaag tgctgggatt acaggtgtga gccgcagtga ctggcctaatt 1440  
 tgactttctt aatcaggaga agatagctct tctcttacat gatggcgaca gaaaagaata 1500  
 stcccttgcc taattttgat gataaatgga taagtacaac aacctgact gagaaacagt 1560  
 ggtgggtgat gaagctattt ataggcccaa caacacgtgc tctcacttgc taaggctgat 1620  
 ctagttactg ccactgctga agatcccagg tgacagcaac agataccatc actgctctc 1680  
 cagtatggct ccatccctca agaagaccaa ccagcttctt aatggcaaat tattcttctt 1740  
 aatgacaaaa tgggtcctt ccaccatgtg attccaccct gtgattttga tacgaatgga 1800  
 cacttatcct attcatacaa cttcagctag acagtgccta ttagcattt gatccactga 1860  
 aacaggatcc tgccaaacat tgcattggac taaagtaact gcttatgtta atggaagttt 1920  
 aaccttaatt acttccttat aggccttaac tccaaataca gtcacattgg gggttataga 1980  
 ttcaacatat gaattttgga aggtctctct tttcccagaa ttgtctttgc tgaaaatcaa 2040  
 ttgaccataa atataacgat ttatttctgg actgtcaatt ctgttcatt ggtctatatg 2100  
 tcttcttact gcaaatacca tactgttgat aactgcagct ttatagttag ttttgaaatc 2160  
 aaggattaaa cattctccaa ctcccttctt cccacgcatg gaaaatcact gatctctttt 2220  
 ctgtctctac agattttacct attctaggta ctttctttt taaacagtggt cttttggcta 2280  
 ttctaggtct tttgtacttc tatgtaaatt ttacaactctg cttgtcagtt cgtgatgaaa 2340  
 aaggctgggt gaattttgag agggattgtg ttgtctatat atcaatttgt agaaagttgc 2400  
 catcttaaca tattgagttt tcaaatctca gaacatagaa tgtagagggt ccctgtntct 2460  
 tttttaattt taaatttctt ttcataattt aaacattttt tctattgagg taaaattcat 2520  
 atagataaaa ttaactattt taaagtgaac aattaagtgg catttattac attcacaata 2580  
 tcgtacaaca actacctcta tctagttcca aaatattttc atcaccacaa aagaaaactg 2640  
 tgtaccatc aaacagttac tcctctttcc tttttctccc aacctcggac accacagctc 2700  
 tctttctgtc tctatggatt tacctgttac tctgtatatt tcatataaat gaagtcatac 2760  
 aacatgtgac ctttgtgtct gacttctttc gttagcacag tgagtgtctt caaggttcat 2820  
 tcacattgta gcatgtatca acttcattcc ttttgatgac caaatgatat cctattatat 2880

```

gtatataacca cagtttgttt attcattgat gaatatttga attctttcta ccttttggct 2940
attgtgaata gtgcttctat gaatatttgt gtataagtag tcatttgaat acttttttta 3000
a 3001

```

```

<210> 87
<211> 1127
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 311
<223> 12-254-180 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 292..310
<223> 12-254-180.mis1

```

```

<220>
<221> misc_binding
<222> 312..331
<223> 12-254-180.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 132..152
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 586..603
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 299..323
<223> 12-254-180 potential probe

```

```

<220>
<221> misc_feature
<222> 952,958
<223> n=a, g, c or t

```

```

<400> 87
ctgccacaat ctccctgagtc cagacaatct agagcagaag ggtagactga ggaaaatata 60
cacagtataa aaaagtaaca aaatcaaaac ctgaaacaaa gatcaacatc caataaatgc 120
ttctgaataa agggagagta gataagaact ggatttttaac cccaacactg ccattttacca 180
gctggccaat actgagctag ttactctaaa gagttcagtt ttctcatttg taaaaatagg 240
atttgtcttt ccatctcact gagttgtgat gagagtcata tgcaacagca tatgaagagg 300
ctagcaaaaag rtatttaaca agcgttcaac attctcatga tgacatgaat aacactgtac 360
atacaacata ccaacttgat aaatacacag cacagttaat agctgagggc agagttatgg 420
ttgggaagag agagagtgca acataggcag agtgaggggg gattcccaca attttctaag 480
acagaaaagt gggggaatca gtagttactg gaaagaatag gcaatgcctg actggataga 540
aaaagattct atgcctttgt caaatttcac aaaagtgact taagcctata ctgcgggatg 600
ttcacactac gtcccttttag tgcagttacg gtacttcagg ctgcaagtaa ccaaatacaa 660
ctaaaattgt cttatacaat aagggcgtaa ttatctcata taacaagaag cttggcatga 720
aggaaatttc aacaatttca caacggcaac aaaaactctg tttcttctac ctttccacca 780
ttcctgtggt ttcagttcca atatggctgc taacatccat atgtcttccc cgcacatctc 840
tttaaaaagct acaaaaagat ttcccaaaag cgtcttggaa aatttcctgt cccatctcca 900
ttggccagac ccacctccca tgggactgcc tcttgtgaag cacacaaagg gncagatncc 960
aaacggtacc gttagggaga cccagaagat ggaccatcca ggatagagac atgaagggca 1020
gaagaggggc cagggatgtg tgtccctcag ctggactaca ggaaggaggt tttggtcagg 1080

```

ggaagaaaag cctcatttcc tatcagtcac tgggtggaatg actaaag

1127

&lt;210&gt; 88

&lt;211&gt; 3001

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 10-214-279 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1482..1500

&lt;223&gt; 10-214-279.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1502..1521

&lt;223&gt; 10-214-279.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1225..1244

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1747..1764

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1489..1513

&lt;223&gt; 10-214-279 potential probe

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 2368..2369,2372..2373

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 88

aatcattgag	ttttgttctc	tatattttct	ctttatctaa	gaatgtcttc	ccccctccat	60
taacaatatc	ctctcatttt	attccattta	aaatatccca	gtggtgcctt	gcaagtgacc	120
tcatctaaact	caagcatttg	gtcatttggg	aaatgtttaa	ggagtgatat	gcagtcgatt	180
ggtttgcata	caaatattaa	gttttttaat	gtgaacattt	agcaaagac	attcatgtat	240
ttgcatgtgt	gtgtgcttgc	acatgtgcac	atgcatgtct	gtctgcaggg	aaaatatatt	300
catgcctttt	gaaaattttt	aaataatgtg	ttatatattat	agaaaagattt	ggaacctttt	360
ctctgaagaa	gttaaagaac	agatgtcatt	gattcatatt	aagcaagacc	ctataaatct	420
tatttctagg	tctcatgtat	ttattaagca	actccacacc	ttaagcaggc	tttctacata	480
gaagaggaag	aagatagaga	tggtttccat	attattttca	tattccacat	tatttgtggc	540
tttaggccag	ctatgtagct	atcctgtatg	tgtgctcaga	caggagactc	agccctgaga	600
gaaggcggtc	ctctggcaca	cctaggatgg	ggaagggtact	cccttggaag	tcccaagctg	660
gcacttcttg	atctccatgg	caatttttct	gcccatcact	ccatggagat	cagaatatca	720
ctctattgtg	tcccctcaac	actgaaggag	tgtctcaata	agaaaagttg	agtcaaaaca	780
ctgtagggaat	tgaagaggtc	cccacttgca	ctacccttgt	aaaccaagag	aagatgttaa	840
aaaataaaaac	gataatgctt	cctgaagggt	tcttcccatc	tttacactag	atgggttcaa	900
ttgagaggaa	ttactggact	gtggaagtgt	aagactgtcc	acataattaa	aatgtacaat	960
agctactcag	gattaccttg	caagtttcaa	catacacaaa	attaacttca	taagatgggt	1020
taaaaagttt	accgttatac	ctaataatct	ggtttaaatt	tttaaaactc	atccattttc	1080
gttaaaattt	aatcaaaaaa	agaacacggg	ttcccatgaa	tttgtctcag	gtcaaacctc	1140
acacagaata	ggtgctccat	gaatattttg	ttaaatgata	gatgatgaat	gttctcacta	1200

tccaatcttc	acacatctta	tagagtaagt	ataacgaatc	caagatttat	agtgctgaaa	1260
gtagtcttta	tatgtttaca	aagcattatt	gtcagtaatt	tttttttact	ttgatgctat	1320
actttctact	tttgctttat	ttaatgcttc	tcaatatgct	cgtttaactg	ttgcagatcc	1380
ccctgaaatt	acgctttgga	ggacttcttc	taacagaaaa	acccattgtt	ctaaaggctg	1440
agtcaaggga	tgagaccgta	agtggagcct	gatttcccta	aggacttctg	gtttgctctt	1500
yaagaaagct	gtgcccaga	acaccagaga	cctcaaatta	ctttacaaat	agaaccctga	1560
aatgaagacg	ggcttcatcc	aatgtgctgc	ataaataatc	agggattctg	tacgtgcatt	1620
gtgctctctc	atggtctgta	tagagtgtta	tacttggtta	tatagaggag	atgaccaa	1680
cagtgcggg	gaagtagatt	tggcttctct	gcttctcata	ggactatctc	caccaccccc	1740
agttagcacc	attaactcct	cctgagctct	gataacataa	ttaacatttc	tcaataattt	1800
caaccacaat	cattaataaa	aataggaatt	attttgatgg	ctctaacagt	gacatttata	1860
tcatgtgtta	tatctgtagt	attctatagt	aagctttata	ttaagcaa	caataaaaac	1920
ctctttacaa	aagtattatt	ggatgtttcc	tgcacattaa	ggagaaatct	atagaactga	1980
atgactgaga	accaacaact	aaatattttg	atcattgtaa	tcactgttgg	tgtgggaact	2040
ggagtgcagt	ggtgcaatct	tggctcactg	cgagctctgc	ctcccaggtt	cacgccattc	2100
tcctgcctca	acctcctgag	tagctgggat	tacaggtgcc	tgccaccacg	cccggcta	2160
ttttctat	ttagtacaga	cggagtttca	ctgtgttagc	caggatgctc	tcgatctcct	2220
gaccttatga	tccacctgcc	tgggcctccc	aaagtgcagg	gattacaggc	atgagcca	2280
gtgccagcc	caatttgatt	attaacatag	gtgagagtta	acccactatg	actttgcca	2340
ttgtttagaa	agaatattca	tagtttannt	annacatttt	tgatgagaca	cagtggctca	2400
cacctgtaat	cccagcactt	tgggaggcca	aggcaggcag	atcatctgag	gccaggagtt	2460
caagaccagc	ctgaccaaca	tgggtgaagcc	ccctttctac	taaaaataca	aaaattagct	2520
aggatgggtg	gcacacgcct	gtaatctcag	ctaccagga	ggctgaggca	ggggaattgc	2580
ttgaacctgg	gaggtggagg	ctgcagtgc	ccaagatcat	gccactgaac	tccagcctga	2640
gtgacagagt	gagactgcat	ctaaaaaata	aaattatgcc	tttttgtagc	acatatattt	2700
tgtaacatac	aactgaagcc	agtattatat	tattagtttt	catttaatgt	tttcagccca	2760
tctcccctga	tatttctggg	agacaggaaa	tatgttttct	tacacctctt	gcattccatc	2820
ctcaactccc	aactgtctaa	atgcaatgaa	catttaataa	aaaaaacagt	tgattgggtca	2880
attgattgga	caacaaggct	gaaactactc	atttcttttc	ttttcctatt	tcttccctta	2940
ttttcccttt	ctgaataatt	tagccctaga	gccattaggt	gggtggcagc	cagatgggtgg	3000
c						3001

&lt;210&gt; 89

&lt;211&gt; 3001

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 10-217-91 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1482..1500

&lt;223&gt; 10-217-91.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1502..1521

&lt;223&gt; 10-217-91.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1414..1430

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1759..1775

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

<221> misc\_binding  
 <222> 1489..1513  
 <223> 10-217-91 potential probe

<400> 89

gattgttgg	acatagaaac	atgcttggct	tttgtttggt	gatcttgtat	catagaacct	60
tgcagagctg	acttagtatt	tctagaagtc	tttttgtata	ttcttgagat	tttatacatt	120
gacaattatg	tcacttgaaa	atagagacaa	ttcttttatt	tcctttccaa	tctgtatgcc	180
ttttaattct	ttttcccagt	ataatgtcaa	ataaatgtgt	tgaatttttg	aattgttccct	240
aatattagga	aggaagcatt	tggtctttca	tcacaaagaa	tgatttagat	gaagtgggtt	300
ttttgtaga	ttctctttat	caaatggagg	aattttctct	ccctagtttg	ctgaattttt	360
aacataaaaag	agtactgtaa	gtactcatta	taaaacaaaa	tatggctgtg	gaagatgaaa	420
gagagtttca	agcatgctgg	cttgataggg	cagatccaag	ctggcaaaaa	taattatctc	480
tttcttcttt	ttttctatcc	atggaataaa	aaattaagag	gaaagaatgt	taatagaatc	540
gcattatttc	ttcaaaatac	gttgtgagtt	ttaaaagtat	tatctacctt	ttttattata	600
ctttttttag	ggtacatgtg	cacaacgtgc	aggtttggtt	catatgtatg	catgtgccat	660
gttgggtgtg	tgtactcatt	aactcatcat	ttaacattag	gtataactcc	taatgctatc	720
cttccccctt	ctccccaccc	cacaacaggc	cccagtgtgt	gatgttcccc	ttcctgtgtc	780
catgtgttct	cattgtatat	ttttttaaat	ctaccacatc	aaggcacctc	tttttcatgt	840
tgcccatggg	ttaggtgaac	ataaagacag	agctcgtctg	aggcaacata	cagtccaaca	900
aagccacctg	cctctctgtc	tccactctct	ctctacactg	cacgcgtgct	aggtgttgat	960
cctgtctatt	ccagtggag	aacaggttcc	gtaccatgtg	gagaatttgc	atgtaaaagg	1020
agactgggat	atacaggctg	gagaccacat	caggtggctg	ggcatgtggg	ataaatccta	1080
ttgagcatct	gtcatagggc	ctgtcactta	gtagacagtc	actaaatatt	tgtaaatac	1140
atgatgcctg	tttaacacat	tttctacaac	catggagacc	tccacaactg	atgtaggaca	1200
aaatctttct	gctttgaact	ctagcctttc	ggggcagtg	gatttatgaa	aaatgccatc	1260
tctatagctg	aggatgaaga	atggaagaga	atacgatcat	tgctgtctcc	aacattcacc	1320
agcggaaaac	tcaaggaggt	atgaaaataa	cttgggtttt	aattagaaac	ttaaagaatg	1380
aatcaggtgg	ggacaggtag	aaagtaagat	cagagttcct	ttccgaggag	tagtctgctg	1440
aatttgagct	tcctaaaaat	agtcttttta	tgtacagaaa	acacatcata	aaattcatta	1500
yacaatgtca	cttattgttc	catgccaggc	aaagtcatgt	ccttctggga	cttatgtctg	1560
cacatttaac	tatgggtggg	gttgtgtttt	gtgcttagat	ggtccctatc	attgccagct	1620
atggagatgt	gttgggtgaga	aatctgaggc	gggaagcaga	gacaggcaag	cctgtcacct	1680
tgaaacagta	agtaggagca	cagccatggg	gttctgagct	gtcatgagcc	cctccagctg	1740
cctgctatgg	agctgatact	cccgtgtttg	ggttattcca	gtgaccagac	aaaaggaggg	1800
ctgtggtaat	gcaacttcaa	tgggtctccc	aagatggggc	agctccgatg	aggaggtggg	1860
gcagctggag	gaaaaggatc	ttctcccctg	tgcacagagg	tcagggttta	catatctgtt	1920
aaattgtcac	cttggatatt	ctggaggact	aaatacatcc	tttaggggga	aaagtgtgat	1980
tgtatcaaag	ttttaagcat	ggagtgtatg	ggatgggtgga	aggggaaggc	acttggtatc	2040
tgttgggttg	cagttagtag	gggtgggaaag	ttataatgga	gaacttagaa	taactttgat	2100
catttcatgt	tttttttctg	agggtatcag	tagaatacta	aatattaaac	attcccacca	2160
tttctttttc	ctccagtctc	aaagagagag	ggtggtaaaa	acgctatagg	tggggcaagc	2220
ctattatttg	ctgtctacac	ttatgcagga	acaacagggtg	taatctgagc	ctgtcctggg	2280
cagacagggg	atatgtggtc	actcactata	gaagtttcca	aatcaaattt	tgagagtttt	2340
ttttaaccag	gacatcattt	gtcattatat	tttcaaaaaa	taattctgcc	atcagggcaa	2400
cctcagctca	ccacagctgg	ggatagtggg	attttccaaa	gcttgagcag	ggagtataga	2460
gaataaggat	gatattttcta	ggagctcagg	acatgggtact	gttgctttgt	aaagtgtgta	2520
agaggaatcg	gctctgggca	tagagtctgt	agtcaggcaa	tgtcacctgt	cttgagcccc	2580
ttagaaagag	tgaatttttc	tactcttgtt	ctgctgaagc	acagtgtcta	cccatcttgt	2640
atcatccaca	attaacacat	gctactgcag	ttgtctgata	gtggatctct	gtctttctat	2700
gactaggctc	cttgacctca	gaggtaagtc	taactcagtt	gagtgtctcc	atcaccccca	2760
gcggagagcc	agctgtgtca	ctgacacctg	ataatcacct	tctgagggag	tgtgatggga	2820
gatgctccag	taaatagttc	tgaaagtctg	tggctgtttg	tctgtcttga	ctggacatgt	2880
ggatttcctg	ctgcacgcat	agaggaagga	tggtaaagag	gtgctgattt	taattttcca	2940
catctttctc	cactcagcgt	ctttggggcc	tacagcatgg	atgtgatcac	tagcacatca	3000
t						3001

<210> 90  
 <211> 410  
 <212> DNA  
 <213> Homo Sapiens

<220>

<221> allele  
 <222> 168  
 <223> 99-28779-168 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 149..167  
 <223> 99-28779-168.mis1

<220>  
 <221> misc\_binding  
 <222> 169..187  
 <223> 99-28779-168.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 390..409  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 156..180  
 <223> 99-28779-168 potential probe

<400> 90  
 tgactgctta acagaccaag ttgcttgcat tttgtatggt tagccctcct ttgccactgc 60  
 ttttagagcc ttggaaggct aagtgtgata gtaatgctag ctctaatagca tatttaaagg 120  
 agactgcctc gcttttagaa gacatctggt ctgctctctg catgaggyac agcagtaaag 180  
 ctcttttgatt ccagaatca agaactctcc ccttcagact attaccgaat gcaagggtggt 240  
 taattgaagg ccactaattg atgctcaaata agaaggatat tgactatatt ggaacagatg 300  
 gagtctctac tacaaaagtc tttgggtatt tgtttcttac atagaaaatg ctaacatgaa 360  
 tagaaagata ctggtgcaag accattcccg ggaaagtaga cataactaca 410

<210> 91  
 <211> 479  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 300  
 <223> 99-28788-300 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 281..299  
 <223> 99-28788-300.mis1

<220>  
 <221> misc\_binding  
 <222> 301..320  
 <223> 99-28788-300.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer



<220>  
 <221> primer\_bind  
 <222> 458..478  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 288..312  
 <223> 99-28788-300 potential probe

<400> 91  
 tctacccatt ctgcttctct gatttttaat gcattgtctc tatcccaggc tactttggag 60  
 ggtcatcccg agtttgcaga taaattcttc ctctctcttt ggactcattt agaagaaagt 120  
 tgtaactatg gaaatgatgt aactagcctg ttaacatccc tcagcttctt gttagaaatc 180  
 cccagtgaat tggggagagg ttggcttttg acctttgtgt tcaccatcat caccatcata 240  
 caatatttat gaaacaccac acacatataa ttctgaactg agccaagcac agagatcacr 300  
 tccactttcc tcaagggact tgtaatttaa ccttgggtctg gtgtgctact tagaccaggt 360  
 gtgggtacat aagaaggagg ctgctgccag caaccacaca ttaataacaa tctctctatt 420  
 ttagaataag tccaggaata tgtaggcat ggatgtagta aagtagccaa gaaagggga 479

<210> 92  
 <211> 499  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 263  
 <223> 99-32052-262 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 244..262  
 <223> 99-32052-262.mis1

<220>  
 <221> misc\_binding  
 <222> 264..282  
 <223> 99-32052-262.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 478..498  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 251..275  
 <223> 99-32052-262 potential probe

<400> 92  
 cagagtgaca aataagtgt atggcttgat agaagtgaag ctcttcacat atattcaaaa 60  
 tacatatcac aaacttttgt aaataggata gtaatctgaa gaacttttgc cctttttacc 120  
 ccatttactg taactcttgt ttctaggtaa tcgttctctc tcaacaaact tctcaagcgt 180  
 ctgtgtaaca agccacatgt tctaacaat tgtctccatc gcacttcaac agccaggtcc 240  
 ctatttttta taacgtatta acyttattat tttcttatta ttttaaaaga atctatgcac 300  
 attagcaaaa ttttaaagat agagaaaaat ataaacagaa aaaattatgt ttacttctac 360  
 caccctaaat caactattat caattttata catattttac tccatctttt ttcaaagttt 420

cttacatttt ccaatgtcat taaaattctc tgtgaatgta aattttaaaa actgtacctta 480  
ctgttttttg gaatctgta 499

<210> 93  
<211> 467  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 244  
<223> 99-32121-242 : polymorphic base A or G

<220>  
<221> misc\_binding  
<222> 225..243  
<223> 99-32121-242.mis1

<220>  
<221> misc\_binding  
<222> 245..264  
<223> 99-32121-242.mis2, potential complement

<220>  
<221> primer\_bind  
<222> 1..17  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 448..466  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 232..256  
<223> 99-32121-242 potential probe

<220>  
<221> misc\_feature  
<222> 72  
<223> n=a, g, c or t

<400> 93  
agcagtatga cagggaccat tctgggtctc tgggaagttc tcagctgcgg ggagctctgc 60  
aggccgcagt tnccagctaa atgaacaact ttaccaaattg attgtccgcc ggtatgctaa 120  
tgaagatgga gatatggatt ttaacaattt catcagctgc ttgggtccgcc tggatgccat 180  
gtttcgtgcc ttcaagtctc tggatagaga tagagatggc ctgattcaag tgtctatcaa 240  
agartggctg cagttgacca tgtattcctg aagtgggaac tgagaagtca agatcctccc 300  
tggaggacag gactgaaaac cttgccaaagc tgtacacagt tgctgatacc ctgtgcaaca 360  
gctctcatTT cctggcaagc tctttcacia ccctacatat ttctgatcat gtgctgcctt 420  
ttactgctga attaaaacag atattcacga aaaatgttct gagtggg 467

<210> 94  
<211> 469  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 169  
<223> 99-32059-169 : polymorphic base C or T

```

<220>
<221> misc_binding
<222> 149..168
<223> 99-32059-169.mis1, potential

<220>
<221> misc_binding
<222> 170..189
<223> 99-32059-169.mis2, potential complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 448..468
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 157..181
<223> 99-32059-169 potential probe

<400> 94
acaagaaccc acctaccttc cggggttaaga aatagaatat ccctacacctg acaagcccac      60
atgcacccca cgccccctaa gcacattcac ccctgttccc tgctctaaaa taaacactat      120
cctgagtttg gcaaacacca cttctttggt ttttctttat aatattacya tctatgaata      180
tatttctaaa caatacattg ttagttttatt cttcttcaaa ttttatgtaa aaggaatcac      240
actacagata ttgttctgtg acttatttgg cccaatatgt ttctgagatt catccttgct      300
gatgggggtg gctgcagttc acttgtttcc agtggtggtt atagtaattc tattgtatga      360
ataataacaa tttattttatt catccaactg tgaaggacat ttggattggt tccagttttt      420
ttttcttttt ggattttgaa caatgctgtc tataaacgct ttaggatgt      469

<210> 95
<211> 450
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 304
<223> 99-32061-304 : polymorphic base A or G

<220>
<221> misc_binding
<222> 285..303
<223> 99-32061-304.mis1

<220>
<221> misc_binding
<222> 305..324
<223> 99-32061-304.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 430..449

```

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 292..316

<223> 99-32061-304 potential probe

<400> 95

cacaaaactc	actattgcca	tagctgcaat	taaaatttag	ataatctggc	tgcttactaa	60
agcaaatagc	ttgataaaat	gtaccccaaa	acagataaaa	attatacagc	aaaatatact	120
atTTTTTTTaa	ttctttaaag	tcaaatcagt	atcatgataa	gaattattgc	acaatctttg	180
gttctttttct	ttaaaaccta	ctgaggtccc	caggaagaat	tataaaactta	ataaaaaaaa	240
atccagactt	gaagatat	cagggccaca	tttcaaagga	gaccagctct	ttggaggagg	300
gccrtaatcc	ctccataacc	tgtcctaata	tgagagcccag	agaagtccag	agttagaact	360
aaggagttac	attgggtaag	tacaaataga	aaagataatg	gtctcatgga	aactccagac	420
agtgggcccc	atccctttcc	tggaagtcag				450

<210> 96

<211> 487

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 303

<223> 99-32065-303 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 284..302

<223> 99-32065-303.mis1

<220>

<221> misc\_binding

<222> 304..322

<223> 99-32065-303.mis2, complement

<220>

<221> primer\_bind

<222> 1..17

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 469..486

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 291..315

<223> 99-32065-303 potential probe

<400> 96

gccccaatgc	caactacatt	atgataatct	tctaaaagtt	ataattgcct	aatgttaaaa	60
tatTTTgttt	tctgagttat	tgccaaatgc	gatacatccc	tagttcggaa	agatacccaa	120
ctactatact	tgaaaccact	gaagctacaa	aataccttgc	tctcagtttt	cacatttgct	180
tttctccctc	tacagctttc	tgaggtggca	taagtggatt	agttatacta	tttttattaa	240
ttacttttagt	agtaatttct	attaaaacaa	ttattaataa	caattattaa	ccagtacagt	300
ctkgttattt	taaacattag	catgaggcag	aatggaaactg	cttttcaggc	attatctaata	360
taagatggta	atagaggaga	aactgatcat	gagttgacaa	agctactggg	aaaagtttat	420
tcttattgaa	cagaaccaa	ttgttgtgat	ctgtatgcct	taaaagtgc	gcctcttatg	480
tggaactc						487

<210> 97  
 <211> 541  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 118  
 <223> 99-32123-118 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 99..117  
 <223> 99-32123-118.mis1

<220>  
 <221> misc\_binding  
 <222> 119..138  
 <223> 99-32123-118.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 520..540  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 106..130  
 <223> 99-32123-118 potential probe

<400> 97  
 cagtaaatag atcagtaaag tacaatataa cacaaaagaa aacgaaatat tgcttgattt 60  
 tttccaataa aagcaagggt aataaaaaca tttttagtaa gaaaatctat catttttrtt 120  
 ttaaaaatct ttcaatttta aacatcatta ccaacacatt aaaagtatta tcaataagtg 180  
 cctttacaat ttcaagcaaa agctactgtg ttttccttat tggaaatact gctttcagtc 240  
 atcttttttg tctgagggtac tctcttcattg cttttcaggg ctgactttat tactggcggt 300  
 ggaggggggt gtctggactt cttttggtta tgaaaacaca tggcacgtct ggaggtctag 360  
 gtatgttgta aatatcttag catattctgg atgctttaag gcaaaacttt taaattcctc 420  
 tagaagagaa agaaaaaaaaa tccaataagt tggggtgaat cttcttttg catgatgcag 480  
 attaataaat gactctaata atgcaattat tacaaaattc tactacccaa cacacaaaca 540  
 t 541

<210> 98  
 <211> 449  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 314  
 <223> 99-32148-315 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 294..313  
 <223> 99-32148-315.mis1, potential

<220>

```

<221> misc_binding
<222> 315..333
<223> 99-32148-315.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 428..448
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 302..326
<223> 99-32148-315 potential probe

<400> 98
tgagtgcatt tgatgtgggs cagcaaagct tcattcaggt ggaaacagat taagaagacc      60
aaagagtggg gaaatggcta agtaggaatg aaaaaacagc cagctacccg yggccagtgc      120
cttattctaa aagaggacag ctagcttgcc caaggactct tgcagaagga aacctgggag      180
agtttccttc tcctcttgca gaagtaaact cttcagggtg aagagtcagg aaggagctcc      240
agggatgagt gaagtcaact gaagttgcct cttttataaa cagctctgca gtggttctct      300
ggaaaccgag gctsgttgca aaccctaaa aagtactgct ctgcaaggct tgtaactgcc      360
atacttggtg ggtcctgctc catctccatg tgtggcagtg ccagctgcaa ccagcctcac      420
acaggggtccg agagtctcag aactgcaag                                     449

<210> 99
<211> 920
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 95
<223> 16-2-76 : polymorphic base A or G

<220>
<221> misc_binding
<222> 76..94
<223> 16-2-76.mis1

<220>
<221> misc_binding
<222> 96..114
<223> 16-2-76.mis2, complement

<220>
<221> primer_bind
<222> 20..39
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 240..260
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 83..107
<223> 16-2-76 potential probe

```

```

<400> 99
ctggggcctg agactgaggt ccagggagac cctaattcct gcacccacc cctcctgggt 60
ccctccagat gggaggcatg gaggtgtca tcacrggcct ggcagatgac ttccagggtcc 120
tgaagcgaca ccggaactc ttacatttg gcgtcacctt cagcactttc cttctcgccc 180
tgttctgcat aaccaaggtg agtaggggtt gggctctggg tcacctgggg gcctctgagg 240
ccgcatttca ataaagtcaa acattcctag ccttagaact gggctgagct cagggagAAC 300
aatgcaggat ccagcatcct caattcagcg gcctgaccca ctagggttag gccagtagt 360
cttcttccat ctctgassct gaggattcca ttcagccctg ttaattgcct tattgacttg 420
agggscagca aaagtccctt tggaacccat ctaactcttt attggctgaa actgagggtga 480
ctgtaacgtc aatacaacag caccacagcc ctatgccctg ggttttcaaa tagagctccg 540
agcaagtggg acagggggca ggtaagagtt gacagacaca acaatcagtt cccacgtttg 600
accaaaggag gcctcttggc ttcttctctc cctgtgccag ggtggaattt acgtcttgac 660
cctcctggac acctttgctg cgggcacctc catccttttt gctgtcctca tggaagccat 720
cggagtttcc tgggttttatg gtatgtgagt gtgtggaaaa gcctcagctc ccagtcctcc 780
tagaatcctg cacctggagg tgtgcaggga ggccttccat ttccaggaca gccacctaaa 840
attccagagt ccagcaagtc acttattggg aacaaatctc aatcctcggc tcattcttgg 900
atgaacctgc ccttaacagg 920

```

<210> 100

<211> 395

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 120

<223> 16-28-93 : polymorphic base A or C

<220>

<221> misc\_binding

<222> 101..119

<223> 16-28-93.mis1

<220>

<221> misc\_binding

<222> 121..143

<223> 16-28-93.mis2, complement

<220>

<221> primer\_bind

<222> 28..47

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 354..374

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 108..132

<223> 16-28-93 potential probe

<400> 100

```

tctgttatct ctaaacctgt gttctgtccg cccacacatg acctaacaat tgggccccca 60
gatactcccc tatcatgtgc agctcagacc aatggtttca gccattgatg aggtccttgm 120
tggttcttac aggagctggc ctagtgttca tcctgtatcc agaggccatt tctacctgt 180
ctggatctac attctgggct gttgtgtttt tcgtcatgct cctggcgctg ggcttgaca 240
gctcagtgag tgacctgct taggatacct atccccatc ccactgggcc tgacccccctt 300
ccccaacaca cagtgtgtgg cctgaagttc ccactattca aacaccaggt taacagttgt 360
ttcccagaag gccctattta aattgcagac aaaaa 395

```

<210> 101  
 <211> 922  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 342  
 <223> 16-3-199 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 323..341  
 <223> 16-3-199.mis1

<220>  
 <221> misc\_binding  
 <222> 343..361  
 <223> 16-3-199.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 143..162  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 374..393  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 330..354  
 <223> 16-3-199 potential probe

<220>  
 <221> misc\_feature  
 <222> 565,643  
 <223> n=a, g, c or t

<400> 101  
 agctcaagaa acagtgtctg gatgagtgc tcaatggacc agctccacaa acaaagctgg 60  
 aggtgtcttg tacagacccc aaatgctatc catgtggggc tgcaggatca aatagcaggt 120  
 ggccctcatc tgcaggtgca gccaggctgc ragaaggggtg tccctggggc aagctgaggc 180  
 ctccctcccct tctcttcctt tcagagactg gcctatggca tcacgccaga gaacgagcac 240  
 cacctgggtgg ctacagagga catcagacag ttccaggtgg gtgaagccta gacccctggg 300  
 gtggagatta caagggcggg ccctggctgt tccctgctgt gyactgcccaggctagaca 360  
 tcacatccag aaaaccaga aaccagtgat gagctgcctt tcccccttg aaacatcggg 420  
 atggggggaca gggaggctca ccttgagccc atggcctcag gcttgccctg tgactttggg 480  
 gaggttctgc tgccctttct gggcctctgt gacaattagg gaatcaactt gcacgttccc 540  
 tgaggtccgt gaaggaaggg ggtgnttttc tgccttctct ctacctctg ctgccccgc 600  
 cagctggccc ttgctccttt ctgtccccac catgtcatca agnccctcgt gtctttctct 660  
 gcagttgcaa cactggctgg ccactctgagc ctgcctggag gagaaggagg aacccccatg 720  
 ccaatgtcca ggtcacaggc atccgctgcg ctcccacctc ggacaccatc ttgggattcc 780  
 tcccctggaa gttgtccttt ctgatccctc cttcttttcc catttacaaa tgatttcgtg 840  
 actgtagttt ttgttcacct tctgtgcate tggcctgggg gctgttagct cagaggagag 900  
 gagcaaacag gaaaatgact tc 922

<210> 102  
 <211> 245  
 <212> DNA  
 <213> Homo Sapiens



```

<220>
<221> allele
<222> 197
<223> 16-50-197 : polymorphic base C or T

<220>
<221> misc_binding
<222> 178..196
<223> 16-50-197.mis1

<220>
<221> misc_binding
<222> 198..216
<223> 16-50-197.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 227..245
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 185..209
<223> 16-50-197 potential probe

<400> 102
agaacctcat gggaggacct ggccctggct atcatggggg ccattggtaac aggcctgccc      60
tgtgtgtgca caggagtga caggttcagc aacgacatcc agcagatgat ggggttcagg      120
ccgggtctat actggagact gtgctggaag ttcgtcagtc ctgccttcct cctggtgtgt      180
agtgtctgca gggaagycct gcatgtgggg agggggctgt gtccaggatg gagctgggtg      240
aggat                                           245

<210> 103
<211> 357
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 181
<223> 16-1-59 : polymorphic base C or T

<220>
<221> misc_binding
<222> 158..180
<223> 16-1-59.mis1

<220>
<221> misc_binding
<222> 182..200
<223> 16-1-59.mis2, complement

<220>
<221> primer_bind
<222> 123..142
<223> upstream amplification primer

<220>

```

<221> primer\_bind  
 <222> 290..309  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 169..193  
 <223> 16-1-59 potential probe

<400> 103  
 gttgccaggg ctgcccattct ctggttcaga ccatgtttcc tctggtctca gagcatcccc 60  
 aggggtttctc agcccttccg gaccagttag gtgttccagt gttgtaggaa gcagaggctg 120  
 atggcttttg tctgctgggt tcaggtatgg attgatgccg caactcagat atttttttcc 180  
 ytggggggctg gatttggagt attgattgca tttgccagtt acaacaaatt tgacaacaac 240  
 tgttacagggt aagattcttc tcagaattct gagaagctct aaatcctggg gattgactct 300  
 tgtgggggtgg cagagagggc tctggtctgg aagccaactc tccctgggca agccaaa 357

<210> 104  
 <211> 920  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 206  
 <223> 16-2-187 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 183..205  
 <223> 16-2-187.mis1

<220>  
 <221> misc\_binding  
 <222> 207..225  
 <223> 16-2-187.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 20..39  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 240..260  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 194..218  
 <223> 16-2-187 potential probe

<400> 104  
 ctggggcctg agactgaggt ccaggagagac cctaattcct gcacccacc cctcctgggt 60  
 ccctccagat gggaggcatg gaggctgtca tcacgggcct ggcagatgac ttccagggtcc 120  
 tgaagcgaca ccggaaactc ttcacatttg gcgtcacctt cagcacttcc cttctcgccc 180  
 tgttctgcat aaccaagggt agtagrggct gggctctggg tcacctgggg gcctctgagg 240  
 ccgcatttca ataaagtcaa acattcctag ccttagaact gggctgagct caggggagaac 300  
 aatgcaggat ccagcatcct caattcagcg gcctgaccca ctagggttag gccagtagt 360  
 cttcttccat ctctgassct gaggattcca ttcagccctg ttaattgcct tattgacttg 420  
 agggacagca aaagtccctt tggaacccat ctaactcttt attggctgaa actgagggtga 480  
 ctgtaacgtc aatacaacag caccacagcc ctatgccctg ggttttcaaa tagagctccg 540  
 agcaagtggg acaggggggca ggtaagagtt gacagacaca acaatcagtt cccacgtttg 600

```

accaaagagg gcctcttggc ttcttctctc cctgtgccag ggtggaattt acgtcttgac 660
cctcctggac acctttgctg cgggcacctc catccttttt gctgtcctca tggaagccat 720
cggagtttcc tgggtttatg gtatgtgagt gtgtggaaaa gcctcagctc ccagtcctcc 780
tagaatcctg cacctggagg tgtgcaggga ggccttccat ttccaggaca gccacctaaa 840
attccagagt ccagcaagtc acttattggg aacaaatctc aatcctcggc tcatctttgg 900
atgaacctgc ccttaacagg                                     920

```

<210> 105

<211> 466

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 311

<223> 99-28761-311 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 292..310

<223> 99-28761-311.mis1

<220>

<221> misc\_binding

<222> 312..331

<223> 99-28761-311.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 446..465

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 299..323

<223> 99-28761-311 potential probe

<400> 105

```

tttctaactc taagaaggca tttttaaaaa gtaagtaggc aataaagaaa tgggtacttct 60
atgtaagtag tgcattgtga gtagtgagtt ttgtgatcaa tacaattgct tttgtatgtg 120
atttgctttt aagatgttgg aaatgagaat ctgatataat agagaatttg acttacaaga 180
tttgcaattt taagtgtaac acctaggagg atttaatgaa ttaattttgt agtcaatggt 240
tggatgctca ggagaacctg aatttatcag ttttaattctc agcagggtga aatgctttaa 300
gagaatttgt rtgctaaatt tagaagtttt gatttattag tcttacaaga actaagtaag 360
tcctgagaaa gattttgttt cttctatttg taagtcttcc tggtagggat ttgaagattt 420
taacaaagcc agatgtatca aatttgtgag tatagtttga aatgct 466

```

<210> 106

<211> 462

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 86

<223> 99-28771-86 : polymorphic base C or T

<220>

<221> misc\_binding  
 <222> 67..85  
 <223> 99-28771-86.mis1

<220>  
 <221> misc\_binding  
 <222> 87..106  
 <223> 99-28771-86.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 444..461  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 74..98  
 <223> 99-28771-86 potential probe

<400> 106		
ttcagagtag taacttccaa aggctaattgg atgaatgtga gtattttccat tctcattgtg	60	
gccaggaaaag atagagataa tcatayagta cccagaaaat gactgcttca tatgatgagg	120	
ctttaatttc cattttaatg gaaacatgtt catttaaaag aaagaaaagc agattttctga	180	
actatgtctc ctctctccgt taacaacctg gatgtgcacc tagaattaat gagctacatt	240	
tttattttcta ttttgctaaa gaggtgacc agggctgttg cattacctga tgtctaattct	300	
ttccagtgtc cctctcacgc ctccctcac tgttttccc cttctgaatg cgatgttagt	360	
attttggctt tgtctcaaataaacttacaa gtcgggtttt tatttctccc caacggagcc	420	
tctcaaatec cttatcttca gctcaacagg aaggagatta ct	462	

<210> 107  
 <211> 452  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 291  
 <223> 99-28791-291 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 272..290  
 <223> 99-28791-291.mis1

<220>  
 <221> misc\_binding  
 <222> 292..311  
 <223> 99-28791-291.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 432..451  
 <223> downstream amplification primer, complement

```

<220>
<221> misc_binding
<222> 279..303
<223> 99-28791-291 potential probe

<400> 107
taaaaaccca cactcaacat gggcagtcaa gccaaagact gggacctttg gagagcctct      60
ggaatgagag ttctctgggg tacttccaaa gggagctggc agtcagtcca ggggacctaa      120
aggaatttgg ttgaacagta tcattctctgt gcatagtaag agggaatgtt ggggtgggtccg      180
ggcagtttcc aatatggcaa agcatctgct tggacagtgc cagcaagcct tcctctgacc      240
cagtctccaa tgtccactaa cttataaaaa tgcatcaac tcccacatgt ragaaacacc      300
atgatttgta ctgtgcatgg gtcacattct tattctagaa atgcatcacc ctgtgtttat      360
ccaagtgtgt ttacttgggt taatgtccag tagtaataga atatgaaata tcaaggaacc      420
atctttgtta cgtgacttcc aaaatgtgag at                                     452

<210> 108
<211> 489
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 66
<223> 99-32077-66 : polymorphic base A or G

<220>
<221> misc_binding
<222> 47..65
<223> 99-32077-66.mis1

<220>
<221> misc_binding
<222> 67..85
<223> 99-32077-66.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 471..488
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 54..78
<223> 99-32077-66 potential probe

<400> 108
gctggagggtg agataaggca tcttcaccgc tgcatttcca gctttgtagg gggaaaacaa      60
tttgcrtttg ggaaataatc caacaagcaa tcctatgggt ttaatacaaa cactcaaaga      120
ggttctggcc atgaccatct ggggtccagcc cttcactgaa ttggaaagac ggcaacgata      180
atggttgaac aggccacat gtgttggtc tgattctgag ttcccctac ccaccgcacc      240
ccatgattga agaggataca ggggtccacc actgtcaggc atcaaggag acacaggctc      300
aggggagaaa tcaacacttc tcagggtcct tttcaaggac taccacagag atggaaggtc      360
atctagtcta tgggtgcctg gacctgcctt ggcagtagtc gtggccattt tggggtaacc      420
taaagaaaac agacaatgtt tgatttgtaa catattgaga gttgtttttg cccttttgat      480
gacctgcag                                     489

<210> 109

```

<211> 489  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 467  
 <223> 99-32078-466 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 448..466  
 <223> 99-32078-466.mis1

<220>  
 <221> misc\_binding  
 <222> 468..486  
 <223> 99-32078-466.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 470..488  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 455..479  
 <223> 99-32078-466 potential probe

<400> 109  
 agcaccacagt ttgttagagt aagactgggc caaagcatcc tgggatgcag tagtggtatg 60  
 gtagactaac tgctgtaaca aatagacccc aaagcggatg gtagctcata cacaacagga 120  
 atttattctt gttctcatta cagtagtgga tatgggaata ataagcaggc tccaatctat 180  
 ctgggtcttt cagggaccca gaattgacaa ggctttgctt tcttcaacac ttggcttcaa 240  
 gggtatcctg gggtgcctt ctattctggc cagccagaag gaacaaaaaa catgatgtat 300  
 ttctatgcgg gaggctttta ggggccagc ccacaaaagg cttacatcag ttccaccaac 360  
 tctccattgg ctggaacgca ggcacagggt ggcacctgac tgtgtgggaa atgtggtcca 420  
 tggctgctca gcacttccca gcatgatgct tggagcaagc aggccayctc tgtctgagag 480  
 aggatacag 489

<210> 110  
 <211> 470  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 426  
 <223> 99-32376-426 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 407..425  
 <223> 99-32376-426.mis1

<220>  
 <221> misc\_binding  
 <222> 427..446

<223> 99-32376-426.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 449..469

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 414..438

<223> 99-32376-426 potential probe

<400> 110

ggggctgaga	attactggca	ttgagacttt	tgatgctggt	agctgcaact	gatgcagttc	60
ctccttaaac	ccagtgaaaa	aacctgtggt	cacgtagctt	tcacacttta	tcctatgtca	120
caaacaaacc	tgaatctgca	aacctcctgg	gatggctctg	caaatgcaag	gtgaccatga	180
acctgctggt	ccccagagcc	ccctttgcat	tgagggcttt	tgaggccatc	tctcatttga	240
tacaagctga	gcagcctcgt	tcctcctgct	cttcctcaaa	tgtccttcag	gctttctctc	300
cttctcacag	catgggtgcta	gatgcttgac	tttttacttc	ctggaaaaaa	aatttcaggt	360
ccatgtggct	tcttgatagt	aaaagaaagc	aatactcatg	tatttattgg	ttcactcaca	420
tctggrtggt	agagccaaat	tccaaagacc	tttgaaagtt	ctcttgcagg		470

<210> 111

<211> 457

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 420

<223> 99-32361-419 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 400..419

<223> 99-32361-419.mis1, potential

<220>

<221> misc\_binding

<222> 421..439

<223> 99-32361-419.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 442..456

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 408..432

<223> 99-32361-419 potential probe

<400> 111

tctctaattct	tctccatcat	cattatctgt	tgaattataa	atgcatcctg	aggcatgctg	60
cccagtggct	ttatatcttg	tctgcacaat	gagattgtaa	gtcccttgag	gaaaaggacc	120
aggttggtg	tgaattatgc	attccttggt	gtgtctagaa	taatatcaag	ttcagaagac	180
tcaggtatca	cttgagatgt	ctctttctgg	cccctccaat	ggtctgaata	aatctgactc	240
aaactcccag	tttaacagtc	ttgatgaagc	ccaaagccct	atccatgata	cgtgagaatt	300
cttattggtt	ttcttttgat	gggtcccatt	gtgactagtt	caaaatactg	gagactatgt	360
cttttttcct	tctcattaac	atggttacia	aactctctct	tttataaact	tccataaaak	420
ctggtgagtc	tcttaagaac	tggtatttag	agacctc			457

&lt;210&gt; 112

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 228

&lt;223&gt; 16-21-228 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 205..227

&lt;223&gt; 16-21-228.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 229..251

&lt;223&gt; 16-21-228.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..25

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 399..424

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 216..240

&lt;223&gt; 16-21-228 potential probe

&lt;400&gt; 112

tagcaggcta	agtcctcctt	ctacttcatt	ccagatgata	cccacttcag	gaagtctttc	60
ccttctgtgg	gatgagatgc	ccattctgca	gggctttcac	tccctgcata	ctgccaaacc	120
tcatcatctc	ttacctggat	tctgctaca	gcctcccagt	tggtgtcccg	cttccactct	180
gggcccctcc	tctccgttct	ccacagtgtc	gtcagaatca	cctattcraa	aggcgaatcc	240
gatcatgtgg	ttcctgctgc	ccttaggatc	atgtataaac	tcctagcatg	acttttaagg	300
ccctctatga	tcttgccctat	tgcaacctcc	ccagactcaa	cccttgccag	gtccctctgc	360
atcagctatc	cagaatctct	ttgaggccct	ccacctgctg	tctacctctc	tacctctgtg	420
cttt						424

&lt;210&gt; 113

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 156

&lt;223&gt; 16-22-156 : polymorphic base C or T



```

<220>
<221> misc_binding
<222> 133..155
<223> 16-22-156.mis1

<220>
<221> misc_binding
<222> 157..175
<223> 16-22-156.mis2, complement

<220>
<221> primer_bind
<222> 1..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 458..481
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 144..168
<223> 16-22-156 potential probe

<400> 113
gcctgacaca tggtaagtcc ttagtattat tacagttatt aggacttagc tgagccagct      60
cagggcctgt actgcaggtc tcagctttat gtgagcaaga gcattaagga atgatgcctg      120
gatgcctggg ggtgtgaaga aaagagcctt gggtytgact aggggaacctg gggccactcc      180
ttcctctgct actaaatcac caagtgatct tgttctgttt tcttctctga ccctccctag      240
ttttgtccac cettgaaata atcatctttc cttttcacat ttcattgctta ccaagtactt      300
gtcacctaata tatctcctct cttgataagc tagatggtyc cttccagggc agcttagtag      360
agagcatggg atgtgatgtt tcagattcca gctctgctgc acacctgcca ggtgaacttg      420
gccacgttac atggcctctc tgggcttcag ttccctcacc tatgagtggg ataagcaagc      480
c                                                                                   481

<210> 114
<211> 478
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 404
<223> 16-23-404 : polymorphic base A or G

<220>
<221> misc_binding
<222> 381..403
<223> 16-23-404.mis1

<220>
<221> misc_binding
<222> 405..427
<223> 16-23-404.mis2, complement

<220>
<221> primer_bind
<222> 1..26
<223> upstream amplification primer

<220>

```

<221> primer\_bind  
 <222> 455..478  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 392..416  
 <223> 16-23-404 potential probe

<400> 114  
 ctaagtggga ataacgctaa acatacttgg attaatgcac aaggccctga gatagaggac 60  
 aggcgtcttg tagacctaga agggcacgca aacatatgaa acacatagga acacaagtga 120  
 gttcaacaga cagagccaag ttatcttgct gcaaacatta aaagggtggcc aacctctccc 180  
 aatacacagg tcagactaaa aagatggttt actcttttaa aagttttctt gtgtcattct 240  
 ttctggatac atcgggttca cttgttatgc ccagacatgg caaaactaat gaccaagtaa 300  
 tgagggaata gtaatggaaa gacttgggag cagtccatca tcacagctta actttttgct 360  
 cacaaccgtg tttttaatac tctggtatct gctgtgctt tgtrtatatc taagatgacc 420  
 aggcagcctt aaacatctag ttgcgttcac attctctgta aaatcgctcc ttgttctt 478

<210> 115  
 <211> 428  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 175  
 <223> 16-24-175 : polymorphic base A or C

<220>  
 <221> misc\_binding  
 <222> 156..174  
 <223> 16-24-175.mis1

<220>  
 <221> misc\_binding  
 <222> 176..194  
 <223> 16-24-175.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..22  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 405..428  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 163..187  
 <223> 16-24-175 potential probe

<400> 115  
 tcgaaccgat cttcagttga cagaagagga aacaggctca gaaagattag gcaactcacc 60  
 cgtctcaaga gttggtgaca ctaagcccag acctgtgtga ctctgaaatc cacacctgtg 120  
 ttctttccac tgacatgagc tgccttatgg atgggcaggt tctggggtag gacgmgcaga 180  
 gcagctgcgg ggactgggtg cggassagtt tgtgtacata gagccctcag gtgcggaagc 240  
 mmagcagacc ccagcctctg ccaggtggta gctgtaccaa catgcaagca gcaggcattc 300  
 catcctccag agggatggag aacagggcca gagaaccac agagggccgc atacaaaatc 360  
 caggtctggt gtccctgcctt cacctgcact gcaagggcag gactctaaga agctgtttat 420  
 gaggcagg 428

<210> 116  
 <211> 433  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 286  
 <223> 16-25-286 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 267..285  
 <223> 16-25-286.mis1

<220>  
 <221> misc\_binding  
 <222> 287..305  
 <223> 16-25-286.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..22  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 412..433  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 274..298  
 <223> 16-25-286 potential probe

<400> 116  
 ggtcccatgc ctcaagtgaca tccttgccctc cctggcaggg tgaccctgtg gtgtttgcag 60  
 gagtcttcag aggggtgaaag ggaggggcca gtgagatggg tggctgatgc ctgggaactt 120  
 gtccggcttt acccagagcc ctctgcctct ggtgcaggag gctgcccggc gagcccagga 180  
 gctggagatg gagatgctct ccagcaccag cccaccggag aggacccggt acagcccat 240  
 cccaccagc caccaccagc tgactctccc cgaccctgcc caccayggtc tccacagcac 300  
 tccygacagc cccgccaaac cagagaagaa tgggcatgcc aaagaccacc ccaagattgc 360  
 caagatcttt gagatccaga ccatgcccaa tggcaaarcc cggacctccc tcaagaccat 420  
 gagccgtagg aag 433

<210> 117  
 <211> 433  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 279  
 <223> 16-25-279 : polymorphic base C or G

<220>  
 <221> misc\_binding  
 <222> 260..278  
 <223> 16-25-279.mis1

<220>  
 <221> misc\_binding

<222> 280..298  
 <223> 16-25-279.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..22  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 412..433  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 267..291  
 <223> 16-25-279 potential probe

<400> 117  
 ggtcccatgc ctacgtgaca tccttgccctc cctggcaggg tgaccctgtg gtgtttgcag 60  
 gagtcttcag aggggtgaaag ggagggggcca gtgagatggg tggctgatgc ctgggaactt 120  
 gtccggcttt acccagagcc ctctgcctct ggtgcaggag gctgcccggc gagcccagga 180  
 gctggagatg gagatgctct ccagcaccag cccacccgag aggacccggt acagcccat 240  
 cccacccagc caccaccagc tgactctccc cgaccctgsc caccayggtc tccacagcac 300  
 tccygacagc cccgccaac cagagaagaa tgggcatgcc aaagaccacc ccaagattgc 360  
 caagatcttt gagatccaga ccatgcccaa tggcaaacrc cggacctccc tcaagaccat 420  
 gagccgtagg aag 433

<210> 118  
 <211> 478  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 393  
 <223> 16-23-393 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 370..392  
 <223> 16-23-393.mis1

<220>  
 <221> misc\_binding  
 <222> 394..416  
 <223> 16-23-393.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..26  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 455..478  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 381..405  
 <223> 16-23-393 potential probe

```

<400> 118
ctaaagtggga ataacgctaa acatacttgg attaatgcac aaggccctga gatagaggac      60
aggcgtcttg tagacctaga agggcacgca aacatatgaa acacatagga acacaagtga      120
gttcaacaga cagagccaag ttatcttgtt gcaaacatta aaagggtggc aacctctccc      180
aatacacagg tcagactaaa aagatgggtt actcttttaa aagttttctt gtgtcattct      240
ttctggatac atcgggttca cttgttatgc ccagacatgg caaaactaat gaccaagtaa      300
tgagggaata gtaatggaaa gacttgggag cagtccatca tcacagctta actttttgct      360
cacaaccgtg tttttaatac tctggtatct gckgtgcgtt tgtgtatata taagatgacc      420
aggcagcctt aaacatctag ttgcgttcat attctctgta aaatcgctcc ttgttctt      478

```

<210> 119

<211> 742

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 364

<223> 16-106-364 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 345..363

<223> 16-106-364.mis1

<220>

<221> misc\_binding

<222> 365..383

<223> 16-106-364.mis2, complement

<220>

<221> primer\_bind

<222> 1..22

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 723..742

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 352..376

<223> 16-106-364 potential probe

<400> 119

```

cccagatggg tgatctacaa tgaccagaaa gtgtgtgcct ccgagaagcc gcccaaggac      60
ctgggctaca tctacttcta ccagagagtg gccagctaa agcctgcctc accccttacc      120
aatgagggga ggggaagacc acctggcatg agggagaggg gctgagggat ggacttcagc      180
ccctctgctc tgtacccttt ttccctttgt ccccggcagc agggaagaag ctggaggccg      240
tggggagaatg gctgggcaga gcagaggggc agcgatagac tctggggatg gagcaggacg      300
gggacgggag gggccggcca cctgtctgta aggagacttt gttgcttccc ctgccccggg      360
aatycacagt gctctgcttc tctgtgtcgc cccgcccagc cccctggtgt ggagggaggg      420
gtctcgtttg tgcgcgtggg tgtagctttg tgcctcctct cccagtggag cgatcacctg      480
tgccctccct ccccttttgt ttgcccctgt gtggttggtc aaggagggat gtgagggaaa      540
tagggacccc ccgacttgcc ctccctgcctc agtctttccc ccaccctgtc tcttccttgt      600
ccttctcttg aaaatgccaa aatacacgat gtgaataaaa gtacaacggc taaattgtgt      660
cctgtttgat accttggggg agaggcttac cttcctgggg ttagcaggag ggcgcttaag      720
aaaactccta actctggccg cc                                     742

```

<210> 120

<211> 535

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 285

<223> 16-16-285 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 265..284

<223> 16-16-285.mis1, potential

<220>

<221> misc\_binding

<222> 286..304

<223> 16-16-285.mis2, complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 516..535

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 273..297

<223> 16-16-285 potential probe

<400> 120

ggtggcaggg	ctgcttctca	ccccaaacca	agggagggag	aggcagggag	gctgagagca	60
gcggtctgcc	ctggagctgt	caggtgggag	gcagagggcg	ggagaggctg	tgggctgccc	120
aggtctgatc	cctgaccac	ttgccaccg	tgccctcagt	tcttcccaa	tgagaggcc	180
atctgcacgg	gctcgatga	cgcttctgc	cgcttggttg	acctgcgggc	agaccaggag	240
ctgatctgct	tctccacga	gagcatcatc	tgcgcatca	cgctcygtggc	cttctccctc	300
agtggccgcc	tactattcgc	tggtctacgac	gacttcaact	gcaatgtctg	ggactccatg	360
aagtctgagc	gtgtgggtaa	gggccagccc	tggtctgtgc	ttctcagct	ggaaggaccc	420
tccccagccc	tccctccca	ttctgtaccc	cccacagct	cccatttcgg	actctcttac	480
tgctgtccct	tgtcactggg	tgactccacc	cctggaatcc	agtaccctt	ggttc	535

<210> 121

<211> 529

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 121

<223> 16-17-121 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 102..120

<223> 16-17-121.mis1

<220>

<221> misc\_binding

<222> 122..140

<223> 16-17-121.mis2, complement

```

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 508..529
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 109..133
<223> 16-17-121 potential probe

<400> 121
gcaggcccag cagacttgag tctgaggccc caggccctag gattcctccc ccagagccac      60
tacctttgtc caggcctggg tggatatagg cgtttggccc tgtgactatg gctctggcac      120
yactaggggc ctggccctct tcttattcat gctttctcct ttttctacct tttttctctt      180
cctaagacac ctgcaataaa gtgtagcacc ctggtacatc tgtgatgttt gccttctact      240
ctcttctggt ccaaaaagac ccagggtccca ttttaaggga gtaatgtgtt acagggtgctg      300
tgataaaggc tgggtactgg atagcttggt ggcttatggg aggaggcctg agatgggtca      360
gggggagaag gtattcagca ggtggctggg ggactgtgtg cagcagttcg ctatggcctg      420
cctgtggtgc ccatgtgttt gtacgggagg gttagcttga gaaggaatca gattataaaa      480
ggtcttgaat gtcaagccag agagtccaga ctttttccta agggcaatg      529

<210> 122
<211> 540
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 185
<223> 16-84-185 : polymorphic base C or T

<220>
<221> misc_binding
<222> 162..184
<223> 16-84-185.mis1

<220>
<221> misc_binding
<222> 186..208
<223> 16-84-185.mis2, complement

<220>
<221> primer_bind
<222> 1..22
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 525..540
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 173..197
<223> 16-84-185 potential probe

<400> 122
tagaatgcct ttaatgagca gtaaatactaa ttttattaaa tctcaaccct tgggtacggg      60

```

```

gtgtcatgaa atgggaagta gcacacagta ctatatgcta cagatgaagt acaatgctgt 120
caaatagggg tacttggtgtt aattgttgga gtcgcaagct gaactagcgt tttcttttct 180
tttcttttct tttcttttct tttcttttct tttcttttct ttttttcaag acagggttctc 240
actctgtcac tcaggctaga gtgcagtggg gcaatcacgg ttcaactgcag cctcaacttc 300
ctgggctcaa gcgacccctc cacctcggcc tcctaaaatg ctgggattat aggcattgagc 360
caccactccc agcccccactt ttttcagact ggaaaacgca cactcacatg tgcattctta 420
aatgatcact tgggctgtgg tatggagaat ggcgaccagt gaggaggcag gagctgttgt 480
ccgagcaagg gatgatattg gcatcttgga ttggcatggg ggcagtagtg gtagtgcaga 540

```

```

<210> 123
<211> 525
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 74
<223> 16-87-74 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 51..73
<223> 16-87-74.mis1

```

```

<220>
<221> misc_binding
<222> 75..97
<223> 16-87-74.mis2, complement

```

```

<220>
<221> primer_bind
<222> 1..22
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 504..525
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 62..86
<223> 16-87-74 potential probe

```

```

<400> 123
gtccatttcc ctttgtccat gtgtccctcc caccctgcag ccggctccct cacatccacc 60
ctgggctgca ggctgtctcg gcaggctccc cacagatcaa agcttgtcca ggggtctgcat 120
tgctgcaaaa ggccaggagg actggtgtac agaccggaag gagctagagc ttagtggcag 180
cctgagaggg gaagctgaaa aaggagaaga ggcaaggggc attccagggg agcccgggag 240
agccagcacg gcctcctggg atatgaggca aagaggaaga cagacacaga cacagggagc 300
tgcaggctgg gggcataagc tgggggctgg gaagcataga tacagaaatg cacagatgtg 360
agctgagaag caaggaggga gagagagaga cagaaagaga gagagagacg tgccagggct 420
tgagggacca gagagccctc ccagcctctc tcggagtgtc ggtatacagg atgtaccgt 480
actagggtta gacacctctg gggacgctga gtatgggaat caaag 525

```

```

<210> 124
<211> 665
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 333

```



<223> 16-91-333 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 310..332

<223> 16-91-333.mis1

<220>

<221> misc\_binding

<222> 334..356

<223> 16-91-333.mis2, complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 641..665

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 321..345

<223> 16-91-333 potential probe

<400> 124

gcccattgctc agggtcagtt ggggaagggt ggaaacgggg agtgaagatt tgcctctgct	60
gctatccctga gctccatctc tctatccctc ccatctgtct ctggatttgt agtttcactg	120
tcagggtctgc atgggaacca tcaattcaca aggactctaa tttgccctcc tttggcgccct	180
gtgacaagct caggagatgg gcttcccttct gccttgctgc ttctcacctt cctttatattt	240
ccccctctt gctcttcttt gaactctcca gctaagggtat gtttgcacca gtgtttgaaa	300
gaaccggcag ctgaacttgt ctgccagtgg gargggggct cttggagtta gctgtctggc	360
ctctggagac caccttctcc agcaactgct ctgccccaaag gatcaatgtg ctctaagtat	420
tcatccccca acccctgacc ttgtcgctcc ctctccagtg ggcaatctgt cccaggctat	480
agaaaatgtc ctgagtgtcc tgctcttcta cccggaggat gaggctgcca agagggctct	540
gaaccagtac caggcccagc tgggagagcc gagacctggc ctcggaccca gagaggtaat	600
cccctctcca cgctcacctg ggaggtagcc ccaaatcaaa caaatagacc tgagaagtaa	660
cctgg	665

<210> 125

<211> 327

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 142

<223> 16-128-142 : polymorphic base C or G

<220>

<221> misc\_binding

<222> 123..141

<223> 16-128-142.mis1

<220>

<221> misc\_binding

<222> 143..161

<223> 16-128-142.mis2, complement

<220>

<221> primer\_bind

```

<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 308..327
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 130..154
<223> 16-128-142 potential probe

<400> 125
ctaggaacag tgcgccagtt tctggtgggc tgcagggcac gaggagatag tcaacttgtc      60
tgactgttaa tccaccctgt cccctgcaga tggaggggcg cagccaggcc ccgtgcccaa      120
gtccctgcag aagcagagggc gsatgctgga ggcctgggtc agcagcgagt gtgagtgcag      180
cccttgcccc gtctcaccca tgcctcccag cctgcacctg cagggcgacc tctccttcct      240
gtgcgactcc atcctggcct gccctatctc acccgtgcct cccagcctgc gcctgcaggg      300
cgacctctcc ttctgtgctg accccat                                     327

<210> 126
<211> 551
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 245
<223> 16-133-205 : polymorphic base A or G

<220>
<221> misc_binding
<222> 222..244
<223> 16-133-205.mis1

<220>
<221> misc_binding
<222> 246..268
<223> 16-133-205.mis2, complement

<220>
<221> primer_bind
<222> 41..59
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 472..490
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 233..257
<223> 16-133-205 potential probe

<400> 126
gttctcctgg cactttgctc acctctgttt cccctccagc tcttcttgga gtacctgtcc      60
tttgtgcaat acacctcctg gaactgtctt tccagtctct gctttttgtc ctgatgattt      120
tcatgtgctt ttctcttaca tcatgaagca tttactccac attatcttcc agtttgetca      180
tttgtcctca cctccactct tctctttctg aatttgcttg ttgcttttcc agtctcttag      240
ctccrtggag tatgttcagt gttgctgtgt tctgatagag gtcctttaag ccatcttgta      300
gattttttgt tgcacttcct ctcttccctt agacctccac aggaggaact tttcaatctg      360

```

tcctcttctc	tctgcttaat	gagcccctgc	aaagggtttg	ggaagtgctt	cagcctctct	420
gtgattgtgt	gttcacatta	atatttatta	ttttctttaa	tgtgcataaa	tctcacaatg	480
tgaacagtga	tcctctttga	gtgatttttt	ttctcctttc	tacttttagt	aattctccaa	540
attttctaca	g					551

&lt;210&gt; 127

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 232

&lt;223&gt; 16-135-181 : polymorphic base A or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 209..231

&lt;223&gt; 16-135-181.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 233..251

&lt;223&gt; 16-135-181.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 52..71

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 482..501

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 220..244

&lt;223&gt; 16-135-181 potential probe

&lt;400&gt; 127

ttggttgtgg	ggaccagaga	cagagcaggc	agggctctcac	gttccccagg	gcctctcaag	60
gtagaccct	cgccctcatc	tccaaaccac	gcctcccaga	caggaaccaa	actcccagag	120
tctccaaact	gcctgagcct	tgcccactcc	ctgggctaac	acacacttta	aaggaatccc	180
acagtcaccg	tgtgaaaagc	ttgctacact	gcatttgatt	ctgggcactg	awagcagtac	240
ttggctgcag	acactcgttt	caaacaggcc	ccatttttcc	atctctgctg	ctggtattag	300
gggagccctt	agactctctt	gcagcgccgg	aataggcgct	caagacgtgt	gttaatattg	360
caacagcaaa	tataatgaat	ctgcagttag	ggacgctgag	gccggagtgg	tggatgaaag	420
gtggccggag	ccttttccac	gggtccaaac	cacctgttac	aggagaaggc	gagcggcctc	480
gctaagcaac	tggacgttcc	gcgggcgggg	cgggggcggg	gccggggccc	gagtcgctc	540
ggaaactttc	g					551

&lt;210&gt; 128

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 455

&lt;223&gt; 16-145-405 : polymorphic base C or T

&lt;220&gt;

<221> misc\_binding  
 <222> 436..454  
 <223> 16-145-405.mis1

<220>  
 <221> misc\_binding  
 <222> 456..474  
 <223> 16-145-405.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 51..69  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 523..540  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 443..467  
 <223> 16-145-405 potential probe

<400> 128  
 gtggaaaaaa ccatatggca ttgtcgctt ctcagcctga cctggcatgc actctcacc 60  
 tcatctgtca tgctcctgc tttccacct ggggggctga gaagtcggc catcgaaacc 120  
 ttggttctcg ccagccacgg gagtttgaa gctttatcag attcctgaag cctcgtttcc 180  
 tcatgggaac agtgcaggtg aaagcacctt cctctcgga cgggggggaa gatgagagga 240  
 aattaaatag atgtatggcc ccgcagcagg actggcgctc tccatttgtg ctgaaattgg 300  
 caggttcttg gtctcactta cttcaagaat gaaaccacgg accctcgagg tgactgttac 360  
 agttcttaaa ggcggcgtgt ctggagtttg ttccttctga tattcagatg tggtccgcgt 420  
 tttctcctt ctggtgggtt cctcctctcg ctggytcagg agtgaagctg cagaccttca 480  
 cggcgagtgt cacagctcat aaacgcagta cagacccaaa gagtgagcag caattagatc 540  
 tatcacaaag a 551

<210> 129  
 <211> 492  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 320  
 <223> 16-177-320 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 297..319  
 <223> 16-177-320.mis1

<220>  
 <221> misc\_binding  
 <222> 321..343  
 <223> 16-177-320.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..22  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind

<222> 472..492  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 308..332  
 <223> 16-177-320 potential probe

<400> 129  
 gaccctatcc gataaatggt gcttcctctt catgacaaaag aaaatgaaca ctcatctcact 60  
 caaaatatcc agcacctgct gtgtgcttca ctcttcctgg cacaggggat gcagaatgaa 120  
 cagagagccc ctgccccact gggaggggtg tttgtgggga gatggaccag gtaccagtca 180  
 gtgaatatag cacaatggca ggtagagaaa agtgctacag tcatctaccg tgagcgctgt 240  
 gatgctctgc ccagtttcac cacattaatg gagcaccac tatatgctgg acacatacca 300  
 tgcattttct catcctagcr gctgttgcaa aatagacacg tccattgtga agactgcggg 360  
 cggtagaatc gcagcccca aagggtgtcca ggtcctaata cccaaatcct gtttgtgtgt 420  
 tcccttgcat ggcaggaggg atgttgcaga tgggattcag ttaaagatct tgataccggg 480  
 gagatgattc tg 492

<210> 130  
 <211> 759  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 354  
 <223> 16-4-354 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 335..353  
 <223> 16-4-354.mis1

<220>  
 <221> misc\_binding  
 <222> 355..373  
 <223> 16-4-354.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 740..759  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 342..366  
 <223> 16-4-354 potential probe

<400> 130  
 cctcggtccc acgtaccatc ttccccccag gtgggtcaagt accccctgca cgccatcatg 60  
 gagatcaagg agtacctgat tgacatggcc tccagggcag gcatgcactg gctgtccacc 120  
 atcatcccca cgcaccacat caacgcgctc atcttcttct tcatcgtcag caacctcacc 180  
 atcgacttct tcgccttctt catcccgctg gtcactttct acctgtcctt catctccatg 240  
 gtgatctgca ccccaagggt gttccaggac agcaaggcct gggagaactt ccgcaccctc 300  
 accgacctgc tgctgcgctt cgagcccaac ctggatgtgg agcaggccga ggtyaacttc 360  
 ggctggaacc acctggagcc ctatgcccac ttctgtctct ctgtcttctt cgtcatcttc 420  
 tccttcccca tcgccagcaa ggactgcac cctgtctcgg agctggctgt catcaccggc 480

```

ttctttaccg tgaccagcta cctgagcctg agcaccatg cagagcccta cagcgcagg 540
gccctggcca ccgaggteac cgccggcctg ctatcgctgc tgccctccat gcccttgaat 600
tggccctacc tgaaggtect tggccagacc ttcataccg tgctgtcgg ccacctggc 660
gtcctcaacg tcagcgtccc gtgcctgctc tatgtctacc tgctctatct cttcttccgc 720
atggcacagc tgaggaattt caagggcacc tactgtac 759

```

&lt;210&gt; 131

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; 99-27199-207 : polymorphic base C or T

&lt;400&gt; 131

```

cccaatgtgg ccagggacac tgayggcctt ttctggggtc ttttgcc 47

```

&lt;210&gt; 132

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; 99-27207-117 : polymorphic base C or T

&lt;400&gt; 132

```

tgtgtggcca gcccctccag ggcygtgtgg acagcttttt gtgtatt 47

```

&lt;210&gt; 133

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; 99-27213-53 : polymorphic base A or G

&lt;400&gt; 133

```

tcacacatgt aattgtttat gcarcgttag ggactctcag attctgt 47

```

&lt;210&gt; 134

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 24

&lt;223&gt; 99-27218-333 : polymorphic base G or T

&lt;400&gt; 134

```

gatattttaat aggtggacca ggtkggggag tgtgtttcac tccttga 47

```

&lt;210&gt; 135

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28108-233 : polymorphic base A or C

<400> 135  
cccgatcatgc aacatctgga cacmactaac agagcatggt gaataca 47

<210> 136  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28109-275 : polymorphic base A or G

<400> 136  
atgtgtccta ggatgaacag taaraattat agactctgca gctctag 47

<210> 137  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28110-75 : polymorphic base C or T

<400> 137  
ggtttccgtg ggaaccagat ccgygcaggt acaaatgggg cccagcc 47

<210> 138  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28125-81 : polymorphic base A or C

<400> 138  
ggaccgagga agctgtaatt ccamaagctc tctgggacct tgatgtt 47

<210> 139  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28134-215 : polymorphic base C or T

<400> 139  
gggtctgtca ccctgtttgg gtayaggctc ctgcacgctg gcggcct 47

<210> 140  
<211> 47  
<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-28137-96 : polymorphic base A or G

<400> 140

aagcagtccc agctcttagc aggrcagact ctgccaggca gagaagg

47

<210> 141

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-32204-305 : polymorphic base A or G

<400> 141

caggtgggtg gacttcagag tccractott aaccccatcc tccactg

47

<210> 142

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-28149-118 : polymorphic base C or T

<400> 142

cccacatacg atactgtgac cttygatggg aggagctagc atgtgat

47

<210> 143

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-28160-285 : polymorphic base A or G

<400> 143

tggatcaagt gctaggggat cgcrataatg ggagtaagta gctgggg

47

<210> 144

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-28171-458 : polymorphic base A or G

<400> 144

actcaagctt tgattccaaa tcttctgtta tttcctactg ggaaatg

47

<210> 145



<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28173-395 : polymorphic base C or T

<400> 145  
ctgggccagt cccaacttat actytgggca atcgaaactc atttgcc 47

<210> 146  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32177-113 : polymorphic base C or T

<400> 146  
taggagaaat taaaaaggga tgaagtactc tgttcaaaaa aaagggt 47

<210> 147  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32181-192 : polymorphic base C or T

<400> 147  
accacaat gggattgcta ctgycagttc ctatgctcct ctacttg 47

<210> 148  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32193-258 : polymorphic base G or T

<400> 148  
aagaggtaat cgtagcttgg actkggttgg agtagtggag acagaga 47

<210> 149  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28722-90 : polymorphic base C or T

<400> 149  
gcatttaaaa gataaaatta tccycttggc actcctcaaa ctgtgct 47

<210> 150  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 99-28730-351 : polymorphic base A or G  
  
<400> 150  
agctgtggag caccaggctg gcartgagct ctgccctcag gcacgcc 47  
  
<210> 151  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 99-32306-409 : polymorphic base G or C  
  
<400> 151  
acagatgccc tgttttgttc cttstcttct aaaacatcac aatgatg 47  
  
<210> 152  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 99-27088-246 : polymorphic base A or G  
  
<400> 152  
agtttggttt ccgctcatgc tacrtgttct gtgagatcag tggggag 47  
  
<210> 153  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 99-27090-203 : polymorphic base A or G  
  
<400> 153  
tgttcagaag ttctcagact gggrrcttggg ttcttgcaact tttcatt 47  
  
<210> 154  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 99-27091-220 : polymorphic base A or G

<400> 154  
agaagcattt ttctttgcat aacrcaacac cagtcctctg tgtttag 47

<210> 155  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27093-145 : polymorphic base C or T

<400> 155  
gagtcacctc gaggtaaaca gaaytccaag agtaacgaag gcccaga 47

<210> 156  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27094-406 : polymorphic base C or T

<400> 156  
aagaccctat gccagttcc gccyggccac caaggccctt ctgaagg 47

<210> 157  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27096-410 : polymorphic base A or G

<400> 157  
cccgggaaaa tggttttcat cacrcacacc aactgcattt atttgca 47

<210> 158  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27097-83 : polymorphic base C or T

<400> 158  
catgacacct gcctgtcatc cccygaaaaa aggtgaacgc cgttcag 47

<210> 159  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24

<223> 99-27098-162 : polymorphic base C or T

<400> 159  
acaagcactc atccacagga cacygccgat gatgccattt actgagc 47

<210> 160  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27550-48 : polymorphic base A or G

<400> 160  
atttttcatg cttgatgtga gccrgaagaa aaatgagctt ctctatt 47

<210> 161  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27558-335 : polymorphic base C or T

<400> 161  
aaatctcatg gccgcatatg ttayacaatc atgccactt atgtagg 47

<210> 162  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27561-106 : polymorphic base A or G

<400> 162  
cccagggtgat gataaaaatg gtcrtcatcg ccaggcttgt gtcctgt 47

<210> 163  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27562-366 : polymorphic base G or T

<400> 163  
tgtgggtaga ggccaggaat gctkttaaac atcctacaag gaaggca 47

<210> 164  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>

<221> allele  
<222> 24  
<223> 16-31-738 : polymorphic base C or G

<400> 164  
taatagatcc tgtataaaag gggstctgga aattcgtgca tttcccg 47

<210> 165  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27110-301 : polymorphic base G or C

<400> 165  
tggactttgg gagtgaactt tgtsagatga ttagatgggtg atgtcct 47

<210> 166  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27563-400 : polymorphic base A or G

<400> 166  
tctctctctg ttaaagatca gctrttccct tctgatcttg gaaagag 47

<210> 167  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27573-443 : polymorphic base G or T

<400> 167  
cccgccctgc tctaattctg cccktccttg gctcagctcc agttcca 47

<210> 168  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28732-133 : polymorphic base A or G

<400> 168  
gtgctggaag gtcacgtgcc ttartgggtca tgagatcctg gtgcaaa 47

<210> 169  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28735-56 : polymorphic base C or T

<400> 169  
tctttacgtg gtgaaagtcc tagycagcca tcattcggca caacagt 47

<210> 170  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28736-399 : polymorphic base C or T

<400> 170  
aatgatttgt tgggttttttg tgytcattgc ttagaagcag tgagtgt 47

<210> 171  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28738-319 : polymorphic base C or T

<400> 171  
ctttggattc tatgcaaaac aggyccctcag ggttgtaaca atgtggg 47

<210> 172  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28739-364 : polymorphic base C or T

<400> 172  
ttctgcatac tgggatgtga ggaygggtaa actaggaaga aattcct 47

<210> 173  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27875-185 : polymorphic base C or T

<400> 173  
aataccatcc ccactaataa gtaycaagta ccagggctcc ttggaga 47

<210> 174  
<211> 47

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-27880-176 : polymorphic base C or T

<400> 174  
caagcaagct taccctcatc actyacttgg cctctattca aatagcc 47

<210> 175  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28747-371 : polymorphic base C or T

<400> 175  
ttctcaatct agatagacag aatyctccct cccaggacat ccccaga 47

<210> 176  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28753-353 : polymorphic base C or T

<400> 176  
atgcagggca ttctacaggg cttyaccatc tggagagggga gcctggg 47

<210> 177  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28755-206 : polymorphic base A or G

<400> 177  
accctatccg ctgcactcag agcrgggacc atccgccaag ggagaca 47

<210> 178  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32333-366 : polymorphic base C or T

<400> 178  
cttgaatgct aggaaaggct ataycccaga caactattat cccattt 47

<210> 179  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-38-323 : polymorphic base A or C

<400> 179  
ttttcagagct gtgggtatatt aaamaaatac atagaaatga actgtaa

47

<210> 180  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28484-179 : polymorphic base A or T

<400> 180  
tacatgcttc tctaggtgtg tgawtaactc ataatccatc catgact

47

<210> 181  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-30853-364 : polymorphic base A or G

<400> 181  
acaaaacggt agtacacttt ctcraattggg ttagctcaaa atatgtt

47

<210> 182  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28485-198 : polymorphic base G or T

<400> 182  
aaacatcaaa gtttaatttct gttktctatc tatcctgccc cttctat

47

<210> 183  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-30858-354 : polymorphic base C or T

<400> 183



ccttcagttt ctccagccat ctttgctgcc acgcccaagc ccaggcc 47

<210> 184  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32002-313 : polymorphic base A or G

<400> 184  
acaccagcac aggggtgggtg agargacatc ctgctgactt tataaag 47

<210> 185  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-15-366 : polymorphic base C or T

<400> 185  
catgttatta cagaatttag taayactgtt tttaaaaagt atgatta 47

<210> 186  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-20-174 : polymorphic base A or G

<400> 186  
tgagcttggtg tcttcaaact aggratacat caattactta attattg 47

<210> 187  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-31-178 : polymorphic base C or T

<400> 187  
cagtcttact ttgcaaattt aagycaaata attaaggatt tgttaaa 47

<210> 188  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-38-395 : polymorphic base A or T

<400> 188  
gatgacttct aaaccatttc acawtgagtc taaattcact gcttaat 47

<210> 189  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-2-192 : polymorphic base G or T

<400> 189  
gatttgcaca gtggcctctt ttaktcatca cttaggttct gttattt 47

<210> 190  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-26921-210 : polymorphic base A or G

<400> 190  
aataagtgcc aaggagattt ggtrggatcc ctgcaatgtc tgctaca 47

<210> 191  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-215-80 : polymorphic base C or T

<400> 191  
ctcgggaagg tgaccgagaa agayatctgg gtacaagaac ctgaatc 47

<210> 192  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-132-368 : polymorphic base C or T

<400> 192  
cagaccagac aacctcttgg ggttycttttc tgcattgagg ttgatt 47

<210> 193  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele

<222> 24  
<223> 18-133-293 : polymorphic base A or C

<400> 193  
gcatctggat agccctcttc tgamgtttcc tttcagaaag agagata 47

<210> 194  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-12-191 : polymorphic base A or C

<400> 194  
agacaatgct ttgactatat gccmttggtg gaaaacattc taaagat 47

<210> 195  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-11-137 : polymorphic base A or G

<400> 195  
actgggggaga agggaggtcc tgcrgggagg agaaaaggga aagtggg 47

<210> 196  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-93-96 : polymorphic base G or T

<400> 196  
tagtggggttg tggcagaaat tgktctctta cagaatatta tottaag 47

<210> 197  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-115-343 : polymorphic base A or C

<400> 197  
gggagggcct ctctcaggcc tggmagggag caggggtcac aaactgt 47

<210> 198  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-42-140 : polymorphic base A or G

<400> 198  
ttgaggagaa ggaggggaag gccrtgctaa acctgctctt ctccccg 47

<210> 199  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-251-176 : polymorphic base C or T

<400> 199  
gtagaagtgg aagacagatt tgcytctctc aggcactagg gcacttg 47

<210> 200  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-269-44 : polymorphic base A or G

<400> 200  
gcttgggcmag atggatggtc aggracttga aaggaacaca tttggga 47

<210> 201  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-218-624 : polymorphic base C or G

<400> 201  
caagtgatct ctttaagtca tttstaatgt gaaaactgcg tgattta 47

<210> 202  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-393-330 : polymorphic base G or C

<400> 202  
aagctagtc ctgtttctca atcstccttc taaagtcact ttaacca 47

<210> 203  
<211> 47  
<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-394-402 : polymorphic base A or C

<400> 203

cttagaagtc cttggtgtcc gagmcttagt cccacaatgg atgtgtg

47

<210> 204

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-217-55 : polymorphic base A or G

<400> 204

cgtagctgga tttcacctcc aggrcagcca gctggacaga caggcag

47

<210> 205

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-284-139 : polymorphic base C or T

<400> 205

gggtggttcc tgtcagtgtg gagygagacc cgaggaaagca tcctggt

47

<210> 206

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-285-305 : polymorphic base A or G

<400> 206

tgctgaaagc cagttgcatt tcaratagtg tctgtgccac cttcaga

47

<210> 207

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-289-239 : polymorphic base C or T

<400> 207

agcctattac aaagacattt tctyctattg ctacctctcc ccattta

47

<210> 208

<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-291-91 : polymorphic base C or T

<400> 208  
atggggggacc tccgcctccc aatygtgctg gctggaactt tctgtg 47

<210> 209  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-186-391 : polymorphic base G or T

<400> 209  
tgggcatgag gtggcaggaa gaakgaaaga gtgaagataa tggagtt 47

<210> 210  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-194-130 : polymorphic base C or T

<400> 210  
tcacatgattt taatcagata atgycttact tctgtagata tagtcta 47

<210> 211  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-198-252 : polymorphic base A or G

<400> 211  
atattgttca tatggcagag gggrgaaaag caatgactta atcaagc 47

<210> 212  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-242-300 : polymorphic base A or G

<400> 212  
acattactgt cttotttatg actrtgaaat aataaaataa aattaaa 47

<210> 213  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 8-15-126 : polymorphic base A or G

<400> 213  
tggcatctct gagccagctg agtrgccacc tgaactacac ctgtggg 47

<210> 214  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 8-19-372 : polymorphic base A or G

<400> 214  
tggaatctgc taattttggc tgcrccttga aggtaggaaa tccaatc 47

<210> 215  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-2409-298 : polymorphic base A or G

<400> 215  
aagtagcgca tggggctgca gccrcagatc tcctgggctc tgggtct 47

<210> 216  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-339-54 : polymorphic base G or C

<400> 216  
catgatggcg acagaaaaga atastccctt gcctaatttt gatgata 47

<210> 217  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 12-254-180 : polymorphic base A or G

<400> 217  
gcatatgaag aggctagcaa aagrtattta acaagcggtc aacattc 47

<210> 218  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 10-214-279 : polymorphic base C or T

<400> 218  
ctaaggactt ctggtttgct cttyaagaaa gctgtgcccc agaacac 47

<210> 219  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 10-217-91 : polymorphic base C or T

<400> 219  
aaaacacatc ataaaattca ttayacaatg tcacttattg ttccatg 47

<210> 220  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28779-168 : polymorphic base C or T

<400> 220  
tctggtctgc tctctgcatg aggyacagca gtaaagctct ttgattc 47

<210> 221  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28788-300 : polymorphic base A or G

<400> 221  
actgagccaa gcacagagat cacrtccact ttcctcaagg gacttgt 47

<210> 222  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24



<223> 99-32052-262 : polymorphic base C or T

<400> 222  
cctatTTTTT ataacgtatt aacyttatta ttttcttatt attttaa 47

<210> 223  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32121-242 : polymorphic base A or G

<400> 223  
ctgattcaag tgtctatcaa agartggctg cagttgacca tgtattc 47

<210> 224  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32059-169 : polymorphic base C or T

<400> 224  
ttgtTTTTTc tttataatat tacyatctat gaatatattt ctaaaca 47

<210> 225  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32061-304 : polymorphic base A or G

<400> 225  
gaccagctct ttggagggag gccrtaatcc etccataacc tgtccta 47

<210> 226  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32065-303 : polymorphic base G or T

<400> 226  
acaattatta accagtacag tctkgttatt ttaaacatta gcatgag 47

<210> 227  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>

<221> allele  
<222> 24  
<223> 99-32123-118 : polymorphic base A or G

<400> 227  
tagtaagaaa atctatcatt ttttttttaa aaatctttca attttaa 47

<210> 228  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32148-315 : polymorphic base G or C

<400> 228  
gtggttctct ggaaaccgag gctsgttgca aaccctaaa aagtact 47

<210> 229  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-2-76 : polymorphic base A or G

<400> 229  
ggaggcatgg aggctgtcat cacrggcctg gcagatgact tccaggt 47

<210> 230  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-28-93 : polymorphic base A or C

<400> 230  
ttcagccatt gatgaggtcc ttgmtgtttc ttacaggagc tggccta 47

<210> 231  
<211> 39  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 20  
<223> 16-3-199 : polymorphic base C or T

<400> 231  
ctggctgttc cctgctgtgy actgccaag gctagacat 39

<210> 232  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
 <221> allele  
 <222> 24  
 <223> 16-50-197 : polymorphic base C or T  
  
 <400> 232  
 ggtgtgtagt gtctgcaggg aagycctgca tgtggggagg gggctgt 47  
  
 <210> 233  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens  
  
 <220>  
 <221> allele  
 <222> 24  
 <223> 16-1-59 : polymorphic base C or T  
  
 <400> 233  
 ccgcaactca gatatttttt tccytggggg ctggatttgg agtattg 47  
  
 <210> 234  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens  
  
 <220>  
 <221> allele  
 <222> 24  
 <223> 16-2-187 : polymorphic base A or G  
  
 <400> 234  
 ttctgcataa ccaaggtgag tagrggctgg gctctgggtc acctggg 47  
  
 <210> 235  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens  
  
 <220>  
 <221> allele  
 <222> 24  
 <223> 99-28761-311 : polymorphic base A or G  
  
 <400> 235  
 tgaaatgctt taagagaatt tgtrtgctaa atttagaagt tttgatt 47  
  
 <210> 236  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens  
  
 <220>  
 <221> allele  
 <222> 24  
 <223> 99-28771-86 : polymorphic base C or T  
  
 <400> 236  
 caggaaagat agagataatc atayagtacc cagaaaatga ctgcttc 47  
  
 <210> 237  
 <211> 47

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-28791-291 : polymorphic base A or G

<400> 237  
aaatgtcatc aactcccaca tgtragaac accatgattt gtactgt 47

<210> 238  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32077-66 : polymorphic base A or G

<400> 238  
ttttagggg gaaaacaatt tgcrtttggg aaataatcca acaagca 47

<210> 239  
<211> 46  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32078-466 : polymorphic base C or T

<400> 239  
tgatgcttgg agcaagcagg ccayctctgt ctgagagagg atacag 46

<210> 240  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32376-426 : polymorphic base A or G

<400> 240  
tttattggtt cactcacatc tgggtgtag agccaaattc caaagac 47

<210> 241  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-32361-419 : polymorphic base G or T

<400> 241  
ctcttttata aacttcata aaakctggtg agtctcttaa gaactgg 47

<210> 242  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 16-21-228 : polymorphic base A or G  
  
<400> 242  
agtgtgtca gaatcaccta ttcr aaaggc gaatccgatc atgtggt 47  
  
<210> 243  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 16-22-156 : polymorphic base C or T  
  
<400> 243  
tgtgaagaaa agagccttgg gtttgactag ggaacctggg gccactc 47  
  
<210> 244  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 16-23-404 : polymorphic base A or G  
  
<400> 244  
tctgttatct gctgtgcgtt tgtrtatatc taagatgacc aggcagc 47  
  
<210> 245  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 16-24-175 : polymorphic base A or C  
  
<400> 245  
tgggcagggt ctggggtagg acgmgcagag cagctgcggg gactggt 47  
  
<210> 246  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 16-25-286 : polymorphic base C or T  
  
<400> 246

actctccccg acccggtccca ccayggtctc cacagcactc cygacag 47

<210> 247

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-25-279 : polymorphic base C or G

<400> 247

ccagctgact ctccccgacc cgtscaccca ygggtctccac agcactc 47

<210> 248

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-23-393 : polymorphic base G or T

<400> 248

gtttttaata ctctggtatc tgckgtgcgt ttgtgtatat ctaagat 47

<210> 249

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-106-364 : polymorphic base C or T

<400> 249

gttgcttccc ctgcccccg aatcacacagt gctctgcttc tctgtgt 47

<210> 250

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-16-285 : polymorphic base C or T

<400> 250

agcatcatct gcggcatcac gtcygtggcc ttctccctca gtggccg 47

<210> 251

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 16-17-121 : polymorphic base C or T

<400> 251  
ccctgtgact atggctctgg cacyactagg gtcttggccc tcttctt 47

<210> 252  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-84-185 : polymorphic base C or T

<400> 252  
aactagcgtt ttcttttctt ttcttttctt ttcttttctt ttctttt 47

<210> 253  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-87-74 : polymorphic base A or G

<400> 253  
cacatccacc ctgggctgca ggctgctcg gcaggctccc cacagat 47

<210> 254  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-91-333 : polymorphic base A or G

<400> 254  
gctgaacttg tctgccagtg ggargggggc tcttggagtt agctgtc 47

<210> 255  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-128-142 : polymorphic base C or G

<400> 255  
aagtccctgc agaagcagag gcgsatgctg gagcgctctg tcagcag 47

<210> 256  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele

<222> 24  
<223> 16-133-205 : polymorphic base A or G

<400> 256  
tgctttttca gtctcttagc tcortggagt atgttcagtg ttgctgt 47

<210> 257  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-135-181 : polymorphic base A or T

<400> 257  
ctgcatttga ttctggggcac tgawagcagt acttggctgc agacact 47

<210> 258  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-145-405 : polymorphic base C or T

<400> 258  
tggtgggttc ctctctcgc tggycagga gtgaagctgc agacctt 47

<210> 259  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-177-320 : polymorphic base A or G

<400> 259  
accatgcatt ttctatcct agcrgctgtt gcaaaataga cacgtcc 47

<210> 260  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 16-4-354 : polymorphic base C or T

<400> 260  
ctggatgtgg agcaggccga ggtyaacttc ggctggaacc acctgga 47

<210> 261  
<211> 502  
<212> DNA  
<213> Homo Sapiens



<220>  
 <221> allele  
 <222> 362  
 <223> 18-473-362 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 343..361  
 <223> 18-473-362.mis1

<220>  
 <221> misc\_binding  
 <222> 363..382  
 <223> 18-473-362.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 482..502  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 350..374  
 <223> 18-473-362 potential probe

<400> 261  
 ggcatttttag caagagatga ctaatcagag aggagttact agtggagaaa agtaatttga 60  
 gatgtattttt tgaagtagga atcatagtag accacaaaga gatcctttat ttctttaaag 120  
 ctatcatttta ttgttagtac tgtaacaact tcacttatgt gatcctattg aatgctcaga 180  
 acaactgaac agctagctcc atttaacaga taagaaaatg catgttcaat accaagattc 240  
 aaaccaggc ctagccagct ccagaaacct gagcttttaa catttacgct ttcctacaaa 300  
 acaggggtgac ttaacaaagt atctgtttct aaagacagtt cttagggcta agaaatcaga 360  
 aygtgccttt agaaataata agtattccta gttgtgtgtt aaaggtagga agctgaaacc 420  
 aacagacttt cctgtcccta agctaaacaa tactgaacca gtcaaaataa cttggctact 480  
 tgtcccagga aatacttgct cc 502

<210> 262  
 <211> 457  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 88  
 <223> 99-12361-88 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 68..87  
 <223> 99-12361-88.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 89..107  
 <223> 99-12361-88.mis2, complement

<220>  
 <221> primer\_bind

```

<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 438..457
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 76..100
<223> 99-12361-88 potential probe

<400> 262
caaggaacac aagagtttga ggscacttct ttagcctttg aactgggttat tcatcctcat      60
tcttacctgg cattatcttg aatgcttyat ttcctctgta cctggccttc actcttgagg      120
agtctagctt gtttgtgcag tttcctactg tttaaacaag agattgttta aactctagcc      180
actgatttcc acagctgttg ccagtgtttt tctttctcac tgaagccaaa catggagtgg      240
ctggagtctg gaaacatgcc ttgagaaatc aaagttccca tctgacattg cagcctactt      300
cctagagcta gtgtcactga ggaaggggtc atttactcat tctaattgtca ggattcccac      360
accaataacc acatcatctt tcaacaaata catcccttcc cctactccac ctcgggcaat      420
aactgtgggt ccggaggcta cagggctttg ggtgtgtg                               457

<210> 263
<211> 502
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 335
<223> 99-12368-335 : polymorphic base A or C

<220>
<221> misc_binding
<222> 316..334
<223> 99-12368-335.mis1

<220>
<221> misc_binding
<222> 336..355
<223> 99-12368-335.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 482..502
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 323..347
<223> 99-12368-335 potential probe

<400> 263
gaacagaagg tattgaacag aaacaaagta ttttcaaact ggtagaaaaa ggattagaaa      60
tcttggctct tcaatttcct catatccttg gccacacata atgaccccaa gagcacttgt      120
tggcaatggg agggagaag gagatcacat cagtcataag gccaccattg ccctgactcc      180
tggcatctgt cctgcttctt actttttatg agcagagtga ggtcaacagg caccatggaa      240

```

```

agagcactgc gttgaagtta cacattccgg gacttcgctt gcttgctagc atcagtctgt 300
agctgtaaaag tggtagacagt aatacctacc actamgggtgt tgtgagaatt aaatgaggca 360
ggatcttgga cttagaaagc tgcccagata tggtaggctac tgtagataag cattctgggt 420
atactcatcg gattccctcc toccacctct tccctggatt gggtcattcc ctccaatgca 480
gcccttctct ttctcatgt at 502

```

<210> 264  
 <211> 461  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 67  
 <223> 99-12370-67 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 48..66  
 <223> 99-12370-67.mis1

<220>  
 <221> misc\_binding  
 <222> 68..87  
 <223> 99-12370-67.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 441..461  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 55..79  
 <223> 99-12370-67 potential probe

```

<400> 264
attacgcaag cactacgcca attaatccaa gacctgtgcc aaatttataaa ggaaaagcag 60
agttcartgc aaattctaga aatagttgtc aaaatcccca tttcttatgt cctagataat 120
acttgatat ttctggatgt ccatagaaaa ataaggatgt cattacatag aacaatagct 180
gtcagcatag agaacaatag cagaacagtg gggaggattt cagatgtgaa cagtgcctgt 240
gagaatgaag caagctacag tgctctccaa ggggacttcg tgagctcaac ttgacattta 300
gtctcacatg actgccttag gctccttggc accagctcaac acagaaggac attggatgtg 360
tttatccaac acttctgtct tgccaacaga gcagcatcag cagacagtcc tcttcagggg 420
aagagtcctc actgtatata gttgagatgt gaggaaatga c 461

```

<210> 265  
 <211> 449  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 314  
 <223> 99-32148-315 : polymorphic base G or C

<220>  
 <221> misc\_binding

```

<222> 295..313
<223> 99-32148-315.mis1

<220>
<221> misc_binding
<222> 315..333
<223> 99-32148-315.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 428..448
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 302..326
<223> 99-32148-315 potential probe

<400> 265
tgagtgcatt tgatgtgggs cagcaaagct tcattcaggt ggaaacagat taagaagacc      60
aaagagtggg gaaatggcta agtaggaatg aaaaaacagc cagctaccgc yggccagtgc      120
cttattctaa aagaggacag ctagcttgcc caaggactct tgcagaagga aacctgggag      180
agtttccttc tcctcttgca gaagtaaaact cttcagggtg aagagtcagg aaggagctcc      240
agggatgagt gaagtcaact gaagttgcct cttttataaa cagctctgca gtgggttctct      300
ggaaaccgag gctsgttgca aaccctaaa aagtactgct ctgcaaggct tgtaactgcc      360
atacttgtgt ggtcctgctc catctccatg tgtggcagtg ccagctgcaa ccagcctcac      420
acagggtccg agagtctcag aactgcaag                                     449

<210> 266
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 322
<223> 19-46-322 : polymorphic base C or T

<220>
<221> misc_binding
<222> 302..321
<223> 19-46-322.mis1, potential

<220>
<221> misc_binding
<222> 323..341
<223> 19-46-322.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 409..426
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 310..334
<223> 19-46-322 potential probe

<400> 266
gatgagtgac tcaatggacc agctccacaa acaaagctgg aggtgtcttg tacagacccc      60
aaatgctatc catgtggggc tgcaggatca aatagcaggt ggccctcatc tgggggtgca      120
gccaggctgc cagaaggggtg tccctgggcc aagctgaggc ctcctcccct tctcttcctt      180
tcagagactg gcctatggca tcacgccaga gaacgagcac cacctggtgg ctcagaggga      240
catcagacag ttccaggtgg gtgaagccta gaccctggg gtggagatta caagggcggg      300
ccctggctgt tccctgctgt gyactgcccc aggctagaca tcacatccag aaaaccacaga      360
aaccagtggt gagctgcctt ttccccttgg aaacatcggg atgggggaca gggagcctca      420
ccttga                                           426

<210> 267
<211> 422
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 315
<223> 19-47-315 : polymorphic base C or T

<220>
<221> misc_binding
<222> 296..314
<223> 19-47-315.mis1

<220>
<221> misc_binding
<222> 316..334
<223> 19-47-315.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 403..422
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 303..327
<223> 19-47-315 potential probe

<220>
<221> misc_feature
<222> 103
<223> n=a, g, c or t

<400> 267
tcctcgctgt ctttctctgc agttgcaaca ctggctggcc atctgagcct gcctggagga      60
gaaggaggaa ccccatgcc aatgtccagg tcacaggcat ycncctgcgt cccacctcgg      120
acaccatctt gggattcctc ccctggaagt tgtcctttct gatcctctct tcttttcca      180
tttacaaatg atttcgtgac tgtagttttt gttcaccttc tgtgcatctg gcctgggggc      240
tgttagctca gaggagagga gcaaacagga aaatgacttc tgttctgtcc ccgctgtttt      300
gggggaagtc tctcycactt tgggatcctg ctgaagctag gttcatgagg tcggaaatcc      360
ccaccacatt tgcctagact ttgggcacag gagtctcttag tccaccaaatt cagagagagg      420

```

at

422

<210> 268  
 <211> 419  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 346  
 <223> 19-51-347 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 327..345  
 <223> 19-51-347.mis1

<220>  
 <221> misc\_binding  
 <222> 347..366  
 <223> 19-51-347.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 401..419  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 334..358  
 <223> 19-51-347 potential probe

<400> 268  
 atcagggtcaa gcccatgtgg tgcattggcag tggctagggt ccctgagtta ggggagagtg 60  
 gccagggtcct gtctccatca gcatgcattt gcaggggactg gtctgtgggc acggcctctg 120  
 tcgtcctccc tgacgacatt taccctgggc ccctcccctc tcctctgggc aggcgtgggtg 180  
 tcctgcacct tcacgagagc agcgggattc atgacatcgg cctgccccag tggcagctct 240  
 tgcctctgtct gatggtcgtc gtcattcgtct tgtatttttag cctctggaaa ggggtgaaga 300  
 catcaggaaa ggtaatatct ctgtgtttct ctttcactta cttgggtgat caaccttggg 360  
 ggggtgtgatt atttctagca ataattatgt agctggtgga caaaaaagat ggagctgga 419

<210> 269  
 <211> 499  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 263  
 <223> 99-32052-262 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 244..262  
 <223> 99-32052-262.mis1

<220>  
 <221> misc\_binding

<222> 264..282  
 <223> 99-32052-262.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 478..498  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 251..275  
 <223> 99-32052-262 potential probe

<400> 269	
cagagtgcaca aataagtgcgt atggcttgat agaagtgaag ctcttcacat atattcaaaa	60
tacatatcac aaacttttgggt aaataggata gtaatctgaa gaacttttgc cctttttacc	120
ccattttactg taactcttgt ttctaggtaa tegtctctc tcaacaaact tctcaagcgt	180
ctgtgtaaca agccacatgt tctaacaaat tgtctccatc gcacttcaac agccagggtcc	240
ctatttttta taacgtatta acyttattat tttcttatta ttttaaaaga atctatgcac	300
attagcaaaa tttaaaagat agagaaaaat ataaacagaa aaaattatgt ttacttctac	360
caccctaaat caactattat caattttata catattttac tccatctttt ttcaaagtgt	420
cttacatttt ccaatgtcat taaaattctc tgtgaatgta aatttttaaaa actgtaccta	480
ctgttttttg gaatctgta	499

<210> 270  
 <211> 3001  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 1501  
 <223> 10-213-292 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 1482..1500  
 <223> 10-213-292.mis1

<220>  
 <221> misc\_binding  
 <222> 1502..1521  
 <223> 10-213-292.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1211..1229  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 1588..1606  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 1489..1513  
 <223> 10-213-292 potential probe

```

<400> 270
gcagaagtat aagatctttg taaaacagtc ctctccctgg ttcattctgct ttctgttacc      60
acaataatgc taagtaaaaa aacatccaaa aacctccctg gcatttaaca atatgcatat      120
tgctcacacg tcttgatagt gagctctgct gatattggca ggacttgctc tgggtctggct      180
gtgatctgat ggagcctggc cctgggtgcg ctgtgcaggt tgactcagct ctgccccaca      240
tgtgtctcat gtttcagtca ggtaaccact ggtgaagaag caagctagga accagggtat      300
ctgacttctg agctaaactc ttaaaactcta taatattgcc tttcaaatat aacactaagt      360
actaggtgcc tatcaaccac actgttttca gacctctgcc aaaacttgga ttctttgtgc      420
tatgaagaga catggctttt gggctggtct ttgtgtggca gtgaggtgag cacaaagggg      480
tgttcttcag agattacagt ccagccctga agcaacaact aggagactgt ttcagcaagt      540
gaggacaggg ctgtgtgggg ttctatcctt ttcataactt tgcctggcac tgaatcaca      600
tgctctgata acatccacca gaactttctt ttgtcatatt tgggtagaa agggactagt      660
ttttcctcaa attattgata gagattttat ataatatagt gtttctctcc acattttatg      720
tatataacaa aagccctgct tttgtgtata tatgcatata tatatatata cacacacaca      780
cacacacata tatataatac aaatcctgct ttgtaactgt tttgtttgt atataataca      840
aaaagagtta tgaaccagaa gtttggccaa taatccttgt cgcacagaga atttgctttt      900
tctatctggt ttcactttct tggttacaga cgtgtaacct cttttttgaa tggtagacaat      960
cactttgtca tattttattt gatgctagtg ctcatagcct attagtcatg tttgcttcca     1020
tgagaaagaa aaaccactac atgggtatgc taaggatttc agtcattggg gtttagagcct     1080
tccgaatgt ctctgctttt cataactcct ccacacatct tagtgggcca ttgagcacat     1140
caaagggcat gacagttatt aaaatacttt atgaatgcta caatcctttg ccagtatgag     1200
ttgttctctg gaacttctaa cagttcaaca gtactacatg gactgagtta aaagttaatt     1260
caaaaatctc aatttatcca aatctgtttc tttcttttca ggcaccaccc acctatgata     1320
ctgtgctaca gttggagtat cttgacatgg tggatgaatga aacactcaga ttattccag     1380
ttgctatgag acttgagagg gtctgcaaaa aagatgttga aatcaatggg atgtttattc     1440
ccaaaggggt ggtggtgatg attccaagct atgttcttca tcatgacca aagtagctga     1500
sagagcctga gaagttcctc cctgaaaggt aggaggcccc tgggaagggg gccctccctg     1560
aaccagcctg gttcaagcat attctgcctc tctacaggac agtctgggct tgtacaatca     1620
tttgcttgtc tttttatggt taaaaggttt tttcaaataca tgaattgat cattgtcaca     1680
ctttacaac cacagactag ataaaagaaa actatagcca gtcacagtcc cagcaactta     1740
agatgaaggt cctcaattat gtccttatgg gtcataagtg tccaaaatgt aaggactctt     1800
ttaaaaacac atgatcacia tgctattatt atgtcccaca aatgaatatt ttttccctgaa     1860
tataatcaaa tcttcaggaa tcaaatttga ataaaaaaca tgcgtctaatt cttcaaagaa     1920
tttataggtt agtgcaacag atagacaaaag aaagcagtga tgacactgct ttccatcaat     1980
acagttagcat catatgcctg tgtaaatatt ctgacttaaa ctattctatg gaggtgtggg     2040
ggagaaagaa ggagagatgg agattagaag aaggaggaga aggaggagag aaggaggggt     2100
aagacaaggt agggaggaga aggaggagaa ttagaaaaaac aagagacgag aggagaagga     2160
aagtgcaaaa taacaatttt gaagtagtgc aagacaattt cttctccttc ctcatgacca     2220
acataaggggt gacttgagggc aggaatctac ttttctgtca gtcattctca tcaattatgt     2280
gccttttgta gtgtgaacac atcaccatcc tgactataat ttgagtgttt agaaataaat     2340
atactttgca acagtattta tctcctctca acaagactga aagctcctat aatgtaagga     2400
gagtagaaaag gatctgtacc ttacaattct catagcaaaa tatgcatagc aggatttcag     2460
tgactagccc acaaaagtat cctgtgtact gctagttagg ggggtgggcc taagtaagaa     2520
accctaacat gtaactctta gaggtattat gtcttttaact tttaaaatat ctaccaatat     2580
ggaaccaggt tcagtaaaaa gaacaaggac aacatagatc cttacatata cacacccttt     2640
ggaagtggac ccagaaactg cattggcatg aggtttgctc tcgtgaacat gaaacttgct     2700
ctagtcagag tcttcagaa cttctccttc aaaccttgta aagaaacaca ggtcagtcac     2760
ttttctgcat taataatggt ttattaacaa ttattttaac tgaatggtct atatatttaa     2820
aaaagaatac actcacttaa tcttttaata atttgttcta tgggccaagg aatctatttg     2880
gacctatcta tgatctttta ggggtgcttca gttctggagt tcaaaagctg tagcattaaa     2940
aacatcatgc aatgtcaatg tagactagca tgacatgatt atctacagtc tccttgaact     3000
t                                                                                   3001

```

<210> 271

<211> 465

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 135

<223> 18-419-135 : polymorphic base C or T



<220>  
 <221> misc\_binding  
 <222> 115..134  
 <223> 18-419-135.mis1, potential  
  
 <220>  
 <221> misc\_binding  
 <222> 136..154  
 <223> 18-419-135.mis2, complement  
  
 <220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer  
  
 <220>  
 <221> primer\_bind  
 <222> 448..465  
 <223> downstream amplification primer, complement  
  
 <220>  
 <221> misc\_binding  
 <222> 123..147  
 <223> 18-419-135 potential probe

<400> 271	
ttccaaccct gttaagactc ttctacagtt gctttttgtg tagctgacca acataacaat	60
catgttcttt attctacatt ccttgataca tttcaaccct tccatactga tcacttcctt	120
tctgttgagg caaaytcagt tttttttgtg aaaatgtttt ctattttacc cttgttcttg	180
aaagggtggc ccaatctcag taagataact tactgaccta ttctaaggct gggcccaaca	240
gagcctcact ccccaaccct gtagggaccc tggatctggg tagaacattt atgcggtagg	300
ggaacagtc ttcttaaaca ggcgcttgga agccctttgc agatgccggt gagaatcggc	360
ggtctgggaa agagtacaca tcttgacagag aagctgaaga gggaagccct tttcctgttt	420
tttcactttc aagaacatga gccacctggc tgctttcttt tgtag	465

<210> 272  
 <211> 527  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 419  
 <223> 18-424-419 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 400..418  
 <223> 18-424-419.mis1

<220>  
 <221> misc\_binding  
 <222> 420..439  
 <223> 18-424-419.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind

<222> 507..527  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 407..431  
 <223> 18-424-419 potential probe

<220>  
 <221> misc\_feature  
 <222> 478  
 <223> n=a, g, c or t

<400> 272  
 cgctttaatt tttagggttc caaaccaaaa gtggcaatca ccatggcata tgtgtacctg 60  
 tgagcatgta gattcatgtg tgctgggggc attttatagc cagttctttc tcagagtccc 120  
 tttttctttt agccaatgga ttctggctag gaaaaacatt aaccgcacct tagtagacta 180  
 gttagaagac tgagaagaac caggtaggga agccagagaa gtgacattca gagatatttg 240  
 gaaacaaact tgagcataca ttttacccaa caggaattag ccaggcattt tatttttaaa 300  
 aaaagaaaga aaaagaaatt ttagcaactc ttgtgtgttg cccctctctg tgtttagaat 360  
 cgtgattttc cagctatgtt cctcacagcc gtaggatttc caagggtaaa aggtagagsa 420  
 ggggggtgtg aggttttgat atgagcatat gggacttcca tagctcctat ttgaaaanwt 480  
 gctgttttag aagagcctgt taagctgagt tttgaacttg acagcat 527

<210> 273  
 <211> 451  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 290  
 <223> 18-429-289 : polymorphic base A or C

<220>  
 <221> misc\_binding  
 <222> 271..289  
 <223> 18-429-289.mis1

<220>  
 <221> misc\_binding  
 <222> 291..309  
 <223> 18-429-289.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 434..451  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 278..302  
 <223> 18-429-289 potential probe

<220>  
 <221> misc\_feature  
 <222> 110  
 <223> n=a, g, c or t

```

<400> 273
gtccagcttc tttagttcca tgctgccaga cagaccgtca gagcagaaca gataccttca      60
ttttgtcata acttttttaa aaatggcaaa aaataatagc cacatacagn tttgttagtg      120
aggtgaaatt cctcatagaa caaagacaac aaagaatata aaatgtttct aatatgttaa      180
aatatatttt atattctttg tattcttttag tctgaaaggc ttaaattctta catttctggt      240
gggatttcag aaaaaaaagt tttcttaggt aaagcgtctt tttcccttm aactagccca      300
tttgaaactc ttctgtttct gaatgaattt cacctaacct gtctacagct atattcacag      360
acactgtttt tccctttaca gactgaccct accctttctg ttacaaaata cagaaacggt      420
gccagtgttt tttggttggt tggttggttt g              451

```

```

<210> 274
<211> 487
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 256
<223> 18-246-256 : polymorphic base C or T

```

```

<220>
<221> misc_binding
<222> 237..255
<223> 18-246-256.mis1

```

```

<220>
<221> misc_binding
<222> 257..276
<223> 18-246-256.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 466..486
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 244..268
<223> 18-246-256 potential probe

```

```

<400> 274
tcataggaag acgagagcaa atatttaatg tgttttgcct tcagttacat aggaaaaatg      60
tctaagaagg tgacattggg acttgtgttt aatgaaacag agaactgtgg gcagcgtcag      120
tgttgggttt ttaggagcgt agggagcaca cagctttgac tctttgtccc attacttgct      180
tctgtgtgaa gccactgagg cccaggggtt cgggttttcc tgccacgcac tctggggtgg      240
cagtgaccgt tccaayatgg atgagtgaga agcagggttct tatgagggtt gtgcaaattg      300
agcaagccac ttggggcatg ggtttttctt cttttctttc tttctttctt tttccacta      360
aagaacagat tgaaagtgct tcacaattaa tcaaaagtcc cctcaacact ctggtgatcc      420
atctaagacc tctcagagat ataaccacca gcacagatat tcaaaccat ttttttcaat      480
ctccttg              487

```

```

<210> 275
<211> 453
<212> DNA
<213> Homo Sapiens

```

```

<220>

```

<221> allele  
 <222> 68  
 <223> 18-355-67 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 48..67  
 <223> 18-355-67.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 69..87  
 <223> 18-355-67.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 436..453  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 56..80  
 <223> 18-355-67 potential probe

<220>  
 <221> misc\_feature  
 <222> 32,51  
 <223> n=a, g, c or t

<400> 275  
 tgccctgttt ctggttctgg tgctgggagg tnaggagtgg agaagactag ntcccctaga 60  
 gctgaggyct gtcttgaagg actcactggg gccctcatcc tcagggggct gattggcagc 120  
 caccctcag tgtggtggac atggagaaaag gaaaggctgg ggaaggtaag gatgctagag 180  
 gcccgagtct ccttggagg ccccaaagga ggaatgtcag ggagcttact ttctttgttg 240  
 cctcagctcc acaccctac caagttggca aatccactta ctcagggaca ctaacaccag 300  
 taagccaacc ctgatgatgt tctatgttgt acctctggac ctctaagcca ggccactgtg 360  
 gggagaccaa ggtcctaccc cagatcctgt cccctgggtg cttatgtgac ttaaggtaga 420  
 cataaggtag tgtgccagtt tagtgcatt acg 453

<210> 276  
 <211> 471  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 266  
 <223> 18-353-267 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 246..265  
 <223> 18-353-267.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 267..285  
 <223> 18-353-267.mis2, complement

```

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 452..471
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 254..278
<223> 18-353-267 potential probe

<400> 276
agttgcctac gtggctgggg aagcggggcg cgggtgtac tcacctcagc tcagggtcct      60
agagacctgc gggttttgct ggtegtgag gtctcccca cttcccacc tacttaagc      120
catcacttcc acctggtctc ccaaattgag gtcctgaagt cctgagacct atgtcccacc      180
caactccgac gtcttttagat cccctttccc tcggtgccag ccttctgaga gtcccaacgt      240
tctggcctct aggggatctg cagttygggc ggtgggcggt tctgattggc cagtcttcca      300
tgaggctctg gggcacccag agtgtgtgtc tggggtaggg tggggagggt ggccaggggg      360
cagaggtctg cccccgtcc cagggtctg atgcctcct cccttcgcct cctcagttga      420
agaagctgga tctggcagct gcggcassac acaccttctt tgtagcaaac c          471

<210> 277
<211> 468
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 306
<223> 18-338-305 : polymorphic base A or G

<220>
<221> misc_binding
<222> 287..305
<223> 18-338-305.mis1

<220>
<221> misc_binding
<222> 307..326
<223> 18-338-305.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 450..468
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 294..318
<223> 18-338-305 potential probe

<220>
<221> misc_feature

```

&lt;222&gt; 84

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 277

ttgtaggtcc	ccaagatggt	gggggtgcag	ggacagagag	cttgetgttc	tgctcctgat	60
gtcacacagg	ggcttcctgb	gcgnctggc	atcaagatgg	ccttccacaa	gtcaagtggc	120
cacatcctca	aggagctggc	tcagccactc	acagctcctc	ccgaaccgga	gggtcccttc	180
cagtcttgtc	ttggaccctc	tggtgcctgc	ggctaggggg	ctctggggaa	gggtctttgc	240
tgggcatttc	ttctctctcc	tcttctctcc	cctcctgtga	ctcctgcagc	agttctttgg	300
cttctrtcca	ctcctggggg	tggggaggag	agtgtggccc	attccctgca	cccaccttcc	360
ctgggtcagc	tcagcccctg	accctcaccg	actgtgagcc	ttctcggggg	ctccttgccc	420
acccttcacg	caccaggaga	accacatccc	ttcctaaccc	gctcctta		468

&lt;210&gt; 278

&lt;211&gt; 3001

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 24-243-346 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1482..1500

&lt;223&gt; 24-243-346.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1502..1521

&lt;223&gt; 24-243-346.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1156..1173

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1652..1672

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1489..1513

&lt;223&gt; 24-243-346 potential probe

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1556,2069,2084

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 278

agaatctctc	tctctttttt	attattattt	tttgagacag	agtttctactc	tcatcgccca	60
ggctggaatg	caatgacaaa	atctcggtc	gccacaacct	ctgcctctcg	ggttcaagcg	120
attcttctgc	ctcagcctcc	tgagtagctg	ggaatacagg	cggccgccac	catgcccagc	180
taagtttttt	tgtattttta	gtagagacag	ggtttcacca	tggtggccag	gctgggtctcg	240
aacccctgac	ctcaggtgat	ctgctgcctc	agcctcccaa	agtgtctggga	ttacaggtct	300
gagccactgc	gcccagccca	gaatctcttt	gagatggaca	cacaccctct	tcattattcc	360
agcttcata	tggcagtggt	gggctcgctc	tgcagaccag	ttagctcagt	ccatgaagta	420
ggagccttcg	tgggctcaaa	ggcaaatccc	agcatgctca	ctgctcagtg	ccagaaagat	480
cacccccaga	agccgggtgc	atcagtgtgg	accaccaaga	accatcaaac	acacgtgttt	540

tctgtgtgct	cgacctccgt	tccttgcttt	ttctgatgac	tgcaccttga	tgtccctttt	600
ggggaacccc	gccactctca	gtcctcatgg	tctgggtggc	actgccccct	cccctgcgct	660
gcacagaagg	cccgaccccc	cacctggcca	atcagagttg	ccagggtcatc	tccctgacta	720
cagcacctgg	ttcagggatg	gacacagccc	agcggagttt	gtgctagaac	tgctgggaaa	780
tgggctttca	ccttctgctc	atcttggcac	gtggatgcca	gcttgaactg	tggaaggcca	840
ccctgtgggc	agagccccctg	agacacaggg	agcacaggaa	agcagagtgg	aatgggggcg	900
ggggagtact	tcctgatgac	atcatctgag	cccctggatc	cagccgtgcc	tgaagcaaac	960
tactctaggc	tctacagatc	tatggactca	tcaatccctt	gccccctctac	ttttttggct	1020
tgtgtcaatt	tatattgaga	ttttgtcact	tacaactaaa	agggctcctga	atctaactca	1080
ttctttgaaa	gtctgcctat	caatcacaaa	atagcagtg	gatcagagct	ggataccatg	1140
ggcagggtctc	cttccctctg	tgaggttcta	tggagaacac	cctacatctt	tttaattatt	1200
tgcatgcac	gggccctatg	gatttgagag	attcatggat	gccacgtgga	atcagtcaat	1260
gacctctact	ttctcaggca	ctacctaggg	catcctccag	gatgcgcccc	ttcccgccac	1320
agcccactgc	catatcttgc	tggaacctgg	gtcatcgctc	atcgctctatc	acagggtccg	1380
ccagccttgc	tggatgccat	ctatgtccgt	gggtctcacc	cgtctcgcca	ccagcttcca	1440
ctacgcagct	ggacagtaca	cagggagcag	acggggattc	caggaggaag	ccactgcaaa	1500
yagggcctgc	agctgccctc	tctccttctg	aaatcctagc	atagtccagg	acacangcac	1560
ctccctggct	gagcagctga	actgccaagc	tcaactccct	gattgagcag	atattctgca	1620
gaaatagaaa	aggatggagg	gaaggcttct	tcccacacaa	tgaacatcaa	acccacccaa	1680
ggggcagtg	ctggggcctc	ccttcccaaa	cagctggctc	aaaacatgca	caaaattttc	1740
ccaaagtggg	ctggggagcag	ggcagctggc	ttccactttc	atattactga	tgcatccaga	1800
catacttcca	tagtgtttaa	aaatttttgg	atgtatgtca	aatgctctta	agagtgcgat	1860
cttaggcctg	tggtaaaataa	atatgatgta	atcctcccgt	ctccaagggg	gctgctgcc	1920
tctccctccc	tccctcactg	gtcctgggca	agcccttgac	ctccacgac	tctctgcgcc	1980
tctcgtgacg	cccacaacaa	ggggctgtgc	caaagggaaa	ggtagaaaga	aaagaggatg	2040
tgctgtgtgc	tgatcatcatc	cctgtgccna	gagacagggc	acanggggtg	tgcccttgca	2100
ccaccggcgc	atccccacac	tggggaagct	ggggtcaccc	tgaccacacg	gcatcccatc	2160
agcctctgtg	acactgacaa	tgattctcgt	gaatggacag	gctgaatgg	cctcagccct	2220
ctctttctat	gctggctgaa	ctctgaggcg	ggaacaggac	agacagtggc	tgagggccct	2280
ggcaggggagg	gcacccttct	aacaggccct	gcgtagccga	gggcacccaa	ctgacaggca	2340
ggacccctga	gctcaccacg	gcctgccctg	ggccaggcaa	gaacgagcac	gtccacccat	2400
gagagttggg	gctgtgtagg	tgactgtaga	catcacccac	agtgggagg	ttcctggagg	2460
tgacgtccga	ggcttggagc	gcaaagtagg	acaggcacac	tgccaagttc	ccagaagact	2520
gagtgccacc	agatcctgtg	gccagtcctc	agtgtggtgt	ggggggctca	gcaggagcac	2580
atcagcaatc	agatgggcca	ggtcaggata	aagaacaggc	gtgacagctg	cttcctaaat	2640
aatcaacggg	gggtgccctg	agtagcacct	cctgctgtgc	ctgtccccag	ggcagcagg	2700
gctcagcgca	ctcccacatc	tgcatcagag	ccccagtcct	tcctggggcc	ccttgtacct	2760
tctaagacta	agctcggacc	ccgcccggaa	ccacccccag	gaccctacct	caggctgtgc	2820
caccaccgtc	cacctggcag	ccccagccag	aaacctggag	gccacccctg	ctttctcccc	2880
tccatgtcta	cctgtccctc	agccttcttg	tggcctggct	actcctctct	ctgctccgcc	2940
tcctgggctg	cctttaatgt	aaacaatcca	tctaacagct	gagccccact	cacgacaatg	3000
c						3001

&lt;210&gt; 279

&lt;211&gt; 3001

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 99-62531-351 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1482..1500

&lt;223&gt; 99-62531-351.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1502..1521

&lt;223&gt; 99-62531-351.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1149..1166  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 1591..1608  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 1489..1513  
 <223> 99-62531-351 potential probe

<220>  
 <221> misc\_feature  
 <222> 755,890,893,1406,1412,2220,2222,2224,2232,2241  
 <223> n=a, g, c or t

<400> 279  
 tgtggtttcc ctttccaggg agtgatgget ctgtaggctc tgggattgct ttttcatttg 60  
 tttgttgttt tgggacagag ttttactctg tcacccaggc tagactgcag tggtaaataca 120  
 cagctcactg cagtctctgc ctccccaggc tcagggtgatc ctccctgcctc cccagggtca 180  
 ggtgatcctc ctgcctcaac ctccctgaata gctgggacta cggtcatttt taattttttt 240  
 ttgtagaggt ggagtctcgc tatgttgtec aggctgggtc tgaactccta ggctgaagca 300  
 atcctcccac cggggcctcc caaagtcctg ggattatggg cgtgagcccc cacacctggg 360  
 cttatttctc gagaaggggc ttgtgtcct cctcacctga tgcctctcct tctcccacca 420  
 gcgtcatcat gaccggggcc tacaacaact tcttcgcgat gttcgatcgg aacaccaagc 480  
 gggacgtgac cctggaggcc tcgagggaaa gcagcaagcc cggggctgtg ctcaagccac 540  
 ggcgcgtgtg cgtggggggc aagcgccggc gtgatgacat cagtgtggac agcttggact 600  
 tcaccaagaa gatcctgcac acggcctggc acccggtga gaacatcatt gccatcgccg 660  
 ccaccaacaa cctgtacatc ttccaggaca aggtaaactc tgacatgcac taggtatgtg 720  
 cagttcccgg cccctgccac ccagcctcat gcaangtcac ccccgacatg accttcacga 780  
 ccgcaatgca aggaggggaa gaaagtcaca gcaactgatga ggacagctgc agaggtggca 840  
 gtgtgtggag acaggaagtt tgggccccct ccttgcccc gctttcctan ggnccagaat 900  
 tgtgtttggc agtaattgtc tgtttaaaaa aataaaaagg aaaggaagcg ttcaccgcca 960  
 caaatcataa aatggacatg actgtggagt cttacagttc agggttcttt cattcacgtc 1020  
 ccttcctgtc tcgggtctgc gtctttacca catcaatagg actttttatg cgtccgggtt 1080  
 aatttttcac tccagtgcgt cctgttgacg ggaccggagc tgatgggagc tgcttctccc 1140  
 ccatgcctca ctggtcccag atcagggctc cagggacaga tgatgagtct caaacgagcc 1200  
 agccaggggt tcttttggtt ataaatggg caattcgccc tgtctcagag ctgatgacct 1260  
 caccgttgtt ttttgatgg tgaattcatg ctgagaattt gcagatgcaa gctcctctcc 1320  
 taggtcttct gaatgtcttg aaacatccca ggtcccaggc ctggtgcggt ttccccgagag 1380  
 gagcggagct gggtttgtct tctgtngtgc cntgtgtcct catctgattc acctgccatt 1440  
 tgctgagcct ctgctgtgta ccaggcgtgg tgcctcagccc tagaggcagt tgacttaacc 1500  
 yctgcagccc tccctgccgc ctccaccttc agcattcact gggcaccttc ccggagcgga 1560  
 cactgactcc catgcacgat tttttggaat cttcctcctg actgtgaggt ggggtgttcat 1620  
 tcatttcctc cataaacacc aacttctcga agcgtgccag gctctgggct ggatgctggg 1680  
 gataagcggg aacccttagg atccctctg tccacgagaa gaagctgagg ctctgagcgg 1740  
 atgcacaggt caccatggc aggtgccgtg cagtgtgtg aggaaccctg ccgggtcttc 1800  
 acacaaggtt ctctccagtc catctcgtgg gcggtcatg ttagagcgac attcaaatgg 1860  
 aagggttgga aaggaatgcc tctgtcttgt gaagtaggac atggcagact tggcgacgac 1920  
 aaggggtccag gagaactgag acgcaggatg aagaccccc agagctcctc 1980  
 gctctgcttg gtggcttcag gagtgtggcc ctccccagga ctccacttca tcttgggctt 2040  
 gcacctcct tgagccaatg cactgaactg cctttgaaag gaaattgcat gttctgacca 2100  
 ttttaggata cctttacttt aaggaccaca cagtcccaga ggacacatcc ctcggaact 2160  
 ctgcccctct gacaatgagg gccacagaga aggtgtgtt tccatggtag atgtcctgn 2220  
 tntnggtgat anccaaacct ngcccacccc tctgagtcgt ctttgtcat ggacttgcag 2280  
 cagagccacg tagtttggca ttttgattca gaaagtgggg agcagagacc cagccaaatc 2340  
 caaacttttt ttttggtttt gttttgtttt gttttttaca agatataaca taaccagga 2400  
 aacagaccca gctgaggtta ttctcagtgg attacagtat acttttgtgt gtgtaaaagc 2460  
 acaaagtgca tgtgtactca cttctggcca tataacattt acacagggaa atggatcatt 2520



```

gatttttttt taatcaacgt gaatgaagaa tgtttgttta tatatcacta taaaatccag 2580
ttgacctgga cagtattata tgtacatatc tattctaatt aaatttaaca atcaaaggat 2640
tggattactt ttttccccct tgtaaagagg ttcgagaatg tggtaattg tatagatagc 2700
gtgttaaagc caaaacccag ctctgagggc cttaccatt acttgatat ttgctacgat 2760
ccatctccct ttgtgagtca aatgttaaga gaagaaactt gtatttgcag ctagagggtta 2820
ctgtcacatc atagatttaa catttaccat cttcaaagta caaatcttac atgtccttca 2880
aaaggaggtc ttaatacagt tcctagtcc ttacttctgt tttaaacttt ggggtacaaa 2940
ccaaaaagaa gaaaaaagaa aggaaaagat cttctttgaa gaaaagtatg tctctggatc 3000
c 3001

```

<210> 280

<211> 3001

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1501

<223> 99-54279-152 : polymorphic base C or G

<220>

<221> misc\_binding

<222> 1502..1521

<223> 99-54279-152.mis1, potential complement

<220>

<221> misc\_binding

<222> 1482..1500

<223> 99-54279-152.mis2

<220>

<221> primer\_bind

<222> 1635..1652

<223> upstream amplification primer, complement

<220>

<221> primer\_bind

<222> 1170..1187

<223> downstream amplification primer

<220>

<221> misc\_binding

<222> 1489..1513

<223> 99-54279-152 potential probe

<220>

<221> misc\_feature

<222> 44,377,423,696,723,1501

<223> n=a, g, c or t

<400> 280

```

ctaaagtgc agagttcaga ctttgagagt ctgaatgagg caanggtaag gattttcata 60
gctctgagag agggttctcc tgagagggga cagacatggc gtttgcacgg actcacacgc 120
tgtggtatga gacacatgat cacactcact catttctctc ataaatcttc acttccttag 180
aacctaccct ccggttagac actagctgtg tcttcttcag cctgacggtc ctctccggaa 240
gggtgcgcgtc tgtctctcag cccaattcaa agaggtggga gaggcggcca cagcctctgt 300
cggcctgctg ggcacctggg gctatagaag agggaccgag gctcagcgag attaatgtgac 360
cacatccac agctacntat ggctgctgca ggatttgaat ttaggacgat ctgctgggc 420
cctactccc agcgagacaa attaacacaa agccccaggg agacaaatta acccaaacc 480
ctggaagaat tttaaaagca gaagctcaag cccccaccc caacacagat tttgattccg 540
ttgggtctggg tgaggctacc cagaaggccc tgctgggtgg cttggggggc tgtgcagaag 600
gccaggtgca ctgctccatg atggcaaac cagcccagct ccctgctctc ttgcaagggc 660
tcagcatctg gtaccagagc aggagatgct cacaangtga gaatttctgt aggggtctac 720

```

aanagcaggt	gctttcaaaa	acagtgtctca	aagaaagtgg	gaattgagag	gcaaacgagg	780
gtgtttctac	ctggggtgca	ggaaggagca	ggcacgtggc	atttgagctt	agctttcgtg	840
aacatatagg	cgttctccga	acacagcttg	cagggagggg	ctcaggtaga	tggaaatggca	900
tctgcagggg	ttcaggttta	cggaaacggg	tcacctccca	tggctctccc	acttcctccc	960
ctgtctgccc	tccaggctca	cggagcagc	cagtgatgtc	tgggctcatc	agtccttgga	1020
caaagccctc	caggagctct	gtcttctcaa	tgtaaaagcc	aaagtccttc	caatgcccc	1080
aaggccttgc	gtggcctggc	ggtgtcaccc	gtgggcccc	tctccacct	ccactgtttt	1140
tttgctcact	ggcctcaagc	tggccttgct	ggtcctggaa	catgctgagc	ctactcctgc	1200
ctcaggtcct	tacacttgct	gttcctctg	cctggatgct	acacagccac	gccagagtt	1260
catgatccca	acacatgtgc	caccttctca	gacaccctcc	ctggccaccc	taggggacac	1320
tgcagccctc	ccatcccgtc	ccccttctt	cctccctgct	gggtgccata	agcttagctg	1380
ttgatttctt	cgctgcctc	ccattagaac	atgagtccaa	agagggaggg	ctccgtttgc	1440
tcaccattgc	ccccgagtg	ctagagcact	gcctggcacc	cggcaggggc	tctataaata	1500
nagatggaaa	gagggaggtg	ggcgggcatg	cgtgggctta	ggtgggcccc	gcaagagatg	1560
cccttgggca	ggacagcttg	gtgtgcatgg	ccaaggaggg	tgggtcccaa	gccaaaggca	1620
ttgaacacca	ggctgaggag	tgaggatgcc	acctgctgta	tcacccaggc	aatagggagc	1680
ctctaaaggc	tttttctttc	cccaagatg	aagtcttgct	cttgctgccc	aggctggagg	1740
gcagtgggtg	gatctcagct	cactgcaacc	tctgcctcct	gggttcaagc	gattttcctg	1800
cctcccgagt	agctgggatt	acaggtgggc	accaccacgc	ctggctaatt	tttgtatttt	1860
tagtagagat	ggggtttcac	catattggcc	aggctggtct	cgaactcctg	gccttgatgat	1920
ccgcacgcct	cggcctccca	aagtgtctgag	attacaggct	tgagccactg	tgcccggccc	1980
ctagaggctt	taagcagggg	agtggcctgg	tcagagccat	gctctgggat	ggtatggcct	2040
accactgtgg	cccagcaggc	ttgaggggtc	cagttagtgc	ccctggagcc	aagcagagga	2100
ctggacagga	tccagcgtgg	ggagggagcc	ctccctgctc	ttgttacctt	ggcagaaacc	2160
ccgagaacac	taggtccgtg	ggcagccctt	gcaggcctgt	cctgctctgc	tggccaaggc	2220
ttggagctct	gcctggggca	ggaggtgccc	atgagaatgc	cagggagtgc	gagctcccc	2280
agagacccag	gcaacaagca	cccactcgac	tccagggtc	agagccctcg	ctaggatgcc	2340
gtcagcatth	gggctgctgc	cttttgact	ccaatacttg	agttcaagtc	ctggctccac	2400
cactgactcc	gggctacagg	gacctgggct	atagccatgt	cctcctctga	accttggttt	2460
cccctctctg	gaaatggctg	gatttggtgc	ctcagctctg	ccctctctta	cctcgacact	2520
ccctacccat	gcccagagcc	tccttgacac	agacaaatgt	gccatcgctt	ctggaatgct	2580
gggcacctta	acagtccagg	cctgccagac	actccaaatt	ctagggcctc	ccagggcctt	2640
aaatgacagg	aagagaaggc	catcttatct	ctggagacag	aagcttgggg	cttggttcta	2700
tttccttggc	aaattctggg	gcacaaacca	gaaagctgca	acaggaaaag	accatacta	2760
tgcaagccca	ggctttaaaaa	ccgagagggg	ccccgggaat	ctcgcgcgcc	aactgcctgc	2820
actttaagga	tagaggcacg	cgggccaagga	gagaagtgc	ttgcccagg	tcacctggtg	2880
gcagtgagtg	ccgtgcaagc	cccaaaccct	ccagtctctg	gttcccacat	ccctgcaggc	2940
tggctcaact	gtagggcctc	cgctgtggaa	atcagtcctc	cgacctcaga	tctggaggcc	3000
c						3001

<210> 281

<211> 461

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 245

<223> 18-168-245 : polymorphic base A or T

<220>

<221> misc\_binding

<222> 225..244

<223> 18-168-245.mis1, potential

<220>

<221> misc\_binding

<222> 246..264

<223> 18-168-245.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 440..460

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 233..257

<223> 18-168-245 potential probe

<220>

<221> misc\_feature

<222> 445

<223> n=a, g, c or t

<400> 281

ttccaactaa cctctatcag tgcattttgt ttgggcagat tgaagatgga agtggttctgg	60
atttgagatt attaaatgaa ttttgtgtgt atgtgtgatt gtctttgggg aacctaagat	120
tttttagcctg ctctctccag acaagtgagc tgggtacagga gctctgcaat actttagaag	180
atgctgaaat ctgatgtgag cctttcccca aaccggaatg acaagctatt tgcatatagg	240
gaagwttccc agtctgcccc tgttctccac cctgcaaaca tgtcacggag aaccctggac	300
aggttctggc aggccccagc ctctggtage ttgtgtactg aggttgggtca ggataaagga	360
atgtatgcag gaaagtggaa catctgttca ggaagcagga ctcccagagt gaaagggatt	420
gaatgaggca ataggaacag ggttnaaatg tgggagttag t	461

<210> 282

<211> 454

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 291

<223> 18-171-291 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 271..290

<223> 18-171-291.mis1, potential

<220>

<221> misc\_binding

<222> 292..310

<223> 18-171-291.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 433..453

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 279..303

<223> 18-171-291 potential probe

<220>

<221> misc\_feature  
 <222> 24  
 <223> n=a, g, c or t

<400> 282  
 tgtcatcagg gagaccagga ggtnaagagg atgtttcata ccttctactg ggagggtgaa 60  
 catggagact gggaagggtga ccagccaccc agctctgcgg aagtttgact gaggcccgat 120  
 ctttgacatt cagcgagacc tatctcagct cctggaggaa ataccaaggg tgaatggcct 180  
 gagtcatttc agcagttccc cttgatccac ttatacctga agtggctctc cagggagagg 240  
 aagtaaccag aagctgccat tgtctgcctg cagagactgt cacaggaata ytgaagaaag 300  
 catcattcct agaagagggg acaccaggg ctcaaggcat gttgccagaa tcccgaacaa 360  
 aatacctctg aatttctcac aggggtggag gtggaggaac tgcagggtca gggcgtatta 420  
 ctgctgaccc acctgttgaa actctctgct gtgg 454

<210> 283  
 <211> 559  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 346  
 <223> 18-172-346 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 327..345  
 <223> 18-172-346.mis1

<220>  
 <221> misc\_binding  
 <222> 347..366  
 <223> 18-172-346.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..17  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 538..558  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 334..358  
 <223> 18-172-346 potential probe

<400> 283  
 tgaggaaata gaaagggaca caccgtctc tctaggtgct gaggccagtt aggatgtgtg 60  
 cattgtcaca tagtgagggg gcctagctgc ttatgtctgc caggacaaag ccaagatggt 120  
 cttagactgt tgtctcatct gtgctattca gggtcattag cagtcattct caagaccgaa 180  
 gaaaataggt ttaaattggt gaaggatgaa tctgaactaa ctgtaaaaca aataaattat 240  
 ttttgacagc aggagcactg gaatccattc ctgaagatgt tagggatttg cagaagcttg 300  
 gcgctcacctg ggcccttaga aaccatccag tcaagcccca ctgagatag atgtcctctg 360  
 cgtaccccca tacagcctgt gcatggtgcc ctccagggga gatgccagca gttttcatta 420  
 tttttaatct ccatttgatt cgggatgggc actaacgcag ctaatagact gaggaggaga 480  
 agtctttccc caattagcga gaggctgtgg atctcacctc ccaaggtagc caactgtcca 540  
 tttcaagaca gttctgatt 559

<210> 284  
 <211> 468

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 406  
<223> 18-177-406 : polymorphic base C or T

<220>  
<221> misc\_binding  
<222> 387..405  
<223> 18-177-406.mis1

<220>  
<221> misc\_binding  
<222> 407..426  
<223> 18-177-406.mis2, potential complement

<220>  
<221> primer\_bind  
<222> 1..17  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 450..467  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 394..418  
<223> 18-177-406 potential probe

<220>  
<221> misc\_feature  
<222> 416  
<223> n=a, g, c or t

<400> 284	
cactcccctc tatttaccta gcgaaggtct actcactatt cagcttaacc atcacctcct	60
cagggagctc ttccctgac tactccagta ggteccatt atatgccttc actgtacctc	120
tgattctcca tattactaac cccaacatag gtatataatc attagtgaac cactttcatt	180
aatgactgga cccctattt gaataagtat ttacgaggat atggagtgtg tgtgttgga	240
gggggtgtct catttttctt atctgctgcc cagtccttgg tccacagcct tcctggccct	300
caatgcatgg ccaacttgac aagtgaatga ctgagtgat gggagcaaag ggaagataaa	360
tgtccatggt gtgtttcagg gccccggag gtgcaatgaa tagctyaccg aagggnscaa	420
cttcattcat agtctctgga taataacacc taccacatcc taactaca	468

<210> 285  
<211> 456  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 338  
<223> 18-298-338 : polymorphic base A or G

<220>  
<221> misc\_binding  
<222> 319..337  
<223> 18-298-338.mis1

```

<220>
<221> misc_binding
<222> 339..357
<223> 18-298-338.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..456
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 326..350
<223> 18-298-338 potential probe

<400> 285
acattgtcac caagaaccag gatctctgga gaaacagttg ggctgttgca tcgagtaatg      60
tcactggact cggcctaagg tttcctggaa cttccagatt cagagaatsy gatttaggga      120
aackgtggca gatgagtggg agactgggtg caagggtgtga cgcagaatc ctggaggaay      180
agagagtaaa gcttctaggc atctgaaact tttgcttcat ctctgacgct cgcaggactg      240
aagatgggca aattgtaggc rtttctgctg agcagagttg gagccagaga tctacttgtg      300
acttggtggc cttcttccca catctgcctc agactggrgg gggctcagct cctgggggtga      360
tatctagcct gcttgtgagc tctagcaggg ataaggagag ctgagattgg aggggaattgt      420
gttgctcctg gagggagccc caggcatcat taaaca                                456

<210> 286
<211> 456
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 110
<223> 18-298-110 : polymorphic base C or T

<220>
<221> misc_binding
<222> 91..109
<223> 18-298-110.mis1

<220>
<221> misc_binding
<222> 111..130
<223> 18-298-110.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..456
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 98..122

```

<223> 18-298-110 potential probe

<400> 286

acattgtcac	caagaaccag	gatctctgga	gaaacagttg	ggctggtgca	tcgagtaatg	60
tcactggact	cggcctaagg	tttcttgga	cttccagatt	cagagaatsy	gatttaggga	120
aackgtggca	gatgagtggg	agactgggtg	caaggtgtga	ccgcagaatc	ctggaggaay	180
agagagtaaa	gcttctaggc	atctgaaact	tttgcttcat	ctctgacgct	cgcaggactg	240
aagatgggca	aattgtaggc	rtttctgctg	agcagagttg	gagccagaga	tctacttgtg	300
acttggtggc	cttcttccca	catctgcctc	agactggagg	gggctcagct	cctgggggtga	360
tatctagcct	gcttgtagag	tctagcaggg	ataaggagag	ctgagattgg	aggggaattgt	420
gttgctcctg	gaggagagcc	caggcatcat	taaaca			456

<210> 287

<211> 451

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 104

<223> 18-299-105 : polymorphic base A or C

<220>

<221> misc\_binding

<222> 85..103

<223> 18-299-105.mis1

<220>

<221> misc\_binding

<222> 105..124

<223> 18-299-105.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 431..451

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 92..116

<223> 18-299-105 potential probe

<220>

<221> misc\_feature

<222> 437

<223> n=a, g, c or t

<400> 287

ttcttggact	gggggctaac	tgtagcaccc	tctctaccag	caggggtgtg	ccaactcatg	60
gtgcatggat	tcaaattgcaa	taaacagtcc	tggggagatg	tccmgctcct	gtagcccat	120
catgggtgtc	tgatttggtg	agtattctag	gtgcttccaa	caacctcatc	cttctgacct	180
gctggcctct	ctgaaggggg	tgtctgctct	aactggatca	agaatagggg	acttgtttgg	240
aggaacattc	ttggtttgtg	atttggtctg	gagtctctgt	ctgcaagtcc	ttctgcttgt	300
ctttttcact	tgagtgtttg	tgtatgtaca	ggaattgctg	atggaagtcc	aacaggctct	360
cctagtttgt	ctgggtctgtc	acatttgctg	aaccctgaag	gaactgttag	cgggaagcgca	420
acaggcctga	ctcgtgntga	ttttccattg	t			451

<210> 288

<211> 451  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 31  
 <223> 18-884-30 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 12..30  
 <223> 18-884-30.mis1

<220>  
 <221> misc\_binding  
 <222> 32..50  
 <223> 18-884-30.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 431..451  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 19..43  
 <223> 18-884-30 potential probe

<220>  
 <221> misc\_feature  
 <222> 438  
 <223> n=a, g, c or t

<400> 288  
 ttgtagttgct ttccttactc ttcagatagt sataaaggac attaaaccta agcaaacaca 60  
 tttagaactat gttactataa cttttcatga aacacttctt ctgtagtgtc tataattcaa 120  
 tttagtggta aataaacctt gagacactga attctgtttt tttttcttta aaaagttttt 180  
 tttaagtata aattaaaatt attcctcttt atttgtattt ctgccctttg tgaacaaagt 240  
 taattctggt ttgattgtga agaatttgct tcttttgctg gtttcttctt gtaggtattt 300  
 aattgtcgct tggtagatct tgacctggcg ttgggttact gcactctctt acctcaaaaa 360  
 gatgtggttg aaaatctctg gaagctcata gataaagcat ggcagaatta cgacaaaatc 420  
 ttggtatgtc ctaaggangc acaccttcaa t 451

<210> 289  
 <211> 451  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 342  
 <223> 18-299-343 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 323..341  
 <223> 18-299-343.mis1



```

<220>
<221> misc_binding
<222> 343..362
<223> 18-299-343.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 431..451
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 330..354
<223> 18-299-343 potential probe

<220>
<221> misc_feature
<222> 437
<223> n=a, g, c or t

<400> 289
ttcttggact gggggctaac tgtagcaccg tctctaccag caggggtgtg ccaactcatg      60
gtgcatggat tcaaattgcaa taaacagtcc tggggagatg tcccgtcct gtagcccat      120
catgggtgtc tgatttgggtg agtattctag gtgcttccaa caacctcatc cttctgacct      180
gctggcctct ctgaagggggg tgtctgctct aactggatca agaatagggg acttgtttgg      240
aggaacattc ttggtttgtg atttggctctg gagtctctgt ctgcaagtcc ttctgcttgt      300
ctttttcact tgagtgtttg tgtatgtaca ggaattgctg ayggaagtcc aacaggctct      360
cctagtttgt ctggtctgtc acatttgctg aaccctgaag gaactgtag cggaagcgca      420
acaggcctga ctctgntga ttttccattg t                                     451

<210> 290
<211> 476
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 140
<223> 99-61513-139 : polymorphic base A or G

<220>
<221> misc_binding
<222> 121..139
<223> 99-61513-139.mis1

<220>
<221> misc_binding
<222> 141..160
<223> 99-61513-139.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind

```

```

<222> 458..476
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 128..152
<223> 99-61513-139 potential probe

<220>
<221> misc_feature
<222> 60
<223> n=a, g, c or t

<400> 290
aagaaggaca ctgggacact cargettctc tctgtctcca cagaaccttg atgcctctcn      60
tacatggcgt ccctgtggcc tctctgtgtg gcccctctat gtggcatcta cacacagcct      120
cttcacatct tctttccacr acatagtctg gactttgtac atggacatac ttagggcttc      180
tgaaggcaca caggcagacc ttctccatcc ctgggcttgg aaaccccaga acatcacctc      240
caccacattc aatcaggcaa aacaaatcac agagccagtc catattccac tgggaggtgc      300
cacctaaggg tgggagtgcc aggaggtaca gcacattggg gctattcaga ctcaccacta      360
cagaatatag atgacactga gtcaggaccc ttggctagca ggaaataagg ggcccctggg      420
cccccaacga aggagatgta gttgtagaag ctgggaagta agggggtaga gaggaa      476

<210> 291
<211> 517
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 179
<223> 99-61514-179 : polymorphic base A or G

<220>
<221> misc_binding
<222> 160..178
<223> 99-61514-179.mis1

<220>
<221> misc_binding
<222> 180..199
<223> 99-61514-179.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 497..517
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 167..191
<223> 99-61514-179 potential probe

<400> 291
atgttcacac agaatcggtc tagaaactgt attccgtgaa aggatgaaag ctcttaactt      60
ctctgtcccc acccccctaa aaaactttac tgtcacataa gagttgacta atgaccttc      120
actaaaaatt acacagtata ctgcctgcca ccaaatacga attcagtaaa tacttggara      180
ataagtgaat aatttcaatt cacagtcaca tgacaagttg tcaaaagcaa ttataaaagc      240

```

aattgtattg gactcagcac atccactgg agaagccagg gcaaggaaac agatccctca	300
gcaccttctt tgaaatacaa agatttgaag aaggtcagag cagattgttt tggtgtgtt	360
cttcttgggc taccaggaag tcacaatgat gacagacgta cagatgtaca tttggacaaa	420
atgtacagat gtacaaagaa atgtaaagat gaaaattgat agatcaatag atcccaatct	480
aaagagcctc attcggcctg aaataaagca ttgattg	517

&lt;210&gt; 292

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 323

&lt;223&gt; 99-61516-323 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 304..322

&lt;223&gt; 99-61516-323.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 324..343

&lt;223&gt; 99-61516-323.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind.

&lt;222&gt; 1..18

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 419..436

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 311..335

&lt;223&gt; 99-61516-323 potential probe

&lt;400&gt; 292

ggagactttc tcttagacac acgcctggag gcgtctgaga gggacaggct gggctcacca	60
attcgaactt ctgccaatgc cctgcatgtc tctctacta agagctaagc caagacttcc	120
cctgtcatca ccaactgctg tggtcagtcc tctattacca acagagggaa acagaatgca	180
attgaggaga accaactaat tgcgaaagca aagcctgaga aaccccatga gtgatggatc	240
caccaattct ggtggccaca gggagggtccc tgggtgtctgg ctgcatgctg gccatggtga	300
ccaggtgtcc ttgggcagga gayggcttca aatgcagacc ggagtcctag cgatccaagt	360
ggttctttga gaaacaaaa caccacaaag ctcccscwgg actgtaccat tgagctctca	420
atcacaaatt cagccg	436

&lt;210&gt; 293

&lt;211&gt; 505

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 70

&lt;223&gt; 18-204-70 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

```

<222> 50..69
<223> 18-204-70.mis1, potential

<220>
<221> misc_binding
<222> 71..89
<223> 18-204-70.mis2, complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 487..504
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 58..82
<223> 18-204-70 potential probe

<400> 293
agaaaagtct gtagcacttc gtaattttat atatgggttaa ggggatctca gagataacta      60
taggatttty aatttggata ataagaagat ggtaatatca ttaaccaaga aaggaaatgt      120
gagaaggaga gggggaacag attgtaacca ttgttatttt actgacacat atcttcacga      180
attcgttgaa acttgatgta atgttataag atagtgatgt ttaagagtat tctcccctgt      240
tccctcgtat ctaccacccc ttctccagga tttgaactca gaggatcaaa aagccttcag      300
tgttgaacat acaagctgca atgaggaaga aaatttcgca aatatgaaaa agaaggccaa      360
aataggcatt catcacaaaa atagtcccc caaagtcact gttccaacta gtggaaatac      420
tatagagtct cctcttcatg aaaacatctc taattcaaca tcatttaaag atgagaaaat      480
catggagact gatagtgaac cagag                                           505

<210> 294
<211> 464
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 442
<223> 18-207-441 : polymorphic base C or T

<220>
<221> misc_binding
<222> 422..441
<223> 18-207-441.mis1, potential

<220>
<221> misc_binding
<222> 443..461
<223> 18-207-441.mis2, complement

<220>
<221> primer_bind
<222> 1..17
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 443..463
<223> downstream amplification primer, complement

```

<220>  
 <221> misc\_binding  
 <222> 430..454  
 <223> 18-207-441 potential probe

<220>  
 <221> misc\_feature  
 <222> 449  
 <223> n=a, g, c or t

<400> 294  
 catccattat agcccagatg aaagttggct gtgacaacac tgtggtgcgc atggtctcca 60  
 gtggaaaaca cgtaaactgt gtgacttttg agtatcgtca gctggagccg tacgagctgg 120  
 aaaacccaaa tggaaacagt atcggggaat tctgtttgtc tggctcttga ataaccaacc 180  
 cagtgattta catgctgata gctaagttag tttttaatgg ccattgtgta tgattttgat 240  
 gcacaactag ttaaaagcct ttcataccag tcagtattcc cagccttgag cgcacgcgcg 300  
 cacacacaca cacacataca cacacgcatt aatttttgta ctttgcttct tttatgtttg 360  
 taatctgtaa atgaacacat ggcagaaaat aaccctgat tggtaggatc atagttctaa 420  
 atggaaatgt ttgtaattct tygatgtgnt acaaacctga aact 464

<210> 295  
 <211> 456  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 65  
 <223> 18-210-65 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 46..64  
 <223> 18-210-65.mis1

<220>  
 <221> misc\_binding  
 <222> 66..85  
 <223> 18-210-65.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 438..455  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 53..77  
 <223> 18-210-65 potential probe

<400> 295  
 ataatatcca thtagctgaa ttcataatgt atacttttta aagacaactt gtttttctct 60  
 ctcarttaca aaagtagact acaaatatct aaccactaa aacagcctta atctatatct 120  
 taagattaga atccaggtaa cctggctttg tattctactg actatgccat tcaataacaat 180  
 gaaaccttct gaaggtctaa gtattagtca tttattcaca tcctactctc taagaataac 240  
 caagtggtcaa cccacaacat tttcaataac atcattaaaa taatgtttac tttctggcag 300  
 atatactaca actcactaac atttttaatg gttttgctct tttatagtta ccagactggg 360

ctatttactt aaataatgat tatttactca ccttcaccc cactatcttc tgcagttaca 420  
 ttgccttcac tggtaatggc ttcgtcataa ctatcc 456

<210> 296  
 <211> 484  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 200  
 <223> 18-212-200 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 181..199  
 <223> 18-212-200.mis1

<220>  
 <221> misc\_binding  
 <222> 201..220  
 <223> 18-212-200.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 463..483  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 188..212  
 <223> 18-212-200 potential probe

<400> 296  
 tttggctagt acaacttctt ggaaattaca cacactttaa gcatttatat tcttggtgaa 60  
 caattagttt taatatactt attgggctga gttaatatga agtacttaca gtttaattcaa 120  
 agatcagctt tgtgggggtga gattcatgtg attattcagc cactactgcct gaggagcata 180  
 ctctgatact tgtggagggg ataccctgat aaagcagcga tttgaagtat tgtgggttgc 240  
 ctactattta tagaacacta gatatgagga ggcagatatg aagccttgac tcttgtggtc 300  
 agcctgactg gacaataaca cagacagcat cactctgttg gtcttgacta cttaattaca 360  
 catatctaga aaagtttatt ttgaacaatt gcaataatg tttacaatac aacaactctt 420  
 tttctctttt tttagactaa aaaatcattt agaaaaataa cacacatata aacatactct 480  
 ctct 484

<210> 297  
 <211> 485  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 334  
 <223> 18-229-334 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 314..333  
 <223> 18-229-334.mis1, potential

```

<220>
<221> misc_binding
<222> 335..353
<223> 18-229-334.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 464..484
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 322..346
<223> 18-229-334 potential probe

<400> 297
aaaccatagc catcatcttc tgccatttat tattagaaaa acattaatgt atactttatg      60
tttattttgt tgggttgctt ttggcttgga tacttatgaa atttttaaaa cttatctttg      120
agactggaaa tttttactgt aattatataat gtgaagtctc tttttgcttg aaacatagtg      180
cgctaagctt ggagtttatc ctgaggtagt tttaggcaag agagttacat ggtgagaact      240
atgtttttaa tataccacct caggcaagta tgagggatgt gtttggaaaa agtacagact      300
agagctgagt agaccagttg gactgttgga ataytgtagg ccagaactga gatattttta      360
agattcagcc tgttcaatat gtagcaggaa gtaataaaca agagaataga tgggagatgg      420
agttgtaag  aagtaactcc aatgtggtct gcggttccca tgtctcactg ctgwtgtgta      480
ctggc                                           485

<210> 298
<211> 457
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 332
<223> 18-230-332 : polymorphic base C or T

<220>
<221> misc_binding
<222> 313..331
<223> 18-230-332.mis1

<220>
<221> misc_binding
<222> 333..352
<223> 18-230-332.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..456
<223> downstream amplification primer, complement

<220>

```

```

<221> misc_binding
<222> 320..344
<223> 18-230-332 potential probe

<400> 298
acaaacacaa tggattctgc cctccacatt gacacctgtt tcatttgcta tactgaggag      60
aatcaacaaa tgcctacatt tgtttgggtt tcatgaaatt cctttgcatt atttttcata      120
aactgaatat tgctttgtca ctacatatac ttgtttcact ttattggcac ttttgtcctt      180
cacatttgct tcaagtgtct cccagaatat aatggaaccc tgggtgtcag gtgcccaccc      240
acatccctgg gaaatagtga agctgagatc agtaacacag acatggaagg aaccttagcc      300
atcatgcagt tcaaaattct tgacataaag ayaaagatgt tgagttccag aaagaaacca      360
tctgcctggg catccatgga ctatctcgct tattcagacg catcatggcc cactaatatc      420
atactaatat catagttaca ttagcatcgc tcctttg      457

<210> 299
<211> 478
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 378
<223> 18-966-378 : polymorphic base A or C

<220>
<221> misc_binding
<222> 358..377
<223> 18-966-378.mis1, potential

<220>
<221> misc_binding
<222> 379..397
<223> 18-966-378.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 458..478
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 366..390
<223> 18-966-378 potential probe

<220>
<221> misc_feature
<222> 55
<223> n=a, g, c or t

<400> 299
gtacaggagg tgttcatcac agtttggcca ctggttccta tgtatgccct ttgnaagca      60
gtatagcatg gtggctttgg catcaaatag acccagcatc aagtactggc tcctttactg      120
ttatgagaaa aacctgagat tgtaatgtcc ccccaactg ggaaggagct gatagtgcaa      180
agaatgactc agacaagtcc agcttgaaga gtggatgagc tcactcactt acagagaatt      240
cctgggcagc agcaagacag ctccagccat cttccccacc tcccatctct aagttgcttt      300
gaagctaatt ttctggctct ttgattactg catatgtgca atgagaatgt tttcctagga      360
atgttccaag ctatgctmca ggatgttgag tttctcaggg acacctgctc ctctgctggg      420
caccatggcc ttggctcacc gcctggcctt cagggttcaa gcagtggaca tacaccct      478

```



<210> 300  
 <211> 463  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 307  
 <223> 18-987-308 : polymorphic base A or C

<220>  
 <221> misc\_binding  
 <222> 288..306  
 <223> 18-987-308.mis1

<220>  
 <221> misc\_binding  
 <222> 308..327  
 <223> 18-987-308.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 443..463  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 295..319  
 <223> 18-987-308 potential probe

<400> 300	
agagacctaa cattcaccca tttgtagcag ttgttttaga acagtgattg ccaaggaggg	60
gaaaaatgag gaagcatagc agaatttctg gggaactgta gaaagagaga gcatattggg	120
aaggtcttgt gatatttgaa aattactctg aaatgtttct gaaactcctt ccactgattc	180
tcatggaaga agtctaacct cttaggatgt gcaagttcaa tggaataaat ttaacacttc	240
atcttgtagc tgaagtgcta tattcagaag caaaatatta aaagctacag gtttttaaaa	300
aattaamtgt taattaaaag caactcaaca ttttaaagat attctacatt ctccctttcc	360
cccgatattt gaaattccca atgatgtctt tcctgagaca tttaaataga cattcaacat	420
tatgagaggt ccttcttttg tggggtttta taagtacgaa gca	463

<210> 301  
 <211> 460  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 118  
 <223> 18-1169-118 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 99..117  
 <223> 18-1169-118.mis1

<220>  
 <221> misc\_binding

<222> 119..138  
 <223> 18-1169-118.mis2, potential complement  
  
 <220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer  
  
 <220>  
 <221> primer\_bind  
 <222> 442..460  
 <223> downstream amplification primer, complement  
  
 <220>  
 <221> misc\_binding  
 <222> 106..130  
 <223> 18-1169-118 potential probe

<400> 301	
gaccaagttc atgttgccaa tttattgaaa catctcactc cttagggcac aaccacaaaa	60
tgccttttgt tccccaataa ctgctttcta actgggccat gttgaacca ctttccastg	120
gggagcagtt cctttaatta caagttggcc agattttgta agttgcagtg atgtttaaaa	180
aagtaatttt aaccctatgc agtttaaaat ttcaatctca acttaactca gagctctcct	240
tcctttccac taataaagac caaacctgcc actggcttta attggtggtg aggggggtgt	300
ctcattacac acttatccct cctccctttt tgagggctag ctcttccagt tcttgggtca	360
gggagaagag caaaaagagg aaatatctct tactcctctg gacagggttg cagtcttctc	420
ccgaatggc agacagtttt cctggttact actgatttgc	460

<210> 302  
 <211> 475  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 138  
 <223> 18-1172-138 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 119..137  
 <223> 18-1172-138.mis1

<220>  
 <221> misc\_binding  
 <222> 139..158  
 <223> 18-1172-138.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 457..475  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 126..150  
 <223> 18-1172-138 potential probe

```

<400> 302
gcaaacaggt aagacatctg atatataaca ggcccccgac cgatgttagt tgccttcatt      60
gccaaacaaat gtggaatgat cccctcctc tgagttccat agagaatgag aataaagagt      120
aggaaggggt ttctcagstt gtaaaacttt caatgctaac atcctggcaa accaggacac      180
attgttcaaa gggctacatt tgataaacta tcccaagtat tcaatatgtg gctgttatct      240
ccttcctaata atcctgaata gcgttttcta ttgttttcagg gagtaggggt gaaaaacagg      300
tattcgtgat gtaaataatt tgttttttca atcacataat tgaagactgt taactggctt      360
tacagcagtg attttcaatg gggagtgcag ttttgcccct cccaagagac ttttagtaat      420
tccggaaga tttttggtta tcataaccag ggagtgggag agggttcttc tgcatt      475

```

<210> 303

<211> 533

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 92

<223> 18-1173-92 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 72..91

<223> 18-1173-92.mis1, potential

<220>

<221> misc\_binding

<222> 93..111

<223> 18-1173-92.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 515..533

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 80..104

<223> 18-1173-92 potential probe

<400> 303

```

ttattgtcag gttgggtctt cttctgaag actcctgtgt attgtgcctt tgcaagttga      60
tttttcagtg aaacttcaga gggccaagat tycccttggt ctccacact gtagtgatta      120
agatagtgag ataacagcag ggggatagat atggggtaga tatatacatc atatcaaagt      180
actcccaaag ttcttattga ttagatatta agtaataagt tcaaaattat tatataactt      240
tatagtagag aagtttggca tacatcaaat taaccaggta ttaaaagttc actgcgccag      300
taatgggaca aatcaacgct atgtgcctcc tcatgtgctg caccgagaag gacacagtat      360
cacttcagca gtgttctggg gccaaaaatg taaaacctca agttgcttat gagtaaacc      420
cagccaaact caaaacaatg gacattctac aaagcaactg gcctgtactt ttcacaggca      480
ttgaggtcat gaaagacaag acagaagagc tgctccagag tgaagaagac cga      533

```

<210> 304

<211> 463

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

```

<222> 387
<223> 18-1174-387 : polymorphic base C or T

<220>
<221> misc_binding
<222> 368..386
<223> 18-1174-387.mis1

<220>
<221> misc_binding
<222> 388..407
<223> 18-1174-387.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 443..463
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 375..399
<223> 18-1174-387 potential probe

<400> 304
gccatttcoct tgccttagat atttgacctt attttttcag acctgtttta tcaccagttt      60
agcttttcagg accctctcta gaggtgggtca tgtgttattg tggaaagtac agattttgga      120
ttcaaacaaa tgcagattca aaccttgggt ataccatcta taagatgttg aaaagtaacc      180
tgaccttgca gtctcagttt cctcaactat aaaatagtggt ctacttggtg ggtaaagggt      240
taatccagca ggtctgcaca gtctaaatcc tgcacattcc aaagaaagggt ttagtcctta      300
ctctactcoct gggagataac ctctaagctt ctagaatata ctgcctgtta agaattgttt      360
tgtttatcta agcccttggg ctacacyaaa tagtttaagc taagaaagtg ggaaatgtgt      420
gattaaatct gagagttgtc ttggtgactt caaaactact tct                          463

<210> 305
<211> 451
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 416
<223> 18-1175-416 : polymorphic base G or C

<220>
<221> misc_binding
<222> 397..415
<223> 18-1175-416.mis1

<220>
<221> misc_binding
<222> 417..436
<223> 18-1175-416.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

```

<220>  
 <221> primer\_bind  
 <222> 434..451  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 404..428  
 <223> 18-1175-416 potential probe

<220>  
 <221> misc\_feature  
 <222> 428  
 <223> n=a, g, c or t

<400> 305  
 gactagaagt tactttccca tgtctctttt ttaaaaacaa ttttcaaaga ccctagaaaa 60  
 tcaaatagtg acttaaggtt tcagaaattt tcaagcctac tagcggagtg atgtggcaga 120  
 atgaacacag acttgagatt gagaaacact tggagctgaa ccttgctcta cctcttgcca 180  
 gctatgtgta cggggcaagg ttctgcatta gggtttcagc ttcttcattt gtaatatgga 240  
 accacctatc tagatggcta ctgtgaggat gaagtgatgc aaacaggtaa gacatctgat 300  
 atataacagg ccccgaccg atgttagttg ccttcattgc caacaaatgt ggaatgatcc 360  
 ccctcctctg agttccatag agaatgagaa taaagagtag gaagggggtt ctcagsttgt 420  
 aaaactbnca atgctaacat cctgcaaacc a 451

<210> 306  
 <211> 450  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 146  
 <223> 18-542-146 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 127..145  
 <223> 18-542-146.mis1

<220>  
 <221> misc\_binding  
 <222> 147..165  
 <223> 18-542-146.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 430..450  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 134..158  
 <223> 18-542-146 potential probe

<400> 306  
 aaactgtgtc ctagagtcag ccaagcaact acaaagccga agaatgactt ttgctaaatc 60  
 actagctact gtattaacac catttcaggt ctattggatt cagggaaata tttttactgt 120

cacaactgct	ttttgttgga	ttgtgraaag	tattacaatt	aatttttaaaa	atgtgtagaa	180
atgcctcagg	ggcaaggata	gaaacagata	tatatttcta	aagaaagctg	gagaaaaatt	240
ctttagaagg	tgagtaattc	caatttggca	tttagcta	aatgttcctt	tctcgttata	300
atctattttt	ttctaacaat	gattaatagt	tttttcttgg	tatttcaaag	cagaattatt	360
gataaactaa	attcattaga	ctaattcatt	agtctttcac	cactcatttg	accacacggc	420
tctacatctc	tccacccaac	tcttacagta				450

&lt;210&gt; 307

&lt;211&gt; 3000

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 8-42-211 : polymorphic base C or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1481..1500

&lt;223&gt; 8-42-211.mis1, potential

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1482..1500

&lt;223&gt; 8-42-211.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1694..1711

&lt;223&gt; upstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1263..1281

&lt;223&gt; downstream amplification primer

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1489..1513

&lt;223&gt; 8-42-211 potential probe

&lt;400&gt; 307

caagtgagcg	agatgagcgc	agcggcgcg	cggggcgctcc	tcttggtcac	gtagtcgatg	60
gggtccgtga	tggcccagta	cctgtccagc	gcgatggcgc	acaggtgcaa	gatggatgag	120
gtgcagcaca	gcacgtcgag	ggcgatgaac	aggtcgcagg	ttacctggcc	cagtgtccac	180
ttgttgagca	cctgatacag	cgcggccatg	ggcagcacca	acaccgacac	catgaggtcg	240
gtgaccgcca	aagagccaat	aagataattg	gccacgttct	gcagggagcg	ctccaaggcg	300
atggcagcca	ccacgcacgc	attgcccagc	accgcgcaga	agatgagcgt	gcccagcagc	360
agagaggtga	tcacttggtg	gctgacggtc	acgtcggaga	taccagtagt	gttgccgccg	420
gtctcaaagg	gagccggtgg	tgatgtggtg	ttgttgccct	gaccagggct	gagcacatcc	480
atgcctgcgc	gcccggcgcg	ggaaggggga	gggaagaaaa	agcagcgcg	agattcgcct	540
cgcccccttc	cctgggggtct	tccgcccttc	tcctgggaag	tttcggagga	aggggaatgca	600
gagacccaag	caggaagtcc	ttactgcttc	ggcgaagggt	atctccgagg	agcagctttc	660
aggcgctccc	tgggctctcg	cagtccagcg	cgttcagaag	ctccagctgg	gaaactggag	720
ttggcctgaa	agcagctcca	ggatctcccg	gcgccggaga	ggtggctgga	acgtctgtct	780
gtcgctgtcc	atcttacttt	gccgctcccg	aactggctgc	cggagctgga	gtctccccac	840
tagcaaacag	tctccaatcc	cagaaatata	tagaacagg	aagccccatc	ctccacgggtc	900
actctgtgac	cctcctctcc	ctatttcctt	ccttcctctc	ctccccctct	ctcctcctct	960
cttctctctc	ttctgctctc	ttctgctctc	ttctccccac	ctgccttccc	tttcagtctc	1020
cctcttctcc	ctcacttccc	tttatttata	cctctgtgag	tcgcttcgaa	agccaggctc	1080
cttccctccc	actetaaccc	tcccctceta	atacttcccc	aaccccgagg	agtgccctctt	1140
tcctctgggt	ccccgccttc	ctctccctct	agctcagcgt	ctttgcattc	gagtctcttt	1200

ttgtcaacag	agactcagaa	ctcacttaca	cacaccagat	ccctgccggt	cagaccaagg	1260
ttgtaacaaa	taaactccgc	ctccaaccca	gcaaaactgg	ggttggaaaa	acttggggga	1320
gggaattcca	actactcctt	gcctcatatt	atctgccaaa	ttcttaaate	gtgtcagcat	1380
cccagagtgg	caataggaga	tgagaaaagg	aagcataggg	agcctgaatg	ggaaggtgaa	1440
cagtctctggg	tcagtctccc	aattattgct	aattgatgga	agaagaccga	gtgtgtcttc	1500
sttttttaaaa	agctacctcc	gttctcgcg	cattgcactc	cagcctgggc	gacagagcga	1560
gactccgtct	ccaaaaacaa	acgaacaacg	acgacaacaa	caacaaaacg	gtacctccgt	1620
tatcatctaa	cagtccagcc	ttactccctc	agggagaata	ttgcctgtga	cttttttttt	1680
aacgttgggg	aaccgggaga	gaacgaaatt	ataaaggacg	tgtcaaagga	caaggagagg	1740
taaacaactg	catctcgaaa	tgaagaacaa	aactcagtgt	gatatatatt	ctaaacacac	1800
acacactttt	ccatcactac	tacacttgta	atttcagtga	cactgccact	tcccatagct	1860
ttgtggctag	taaattcagg	gatggaaata	ttttgcatat	gtgttctaag	tgaagcctgg	1920
catttcacat	ggccttttgc	acttcttacc	agagcctgca	aacctctggg	ggaaacttgg	1980
tggaatcccc	gttcgctagc	cggttagcct	ctcttaatct	cagaaactgg	gttcagcacc	2040
tgggacagtt	ctaagcaatg	aggttttatg	tcgccacctt	ctggcaaatg	tttttagagt	2100
ccatctggaa	acccttatgc	agaaatgaag	caagtattga	ggaaatacaa	caacttttag	2160
aaagaggaag	acagttatta	aaagacaagg	tagtattgag	ttttgtctcc	ttcctatttt	2220
ctttaaaaat	ttattttagt	gccctctttt	gctctgaacc	ttatatatca	ggcctattat	2280
atgttttagc	ttccttcgaa	agcctgaagt	atctgtcatt	cacaagttct	aactgggaat	2340
gccattttta	taaagctagg	ctaacacttt	cacctgtgtt	ggttttgtgc	tgtcataacc	2400
tgaacttttg	aactgacata	aatttacctt	ttgttggaga	aacgaatagt	attgcatttt	2460
ccaaatgatt	taacatttgg	aaatgttaaa	tcaactgaaa	taaagatact	tacaagggtt	2520
tgttctaaagc	tgtttccctt	aacaagaaaa	acaaatttaa	tcacatttga	gcattggtta	2580
agaatgggac	ttctaagcaa	ctacagtaaa	cataccacac	aacatttcac	ttatacatcc	2640
tgattgcatg	cctgaggtga	aaggaatgca	atctcaaaag	cagttgacac	tggataacat	2700
gaacagattc	actacagatt	gcaataatct	taatattgtg	ttcaaactctg	agctctgaat	2760
ttcatagctc	tgaattctcc	aagcccaaac	aaaagagcaa	tcaccaaagc	atcaaaaaga	2820
atccacttgg	gccaatgcat	tacaatacag	gacagtgtgt	ttggataagg	ttttgtttgt	2880
tttttttttt	tatagttcag	tgctggggcac	agttcccact	caatcatttc	agcatgccac	2940
cacaatgagc	ctgccatttg	tgatgattca	tggcattgaa	aagaaagaga	taagtataca	3000

&lt;210&gt; 308

&lt;211&gt; 3001

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 1501

&lt;223&gt; 8-45-389 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1481..1500

&lt;223&gt; 8-45-389.mis1, potential

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1502..1520

&lt;223&gt; 8-45-389.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1114..1133

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1516..1533

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 1489..1513

&lt;223&gt; 8-45-389 potential probe

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 11,126,133,286,315,1042,1228,2645..2646,2799,2964,2986..2987

&lt;223&gt; n=a, g, c or t

&lt;400&gt; 308

catatgcaaa	natatttcca	tccctgaatt	tactagccac	aaagctatgg	gaagtggcag	60
tgctactgaa	attacaagtg	tagtagtgat	ggaaaagtgt	gtgtgtgttt	agaatatata	120
tcacantgag	ttntgttctt	catttcgaga	tgcagttgtt	tacctctcct	tgctccttga	180
cacgtccttt	ataatttcgt	tctctcccg	ttccccaacg	ttaaaaaaa	agtcacaggc	240
aatattctcc	ctgagggagt	aaggctggac	tgtagatga	taacgnaggt	accgttttgt	300
tggtgtgtgc	gtcgtgttgc	gtttgttttt	ggagacggag	tctcgtctctg	tcgcccaggc	360
tggagtgcaa	tggcgcgaga	acggaggtag	ctttttaaaa	acgaagacac	actcggctctt	420
cttccatcaa	ttagcaataa	ttgggagact	gaccaggac	tgttcacctt	cccattcagg	480
ctccctatgc	ttccttttct	catctcctat	tgccactctg	ggatgctgac	acgatttaag	540
aatttggcag	ataatatgac	ccaaggagta	gttggaaatc	cctcccccaa	gtttttccaa	600
ccccagtttt	gctgggttgg	aggcggagtt	tatttggtac	aaccttggtc	tgaccggcag	660
ggacctggtg	tgtgtaagtg	agttctgagt	ctctgttgac	aaaaagagac	tcgaatgcaa	720
agacgctgag	ctagagggag	aggagggcgg	ggaccagag	gaaagaggca	ctcctcgggg	780
ttggggaagt	attagggagg	gagggtaga	gtgggaggga	aggagctcgc	tttcgaagcg	840
actcacagag	ggataaataa	agggaaagta	ggaggaagag	ggagacttaa	aggggaaggca	900
ggtggggaga	agggggacga	aagaggcaga	agagagagaa	gagaggagga	gagaggggga	960
gagaggggaag	gaagggaaata	gcgagaggag	ggtcacagag	tgaccgtgga	ggatggggct	1020
tctcggttct	agatatttct	gngattggag	actgtttgct	agtggggaga	ctccagctcc	1080
ggcagccagt	tcgggagcgg	caaagtaaaa	tggacagcga	cagacagacg	ttccagccac	1140
ctctccgcgc	ccgggagatc	ctggagctgc	tttcaggcca	actccagttt	cccagctgga	1200
gcttctgaac	gcgctggact	gcgagagncc	agggagcgcc	tgaaagctgc	tcctcggaga	1260
tacccttcgc	cgaagcagta	agaacttcct	gcttgggtct	ctgcattccc	ttcctccgaa	1320
acttcccagg	agaagggcgg	aagaccccag	gggaaggggc	gaggcgaatc	ttcgcgtgc	1380
tttttcttcc	ctcccccttc	ccgcgcgggg	cgcgaggcca	tggatgtgct	cagccctggt	1440
cagggcaaca	acaccacatc	accaccggct	ccctttgaga	ccggcgccaa	cactactggt	1500
rtctccgagc	tgaccgtcag	ctaccaagtg	atcacctctc	tgctgctggg	cacgctcatc	1560
ttctgcgcgg	tgctgggcaa	tgcgtgcgtg	gtggctgcca	tcgccttggg	gcgctccctg	1620
cagaacgtgg	ccaattatct	tattggctct	ttggcggtca	ccgacctcat	ggtgtcggtg	1680
ttggtgctgc	ccatggccgc	gctgtatcag	gtgctcaaca	agtggacact	gggcccagta	1740
acctgcgacc	tgttcatcgc	cctcgacgtg	ctgtgctgca	cctcatccat	cttgacactg	1800
tgcgccatcg	cgctggacag	gtactgggcc	atcacggacc	ccatcgacta	cgtgaacaag	1860
aggacgcccc	ggcgcgccgc	tgcgctcatc	tcgctcactt	ggcttattgg	cttcctcatc	1920
tctatcccgc	ccatgctggg	ctggcgccac	ccggaagacc	gctcggaccc	cgacgcacgc	1980
accattagca	aggatcatgg	ctacactatc	tattccacct	ttggagcttt	ctacatcccg	2040
ctgctgctca	tgctggttct	ctatgggcgc	atattccgag	ctgcgcgctt	ccgcateccg	2100
aagacgggtca	aaaaggtgga	gaagaccgga	gcggacaccc	gccatggagc	atctcccgc	2160
ccgcagccca	agaagagtgt	gaatggagag	tcggggagca	ggaactggag	gctgggcgtg	2220
gagagcaagg	ctgggggtgc	tctgtgcgcc	aatggcgccg	tgaggcaagg	tgacgatggc	2280
gccgccctgg	aggtgatcga	ggtgcaccga	gtgggcaact	ccaaagagca	cttgccctctg	2340
cccagcgagg	ctgggtcctac	cccttgtgcc	ccgcctctt	tcgagaggaa	aaatgagcgc	2400
aacgccgagg	cgaagcgcaa	gatggccctg	gcccagagaga	ggaagacagt	gaagacgctg	2460
ggcatcatca	tgggcacctt	catcctctgc	tggtgcctt	tcttcatcgt	ggctcttgtt	2520
ctgccccttct	gcgagagcag	ctgccacatg	cccaccctgt	tgggcgccat	aatcaattgg	2580
ctgggctact	ccaactctct	gcttaacccc	gtcatttacg	catacttcaa	caaggacttt	2640
caaanngcgt	ttaagaagat	cattaagtgt	aagttctgcc	gccagtgatg	acggaggagt	2700
agccggccag	tcgaggctac	aggatccgtc	ccattcacta	tgcttcccc	aacctagggg	2760
aatcaacact	taagataatt	cgccacttct	cctctttctt	ctctgctccg	ctcacggctt	2820
gcagacctgg	ttccctcccc	acttctctgt	ccacggcagg	gccctttgtg	caaaggagac	2880
ccagcgaggg	agcgttgaga	gcccaggaaa	ttcagagagt	ttgtgagaag	cgacattggc	2940
tcagactttg	cctgtatcat	cagnttttga	tcccagcaat	tgccctnnttc	tctcttctat	3000
c						3001

&lt;210&gt; 309

&lt;211&gt; 498



<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 270  
<223> 18-994-270 : polymorphic base C or T

<220>  
<221> misc\_binding  
<222> 250..269  
<223> 18-994-270.mis1, potential

<220>  
<221> misc\_binding  
<222> 271..289  
<223> 18-994-270.mis2, complement

<220>  
<221> primer\_bind  
<222> 1..19  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 481..498  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 258..282  
<223> 18-994-270 potential probe

<220>  
<221> misc\_feature  
<222> 477  
<223> n=a, g, c or t

<400> 309  
actatggaaa accacatact tctctgcaaa tgtaattctt ggcaaagatt tgtctccatt 60  
ctggacattt gaaatttctt tcccagttta gaatgatagt gtcccagctt acacctaata 120  
tattgcttta atattctttg ttgagtggt tagtgaaaag ggagtgcaaa ggaaattcac 180  
tcaactctcc actggaaatg aatacccat catttttatc atgagttccc gtagcaataa 240  
agcattgtaa atgtgtagca attactgaay ctgtggtata acaattttct ccacacaaat 300  
ataattttat atttctttaa agaagatttt aaaaatatct aacaaagaga aagcctgcca 360  
agataatctt aagcaaattc ttgtttgatg tgcaacagtg gatgggaaag taggaccagg 420  
ggtcctgctg ggatgttctg tccaacattg aactcctcaa agaacccttg tcaaagncaa 480  
gttcctctgt ccttagaa 498

<210> 310  
<211> 467  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 165  
<223> 18-912-165 : polymorphic base C or T

<220>  
<221> misc\_binding  
<222> 146..164  
<223> 18-912-165.mis1

```

<220>
<221> misc_binding
<222> 166..184
<223> 18-912-165.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 447..467
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 153..177
<223> 18-912-165 potential probe

<220>
<221> misc_feature
<222> 450
<223> n=a, g, c or t

<400> 310
catttttctc accccgacta tgctcttact ctttcaaaag tgaacaataa aaatattgac      60
agaaggacag cattgtaaaa gtacatttat taatgcttgt cactataaat ctgataattt      120
ctcacataaa aaatactctt tttgggtttt tactgaactt taaayatttt attaggactt      180
acaaatttca aatacttatt ttatgctttt gaacaaatgc atgaacttcc agggaaagag      240
tagggtcggt ttcaatactg atcattgaac tttcattggc atgttctttt attcccttca      300
ctaacttctg attatgtaaa gaagtctcag aatgcagcaa tcacatcttg ttttctactt      360
gtcttttact cagaatttcc cagagaactg gaagcttacc aaatacttta aagaatgggg      420
agaatgtaac atccacatgc aaatctcttn cctaatatat cctccca      467

<210> 311
<211> 463
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 124
<223> 18-991-124 : polymorphic base C or T

<220>
<221> misc_binding
<222> 105..123
<223> 18-991-124.mis1

<220>
<221> misc_binding
<222> 125..144
<223> 18-991-124.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind

```

<222> 444..463  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 112..136  
 <223> 18-991-124 potential probe

<400> 311  
 cattcctcat atactcatcc aaatggcaga ttgttctaata gctgtgatat gtattttatac 60  
 cttttcagca ggcccctgcc atctggattt ggaattcttt tagcagaaga caaagccttt 120  
 tcaygtttac cgatgaagct gcaaaaggaa agaccacacag gaaaaacaat ccctgacttt 180  
 ccctttctgt cattcgccca aatctccctg gctcaaaacc tcacagcat cttctactcc 240  
 ctctctcttc acatccagac accaagtccct gccagttcct tctttgatgc atttttcac 300  
 atcttaacttg ttttccattc cttctgccag cttcccatat tcaggccttt attgctctac 360  
 acctgcctca ttgaaatcac ctccaaagag aacacatctg ctttcgttat tagtggtctc 420  
 cactggctaa aaccacagtt tcagcttttt aacctggcat aag 463

<210> 312  
 <211> 551  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 219  
 <223> 18-920-219 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 199..218  
 <223> 18-920-219.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 220..238  
 <223> 18-920-219.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 534..551  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 207..231  
 <223> 18-920-219 potential probe

<220>  
 <221> misc\_feature  
 <222> 536  
 <223> n=a, g, c or t

<400> 312  
 taccctctaaa cacaactaca atctctggac attatatata aaaaatgatt taaaaaattt 60  
 aaacagtgga tagagacaga ctggctaggg acctcaaaat atgaagagca acttatggtc 120  
 cttgggtttt tcttttctta cattaatatc ttagacatag agtttatgaa gccagcaacc 180  
 tggaaaggcc aatgggcata gataaaaact gcccacayc cccaagtaaa agtctgctct 240

ctctagggaa	aaattcagga	aagaagcatc	caagaagaga	aaaaaatttt	agataataac	300
tactcaattt	agccaaacat	tggaagaaa	aaacaaagta	ttctgtcccc	tgccccacac	360
cagcaaagac	catatgagta	acctagactt	tcacccacag	cagcctgaaa	taatctcctc	420
caagcctctt	agaggtggta	ttaaaaaaag	tccaagtagg	aaaaaacatg	actttatcct	480
tcctaggtgg	taacaagacc	ccctcctgat	gcaaggtcag	tggtgacaat	ttaggnagta	540
tggtcttcta	t					551

&lt;210&gt; 313

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 312

&lt;223&gt; 18-911-312 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 293..311

&lt;223&gt; 18-911-312.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 313..331

&lt;223&gt; 18-911-312.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..19

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 437..457

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 300..324

&lt;223&gt; 18-911-312 potential probe

&lt;400&gt; 313

ccacatttcc	caaattatgt	aaggaaaatt	tcctataagt	tgtttctcct	agtcatttcc	60
aatcaaaatt	catagtcttg	aacaaaacac	aattgcccta	ctgctacagt	atttggggat	120
tggaagaagt	taaatttaga	ataatatatt	taacctaaca	aaataattga	ttctaatttc	180
aattacatga	aaaaaaagta	aaaacttttt	tttcagtagg	agctttttaga	aacaactttt	240
ataatctcat	aagcaaatat	tcaactcttt	actgtataga	ttctttcttc	agtaataaaa	300
acaattcagc	crtagtttgg	ggataatgga	caaacatacc	aattactgag	aaactccaac	360
catcagcctt	cagtaatgat	agggcttcaa	ggttcacagc	aaaacttcag	cttaaatctt	420
tttagtttgt	gtccctggtc	aaggaatwac	attgaaa			457

&lt;210&gt; 314

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 368

&lt;223&gt; 99-65963-368 : polymorphic base A or G

&lt;220&gt;

```

<221> misc_binding
<222> 349..367
<223> 99-65963-368.mis1

<220>
<221> misc_binding
<222> 369..388
<223> 99-65963-368.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 459..477
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 356..380
<223> 99-65963-368 potential probe

<220>
<221> misc_feature
<222> 460
<223> n=a, g, c or t

<400> 314
gcttctgtat tctaaactgg aagtagacat catatcccag ctaaacaggg aaagtttttag      60
aactttggga atagtttgtc tatgcatgta taatgctgag aagggctctgc agtgaagaag      120
ataagataga cttctccagc acaactatta ctcatttgat aattcagttt catttttgct      180
cacataatct aagtaaagcc atatcagaaa ccaagttttt ctgtatgtta cactaaattt      240
taagaacaaa gtctatatatt aaaataatcc aaaccccaaa ttgctcatc caaattatgt      300
cttgccagc aagttttaca ttagaagttt tgagacttcc atttatttgt gtcttttaca      360
gaattgtrtg acaatgactt ttggacattt gttctttcgg ctttgaata tttacacaag      420
aatggagaag gaacatccaa ctggagcata attgtcaagn caatagagaa tttagag      477

<210> 315
<211> 502
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 225
<223> 99-65966-225 : polymorphic base C or T

<220>
<221> misc_binding
<222> 206..224
<223> 99-65966-225.mis1

<220>
<221> misc_binding
<222> 226..245
<223> 99-65966-225.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

```

<220>  
 <221> primer\_bind  
 <222> 486..502  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 213..237  
 <223> 99-65966-225 potential probe

<220>  
 <221> misc\_feature  
 <222> 485,490  
 <223> n=a, g, c or t

<400> 315  
 tacctccata tacaatctct agcacctttt tctgtactta acactactct gtgaaccttc 60  
 tgcttttagct aaaatgttct aattgggtatt tctaaccaga tctgctactt caaattttaag 120  
 tggcacatta tgtgtaaaaa ccagggtggca aaattataaa cattatataa gtttgaattt 180  
 tttgccttgt acctaccctt ggccaccctg ttgcaactct ttaaygggta atgattctct 240  
 cctcattctg atgctctcct ccttactctg ctcaaaactt tcttcctctc atctagccat 300  
 tcctttgggt ttagacccat cttttcctct ctcttccaag accctttcgg gttaatacaa 360  
 cacatgggag gttttgagtc tgcattcttc tcaaggatca acatttgcac aatcaaccca 420  
 ggcaattaat caacatccag caatcagata gaaatttcat actaggccct cacttgccag 480  
 gaagnaaggn atcagggtgt tt 502

<210> 316  
 <211> 452  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 75  
 <223> 99-65968-75 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 56..74  
 <223> 99-65968-75.mis1

<220>  
 <221> misc\_binding  
 <222> 76..95  
 <223> 99-65968-75.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 432..452  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 63..87  
 <223> 99-65968-75 potential probe

<220>

<221> misc\_feature  
 <222> 439  
 <223> n=a, g, c or t

<400> 316  
 cctgaccttt gtttactgga ggtttaccca tgctcacttt gccctgcagc catcattctg 60  
 acaccagaaa gcagyagaat gaacaaacat aacaacagaa acaagagggtg tttttgacta 120  
 cttaagtagg gaaataatag agcataataa ttaatttttaa catagtaata cgtcatatat 180  
 acaaaaccct actatggaag aagaccacgc cagaaaataa aatgcccctc tacttttaat 240  
 tgatgaaccc caaaacaatc aactgtttct tttgaaacag gggagggttat tttcctccag 300  
 ctgaatgttg cagggtagac agaggaggga tctcagcacc acccactgtt ttaaaaaggc 360  
 agattggacc cctgttgctt tccccagaga ctgtagtttt cctccatata tcttcaattc 420  
 tgtccatgtt agaaagaanc ctatatgtta cc 452

<210> 317  
 <211> 2512  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 1501  
 <223> 99-5069-331 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 1482..1500  
 <223> 99-5069-331.mis1

<220>  
 <221> misc\_binding  
 <222> 1502..1521  
 <223> 99-5069-331.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1171..1189  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 1702..1719  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 1489..1513  
 <223> 99-5069-331 potential probe

<220>  
 <221> misc\_feature  
 <222> 572,758,2175..2176,2329,2494  
 <223> n=a, g, c or t

<400> 317  
 cccattcagg ctccctatgc ttccttttct catctcctat tgccactctg ggatgctgac 60  
 acgattttaag aatttggcag ataatatgac ccaaggagta gttggaattc cctcccccaa 120  
 gtttttccaa cccagtttt gctgggttg aggcgaggtt tatattgttac aaccttggtc 180  
 tgaccggcag ggacctggtg tgtgtaagt agttctgagt ctctgttgac aaaaagagac 240  
 tcgaatgcaa agacgctgag ctagaggagg agggggcgg ggaccacagag gaaagaggca 300  
 ctctctgggg ttggggaagt attaggagg gaggggttaga gtgggaggga aggagctcgc 360  
 tttcgaagcg actcacagag ggataaataa agggaagtga ggaggaagag ggagacttaa 420  
 aggggaaggca ggtggggaga agggggacga aagaggcaga agagagagaa gagaggagga 480

```

gagaggggga gagaggggaag gaaggaaata gcgagaggag gggtcacagag tgaccgtgga 540
ggatggggct tctcggttct agatatttct gngattggag actgtttgct agtggggaga 600
ctccagctcc ggcagccagt tccggagcgg caaagtaaaa tggacagcga cagacagacg 660
ttccagccac ctctccgccg ccgggagatc ctggagctgc tttcaggcca actccagttt 720
cccagctgga gcttctgaac gcgctggact gcgagagncc agggagcgcc tgaaagctgc 780
tcctcggaga tacccttcgc cgaagcagta agaacttcct gcttgggtct ctgcattccc 840
ttcctccgaa acttcccagg agaagggcgg aagaccccag ggggaaggggc gaggcgaatc 900
ttcgcgctgc tttttcttcc ctcccccttc ccgcgccggg cgcgcaggca tggatgtgct 960
cagccctggg cagggcaaca acaccacatc accaccggct ccctttgaga cggcgccaa 1020
cactactggg atctccgacg tgaccgtcag ctaccaagtg atcacctctc tgctgctggg 1080
cacgctcatc ttctgcgcgg tgctgggcaa tgcgtgcgtg gtggctgcca tcgccttggg 1140
gcgctccctg cagaacgtgg ccaattatct tattggctct ttggcgggtca ccgacctcat 1200
gggtgtcggg ttgggtgctgc ccatggccgc gctgtatcag gtgctcaaca agtggacact 1260
ggggccaggta acctgcgacc tgttcatcgc cctcgacgtg ctgtgctgca cctcatccat 1320
cttgacactg tgcgccatcg cgctggacag gtactgggcc atcacggacc ccacgacta 1380
cgtgaacaag aggacgcccc ggcgcgccgc tgcgtcatc tcgctcactt ggcttattgg 1440
cttctcatc tctatccgc ccattgctgg ctggcgacc ccggaagacc gctcggacct 1500
ygacgcatgc accattagca aggatcatgg ctacactatc tattccacct ttggagcttt 1560
ctacatcccg ctgctgctca tgctggttct ctatggcgcc atattccgag ctgcgcgctt 1620
ccgcatccgc aagacggtca aaaagggtgga gaagaccgga gcggacaccc gccatggagc 1680
atctcccgcc ccgcagccca agaagagtgt gaatggagag tcggggagca ggaactggag 1740
gttgggctg gagagcaagg ctgggggtgc tctgtgcgcc aatggcgcgg tgaggcaagg 1800
tgacgatggc gccgccctgg aggtgatcga ggtgcaccga gtgggcaact ccaaagagca 1860
cttgccctctg cccagcgagg ctggtcctac ccctgtgtcc ccgcctctt tcgagaggaa 1920
aaatgagcgc aacgccgagg cgaagcgcaa gatggccctg gcccagagga ggaagacagt 1980
gaagacgctg ggcacatca tgggcacctt catcctctgc tggctgccct tcttcatcgt 2040
ggctcttgtt ctgcccttct gcgagagcag ctgccacatg cccaccctgt tgggcgccat 2100
aatcaattgg ctgggctact ccaactctct gcttaacccc gtcatttacg catacttcaa 2160
caaggacttt caaanngcgt ttaagaagat cattaagtgt aagttctgcc gccagtgatg 2220
acggaggagt agccggccag tcgaggctac aggatccgtc ccattcacta tgcttcccc 2280
aaccctaggg aatcaacact taagataatt cgccacttct cctctttcnt ctctgtccg 2340
ctcacggctt gcagacctgg tccccctccc acttctgtct ccacggcagg gccctttgtg 2400
caaaggagac ccagcggagg agcgttgaga gccaggaaa ttcagagagt ttgtgagaag 2460
cgacattggc tcagactttg cctgtatcat cagnttttga tcccagcaat tg 2512

```

<210> 318

<211> 493

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 175

<223> 99-5070-176 : polymorphic base G or T

<220>

<221> misc\_binding

<222> 156..174

<223> 99-5070-176.mis1

<220>

<221> misc\_binding

<222> 176..194

<223> 99-5070-176.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 476..493



<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 163..187

<223> 99-5070-176 potential probe

<400> 318

cttattggct	tcctcatctc	twtcccgccc	atgctgggtg	gcgcaccccg	gaagaccgct	60
cggaccccg	cgcattgcacc	attagcaagg	atcatggcta	cactatctat	tccacctttg	120
gagctttcta	catcccgctg	ctgctcatgc	tggttctcta	tgggcgcata	ttckagtg	180
gcgcttccgc	atccgcaaga	cgggtcaaaaa	ggtggagaag	accggagcgg	acacccgcca	240
tggagcatct	cccgcgccgc	agcccaagaa	gagtgtgaat	ggagagtcgg	ggagcaggaa	300
ctggaggctg	ggcgtggaga	gcaaggctgg	gggtgctctg	tcgccaatgg	cgggtgaggc	360
aaggtgacga	tggcgccgcc	ctggagggtga	tgcagggtgca	ccgagtgggc	aactccaaag	420
agcacttgcc	tctgcccagc	gaggctggtc	ctaccccttg	tgccccgcc	tctttcgaga	480
ggaaaaatga	gcg					493

<210> 319

<211> 450

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 348

<223> 18-511-348 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 328..347

<223> 18-511-348.mis1, potential

<220>

<221> misc\_binding

<222> 349..367

<223> 18-511-348.mis2, complement

<220>

<221> primer\_bind

<222> 1..20

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 430..450

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 336..360

<223> 18-511-348 potential probe

<400> 319

agtattagat	gtgacattgg	ttacatgaag	gcatttgatg	gtgctgcatg	tgagtggaa	60
agagaaataa	aaatgcatca	attctgaaat	caaataattgt	gtcatgctta	gttataggca	120
aatagaaaac	ccattactct	gagcaaatgt	attaaatgtt	aatagaaaat	gttaaaatat	180
atataaatac	agaattttcc	tgattgtata	ccacaatgg	atggcttatg	ttttaaagga	240
ctatgattct	ttttctaata	ttcaccatct	ataagcttaa	gaatgtcaac	aatgtttacc	300
tacatgtgaa	tggaaattga	gaaaagaagg	ttactacttg	tcaaattycc	tgctagacca	360
gttggtaaat	ttctatgcaa	ctaaatgata	tatttaattgt	taatttggat	gatttcattt	420
tagcataatc	taaacagaaa	ttctaacgtc				450

<210> 320  
 <211> 475  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 352  
 <223> 18-523-352 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 332..351  
 <223> 18-523-352.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 353..371  
 <223> 18-523-352.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 455..475  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 340..364  
 <223> 18-523-352 potential probe

<400> 320  
 ttcagccctt tctcgtcacc gagcccggtg aaatagtact acacacaaaa tacaaaccag 60  
 cagggtgagg agtgggagag aaggccaact gtgaaggcta ttcacaatat taggatgcac 120  
 aaaggagttg atgagatcag ttacatgatg gtactcagtg tgaaatgtag tatcttttca 180  
 atactgtttt gctgtgattt ccttaggaag attaataagcc ttgtgagacc ttgttaatta 240  
 tttttgctat gcttaaagta agtagataat tttctccac aagtgtctcc taatagatag 300  
 taaattccct agatcatcct ccacacgaga cattggggag gtggtaatgt trggctctgt 360  
 gatgtaaaat caacccttct gtctccacca ttagttcttc ataccactct tggggtcaaa 420  
 acaactaaac aagaaatctt ctagtcacga gtttgtggkt tctgttttag agtgc 475

<210> 321  
 <211> 509  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 480  
 <223> 18-545-478 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 461..479  
 <223> 18-545-478.mis1

<220>  
 <221> misc\_binding  
 <222> 481..500

<223> 18-545-478.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 489..509

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 468..492

<223> 18-545-478 potential probe

<400> 321

cattcatatt	tcctgaagaa	ccactggaaa	cagttattta	atagtgtggc	taaattgtata	60
ttcagagaaa	cacttcctgt	atatttgcac	atztatgtat	atztatgtcc	tattcctgga	120
atagatttac	aagttttgtt	tttcagaaaa	tttcagaatt	tctggaatgt	gcagaagtat	180
taacaggtaa	cttagatttg	gaatacactg	tattagagat	aactggaaaa	atgagaggct	240
tcctacactg	gaaggtcaaa	gatctttcct	ggaggggagt	taggaatttg	cctttactta	300
ccattattct	gttaaaagag	attatgaata	atgcagtttc	acaaaaggaa	tgggacaatg	360
gtgtaagtaa	acctcccat	cacgttttca	gtggctttcc	tttgagtctt	gaacgttttc	420
cactgggtgt	tatagtcgag	agtcccccac	ctcctgagga	agcaagacct	ggcaaaccr	480
agacgatgcg	ctcttacttg	tgttgtttg				509

<210> 322

<211> 477

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 194

<223> 18-522-194 : polymorphic base G or C

<220>

<221> misc\_binding

<222> 175..193

<223> 18-522-194.mis1

<220>

<221> misc\_binding

<222> 195..214

<223> 18-522-194.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 457..477

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 182..206

<223> 18-522-194 potential probe

```

<400> 322
gtagcaaaat aggattttca gctggggttag aaaataccaa caacttggat taaaaaaaaa 60
atgctttttt gatctgggtg gttttgatag actgtcaaaa atattaatct taaaatttat 120
cgtaaatagt agtcatgcaa acctttcatt atatatctc tcaaattgat ttttttcaaa 180
gaacaagttt tcaaaaatac actggattca acaatttttg aattacagtc agatttgaat 240
ggtcttgtgc agatccactt aacttgtgag tagtaatgac cacttaacta gtaaataata 300
ctatctcata agcagtaaat aacttttatg aaaaatgaaa cgatataatt gctaaattaa 360
gtttctcact ttatactttt gctgtatcta aagataattg gtattcctac aggttaacat 420
attgttgatt catatatatg gctaccatat taagtgctaa tacttcattg ttgcatg 477

```

<210> 323

<211> 450

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 284

<223> 18-524-284 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 265..283

<223> 18-524-284.mis1

<220>

<221> misc\_binding

<222> 285..304

<223> 18-524-284.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 430..450

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 272..296

<223> 18-524-284 potential probe

<400> 323

```

actacttcgg tggatattct tagaccaaca aatgagaatt gataaagcct ccaggatctt 60
gtgtcgccca cttcaacaga acttcgcttc cattgataaa caatttcctc acgtggatag 120
ccatctgccg tgagatagga aagctcacat taaaaatgat tataaattag catatgtagc 180
aaccatcttc tatgaacatg aactgaggt aaagactgag aaagatagtt acaagctaaa 240
tgaggatctt ggaccaaagg gcattgcaat gagaacataa attrcaatga ctttgcattc 300
taatgggaag ttagattcaa aaatccaaag gtcaaattta ctcttgaaaa taatttaa 360
gacatagaag gtatactaca tgtgatttta tatatgccat atgcatactt tacatcatct 420
ggaatagtgc ataccaagtg accagtctat 450

```

<210> 324

<211> 505

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 52

<223> 18-626-52 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 33..51

<223> 18-626-52.mis1

<220>

<221> misc\_binding

<222> 53..72

<223> 18-626-52.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 485..505

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 40..64

<223> 18-626-52 potential probe

<400> 324

gaaacagaga	ggaagtctctg	gcacctgtgg	aaagttgggt	tggttgagca	gygagggata	60
aattgagggg	gtagaagtct	attctgtagg	aagtggaggg	cccctagggg	tttatgagca	120
ggacagtcac	ttgttggtag	ctgcatcctg	cagctggcag	caggggagag	gtgaggagca	180
tctggctcgg	gaaggcagag	gtgggaaggg	agagagggcat	aaggagaatg	tgaaagggag	240
tgagacaaga	tttggcagct	gaatctgtct	gggcttcaaa	gcatcacatt	tattcttcca	300
gtcagcactt	ccactgggtg	accctccca	ggcccatcca	agatgaccct	ttctgaaaag	360
cccccaagct	gtggttgctc	ctgaaatctg	cttttgggag	aatccctgtt	gcttcttgcc	420
catggctgct	gctggatttg	gctgaaggtc	tatttctctg	ggtatcctgg	actcattagt	480
gtgtgcgaca	agttgaagtg	ctctc				505

<210> 325

<211> 486

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 189

<223> 18-629-189 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 169..188

<223> 18-629-189.mis1, potential

<220>

<221> misc\_binding

<222> 190..208

<223> 18-629-189.mis2, complement

<220>

<221> primer\_bind

<222> 1..20

<223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 466..486  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 177..201  
 <223> 18-629-189 potential probe

<220>  
 <221> misc\_feature  
 <222> 470  
 <223> n=a, g, c or t

<400> 325  
 cgatcactcatt tattgtgtgc actacaggtc atcaataacc tgtaaataat gataaaaatt 60  
 tagtggtttca caagtgtatt tgggtttcac ataggctgac tctagargct gtgggcgtac 120  
 atcacccctgc tgtttggctt ccacaggttc tgactaccct aaaagtaaga tgattgcctt 180  
 tttcccttyg aaccaaataa aaagatgaga agagactata gcttgcatgt agcgctaagg 240  
 agaccagctg gcagcaggtt cacgtggaaa tactctgaat caagcaagtt tgcctagctt 300  
 agctcgggtat ccagtctttg gaatggaagt ggaaattggt ctccgcattg ggcacgccat 360  
 tgtcacatcc acatccaaad atgccttctg agcatgacag ccgcgttatc ctgaaagaca 420  
 atacatcaag ccaagggcaa ataatatcca atgtcaaag ctctcggggg tttgagaggt 480  
 ggatat 486

<210> 326  
 <211> 457  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 71  
 <223> 18-1131-71 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 51..70  
 <223> 18-1131-71.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 72..90  
 <223> 18-1131-71.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 437..457  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 59..83  
 <223> 18-1131-71 potential probe

<400> 326  
 cgaagaccaa aaaagaggaa gcattcagcc agctcaaaga aattattgca tcatttcctt 60

```

gtgtgcggtt yagggttaaaa ataacctcta atccttgtca agagttaaact gtcttgtcaa      120
agagaattag gaaattacct cagggcgggg gttacagggt ggggtagaga aggagcagtt      180
catcaggaag aaattacttg ctgcattttg agatgaacat ttctgaatga ctgaagaaaa      240
tgtggggcta agggaatagg gactccgatg ggagacagga ggaacgtgca tggggcatgt      300
gtgtgtgttg tgggggtagg tgaagagggg ggcactggag tgtccctgcc atggaggtgg      360
ctgccctggg tggcttgaac tgctgggcca tgggggtgttc ttctcttctc cgtcttgggc      420
agcctgcttt ggccttgggt gctcacagag atagagt                                457

```

<210> 327

<211> 517

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 126

<223> 18-534-126 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 106..125

<223> 18-534-126.mis1, potential

<220>

<221> misc\_binding

<222> 127..145

<223> 18-534-126.mis2, complement

<220>

<221> primer\_bind

<222> 1..19

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 497..517

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 114..138

<223> 18-534-126 potential probe

<220>

<221> misc\_feature

<222> 443

<223> n=a, g, c or t

<400> 327

```

gtagttagtt gcaccagagt ataaatactt ggtaaaacac acaagaggaa gtagaattta      60
cacacaagtg btaactttca ccagcaaatt cagctgggca cttggacata aaaaaaata      120
aaaaaaycctt aagataatta tatttataat atggatacag ttacagtacc atgataaagg      180
agtataaaaa ggtattttcc caatgaatca ttagctcaat aacatactag acaacagaag      240
tagagtttga attttattta agatctgccc agccctctc cctttaaaaa atatttaatt      300
tctttttgtg caagtaacat cttctgtgga ttttgtaatt cctaactg tgcaaaaatg      360
gcattttgaa ccactccttt tttttgtttt tgtttttatc cacatgtgca gtaatctgaa      420
ctgtttctct ctctcgctct cbntttaatg tcctgtcttc aattgacaga gtcacatgtc      480
acagagagag gctctgcgcc tggtccttcc aactaat                                517

```

<210> 328

<211> 514

<212> DNA

<213> Homo Sapiens

<220>  
 <221> allele  
 <222> 59  
 <223> 18-596-59 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 40..58  
 <223> 18-596-59.mis1

<220>  
 <221> misc\_binding  
 <222> 60..79  
 <223> 18-596-59.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 495..514  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 47..71  
 <223> 18-596-59 potential probe

<400> 328  
 tcaactccag taggtggcag gtatatagat atctgtttct aattatgggtt actttttctrt 60  
 tctcttcact tttctgttta acaaaatgta aaatgttaag gaaaaggaaa acctagttga 120  
 gttcaacaga accaaatgat ggatgggtgg aaccatgaat gaagtagctg ttattggaag 180  
 gaaacaatca taaactccaa tggtcaaaaa taaaatctga tggtcctttg ttaattctt 240  
 ggatgaaaat gaacatcca tcgaacagaa acctcctgat gctgctgttg gtaacgtctg 300  
 gttgtcacca gccacggacc ttgttttctt ttcactctg tcatgtttct tctccctctt 360  
 tggggatctg tcttccatgt gttttctata aaatcagcat aacagttcct agtgaaaaaa 420  
 tattttactg cacatgtgta agatttggga gtatagacta aaggcaggca aattacaagt 480  
 aagtttctgc catgctgtgc ttacaccttg attc 514

<210> 329  
 <211> 470  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 27  
 <223> 18-597-27 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 7..26  
 <223> 18-597-27.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 28..46  
 <223> 18-597-27.mis2, complement

<220>



```

<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 450..470
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 15..39
<223> 18-597-27 potential probe

<220>
<221> misc_feature
<222> 428,455
<223> n=a, g, c or t

<400> 329
atgtgggagc ttgcgttctg tcaagasctg acaccaaaaca gttattgggc actccaagat      60
ttaattcctc cctagtctcc cactcacagc aatctacctg attcaacttc ctctgttttc      120
caagctcttg tggttaggac agattctctt agcctctcag ctactgctcc tcatttttga      180
gatctgtctt ttgcggctgc cagctgatgt ctttattctg tgctggtcac ttttccagcc      240
ctgcaatttg aaattactca tctgatttca tgggtggctg gcaaagggat ctgtcaaadc      300
tgcatacatt taggggaaac tgaaaatgaa actacatgct ggaatttttt aaagtataga      360
cttttctata gagaaaagaa aaatgtagaa atacagggca ggggaggtag atatctgtag      420
ctactggntg accccccgcc ccccaaaatc agttnctagt tctccatgct      470

<210> 330
<211> 476
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 203
<223> 18-730-203 : polymorphic base A or C

<220>
<221> misc_binding
<222> 184..202
<223> 18-730-203.mis1

<220>
<221> misc_binding
<222> 204..223
<223> 18-730-203.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 456..476
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 191..215
<223> 18-730-203 potential probe

```

```

<220>
<221> misc_feature
<222> 458
<223> n=a, g, c or t

<400> 330
tgaagctgga ctcttgactg gaggcagagt gatgatcaga cgggagcacc cctgtgccac      60
tcactcctga actccctgtg ctcttgatca gcctacaccc tgggggagca ttaagataaa      120
atgcacgcta atattttcct gctttggaaa ggaaactgca atagcaaata ctgatgtgtg      180
aatcgtactt tacagtttac aamgatgtga gcatccagga tcacgactga ctggcaaaac      240
tgccttttagt atcttcctga atctgaggaa gctgagcttc gaggtaatta agactcagac      300
gctcaactgt gcctgctggg ccgagggtacc tcctgagtta gagctctccc aatttagttt      360
atgtcttagg gatgtaaaat gatgctgctc tagattctta ccaggtatat atatttaatt      420
tattactatt gtatctcatt gattgttatt tgggtggtnaa ttttaaagtg gcaggc      476

<210> 331
<211> 453
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 89
<223> 18-734-89 : polymorphic base A or G

<220>
<221> misc_binding
<222> 70..88
<223> 18-734-89.mis1

<220>
<221> misc_binding
<222> 90..108
<223> 18-734-89.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 433..453
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 77..101
<223> 18-734-89 potential probe

<220>
<221> misc_feature
<222> 435
<223> n=a, g, c or t

<400> 331
tcagccgatg aggagctaac aactcaatgc caaatctgct caaggatgaa agggaagcag      60
ggagaggaag agaaggagag atgcagggrg gaggatatag gggtcctctg ggacttgtag      120
aggctcgagg gtggagaggc ctctgc aaa ggccctggagg gaggcagact gaggacatga      180
gacgcgatgg gattcgtgaa gtgtggaggc tgtggccac tcactacttt cctcaatcgg      240
actggggacg gcacagtcac tgatggctcc tcctggactc gaggccaaagt ggcataactaa      300
cccagagacca ggggcacgtg cctgagcact gccagcaagg agagctgtgg ggaggccggc      360

```

```

tggggcccag gccagcctga cctgaggcct cgctgggtgc aagtcctgtg agccgctttc 420
tccatggtta ggggncagag gttggatgat aat 453

```

```

<210> 332
<211> 455
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 321
<223> 18-895-321 : polymorphic base A or C

```

```

<220>
<221> misc_binding
<222> 302..320
<223> 18-895-321.mis1

```

```

<220>
<221> misc_binding
<222> 322..341
<223> 18-895-321.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 435..455
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 309..333
<223> 18-895-321 potential probe

```

```

<220>
<221> misc_feature
<222> 428
<223> n=a, g, c or t

```

```

<400> 332
aggaaggga ataaataggg gcttgatgta ttttatgatg tcttttgtgg ctgttgaaaa 60
acatgccctg ctggccagaa tgtgtgaacc tggttcccg ctttgctaga aacccactt 120
cttcaaaagc aattgggagc gcagggtcaa gaggtaaaag tgctcaaaga acctgatgta 180
aaattcctct tacaaaaata tcttctaata taaataatct caaataccta agaaaacttg 240
taagccaaat acgttcaacta caggaaaatt tataacagca aaatcattca ctacgtaaac 300
atccccaatt agggaagaag mtaacacaag gcgctcttgc cctgtcaaat atgcagccat 360
ttaaataat acattttaaa gaaattgtga tcatgtattg ggtaggaaaa aagcacagta 420
ccaaactngc acagcctgat cccaactgta taaa 455

```

```

<210> 333
<211> 561
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 69
<223> 18-896-69 : polymorphic base A or G

```

```

<220>
<221> misc_binding
<222> 50..68
<223> 18-896-69.mis1

<220>
<221> misc_binding
<222> 70..89
<223> 18-896-69.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 544..561
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 57..81
<223> 18-896-69 potential probe

<400> 333
ttttaccaca catcgttttca tttaaaaata tacagctctt ggaaacatgc gtctatttcc      60
ccttatgcra acagcaacag aaaagcattc tttcaacaga tgagcatggt gaatctagct      120
cctggccaaa gtcttggtgt tgatttttca ggccaactac agacaattac agatgcttta      180
cctggcagtc tcatggggta agctgccctc cccacaccag acctggtgca cagtcagtg      240
actgcagtct ctgatgggag cggctgcaac taccaggccc tggccagcca tgctgttagg      300
catctctcta ttcctatctc ccaggcctgt tgactgggga cccttcttat caggcataga      360
tgactttgaa ggcacgttct ccactgtgac tcagggttta gtacttttcc actcctagcc      420
cttgccctga cccatcctcg tagccccag gttcataaat gtaagcagcc tttctttgga      480
gaagagctat gatccccacc tctgagctga tccacctgcc ccacacctta cactgttctg      540
tgggaaaatg ggctggtgag t                                     561

<210> 334
<211> 459
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 58
<223> 18-903-58 : polymorphic base A or G

<220>
<221> misc_binding
<222> 39..57
<223> 18-903-58.mis1

<220>
<221> misc_binding
<222> 59..77
<223> 18-903-58.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>

```

<221> primer\_bind  
 <222> 442..459  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 46..70  
 <223> 18-903-58 potential probe

<400> 334  
 caggggttcca aataacagct ttcccctctt aagggtggaaa acatggacag gcaccacrctt 60  
 gttttatgag gctctgagtc tgtgccatgg aacatcatgc tagaactctc cgatattcct 120  
 gccaaatcct aaaatcccc agttctccct gcagctcctg aaatcctact gaagtgtatt 180  
 cctcaatctt catggagggt ctccattctt gcccttggca ctgctgcccc actcagaatc 240  
 ctgctgcccc caaggtaaaa cccaagccct atggccccac aggccagagc cacctctccc 300  
 accctgccct ccttcctaga ctgagccctg ttctctctcc cagccacact ggggggtcctg 360  
 cataggtgat gacacagtga tggtccatcc cagtccttac acacattctc cccattctct 420  
 tgccatgccc atcagcaagc acatccgctc taataccac 459

<210> 335  
 <211> 453  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 216  
 <223> 18-590-216 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 197..215  
 <223> 18-590-216.mis1

<220>  
 <221> misc\_binding  
 <222> 217..236  
 <223> 18-590-216.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 434..453  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 204..228  
 <223> 18-590-216 potential probe

<220>  
 <221> misc\_feature  
 <222> 417..418  
 <223> n=a, g, c or t

<400> 335  
 cattgtgggg tggcgttttg tggtctgaac cgtttcgtct cctcttgcc cacactgagg 60  
 ttcacaggcg cctgcagagg agctggtgtg ggacgatggg gagattggga ggcaacatcg 120  
 cctcctctgc atgaaatgct catgggcaca tgtctgctgc ctctacctac caaaggacag 180

```

aaccagccaa ctggcatggc aggcagggag ccagckcagc ctccaggccg tccatcctct 240
ctcctcagta ccagggcctc ccgtcaacgc cagcgccaac agagagcctg ggcccccccg 300
acccctccct cctgctggct ctcttcttc cttctagggc cctgctgce cctctgtctc 360
cagaattgtc ccctgcttgc catttaaccc attcccagtg cttgttktcc ccgaggnncc 420
cagcctctca gccctcaatg gtcacctgtc cca 453

```

```

<210> 336
<211> 534
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 433
<223> 18-817-436 : polymorphic base G or C

```

```

<220>
<221> misc_binding
<222> 414..432
<223> 18-817-436.mis1

```

```

<220>
<221> misc_binding
<222> 434..452
<223> 18-817-436.mis2, complement

```

```

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 514..534
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 421..445
<223> 18-817-436 potential probe

```

```

<400> 336
ccatcatttt cacttgaata cttcttgcag ttttattcat ttccttgccat catactacaa 60
aaattttaatt gtgcagtcac taacaaaaat taggatggaa aatatcaacc tgggggttgtt 120
ttttccactc atatggagaa ggcttcttca gcttactgag ccagtaaaag atgtctgtca 180
tcatttgctg ttgattgtgg catatataacc attgcaacat gcatcattag cgcagttagt 240
accttggtac agcttttggc tttatattct tactgtgtct taggggtctca gatgggttgc 300
gttacatttc tcagatgtaa tacaagtata tctctgtgac aagtttctat ttttaatttt 360
tttaacctct ttttatgtgc agttacctaa aattattctg tagggacttg actccaatcc 420
ctgaagtaga ggsatttttg catagtcacg ttctgtctgt cttgtccagg gacttttcct 480
gtgtgctgtg tttatatatt tgattcctaa cacgtaagac ctttttcgga gcaa 534

```

```

<210> 337
<211> 483
<212> DNA
<213> Homo Sapiens

```

```

<220>
<221> allele
<222> 85
<223> 18-829-85 : polymorphic base G or T

```

```

<220>

```

```

<221> misc_binding
<222> 66..84
<223> 18-829-85.mis1

<220>
<221> misc_binding
<222> 86..105
<223> 18-829-85.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 464..483
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 73..97
<223> 18-829-85 potential probe

<400> 337
caagggtcta gtgttttttag ctgtcttccc agccctgctc cagagccccc atgtaacctg      60
ctgccctgca gtgccagca cagakcagtg tctgttgaat gcgtgagtca agcaaaacat      120
caaacagaat ccttgacatg ggaaaaacat gctcccagcc accaccagct gaacattgac      180
atccagctgc tttcccactg ggcagtggct tgtgaagatg gggacagagt atcataaatc      240
atctcctttg tggacagcag ggatgatcct gaccttcttg tcacagacta aacagactaa      300
gtagccagaa gaaaaaaaaa gaaagaaaga aaaaaggggc ttaaaggcac tcagctgtca      360
aaattataag gagggtttgt taaaactatt ttttaaaaaa gaaaagtggg taagttatgc      420
agtaggatat aatattctat aataacttat taccaaactt ttagccttaa tccagttgct      480
att
                                         483

<210> 338
<211> 597
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 387
<223> 18-832-387 : polymorphic base A or G

<220>
<221> misc_binding
<222> 368..386
<223> 18-832-387.mis1

<220>
<221> misc_binding
<222> 388..407
<223> 18-832-387.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 580..597

```

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 375..399

<223> 18-832-387 potential probe

<400> 338

cagtctatgt	gttggttcctt	gtgtaagagc	aggtaacttta	ccataaatcc	tgcccttagg	60
tcaaacaacc	gtgatatcat	atttcaattg	tcctacacat	ctcttctgaa	gcatctacac	120
cctttcccga	tgggtgtgtaa	accctgggtc	tggggatgat	ggcgcagggt	ctaccatctc	180
aactcgcagt	gaccagagac	acaaacctgg	cttctgtttg	taagtcccta	ttaaagtgtt	240
ctttctaaga	aactggattt	gtcagcctcc	tttttgggcc	tctcagcttc	cttggatttg	300
ggaggcaggt	ttgcatagac	ctgctcacca	caaaacaggt	agctaccaac	cttaggggtg	360
gggaaacagg	ggcagagggt	gaggtrtca	gaacctggaa	gctgggagga	ggagtgtcac	420
agagctggga	gctggacctc	tgtgcaggac	actgctgcag	ctgccatggc	aggctcagag	480
ggggacttta	aggaatggct	ggtgcyatga	cccctgcagg	gcacagagag	tctgggtcag	540
agtgtgggga	gagctggagg	gaggccgaca	aggacagcag	gtgagcaggt	cccttct	597

<210> 339

<211> 461

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 259

<223> 18-833-259 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 239..258

<223> 18-833-259.mis1, potential

<220>

<221> misc\_binding

<222> 260..278

<223> 18-833-259.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 441..461

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 247..271

<223> 18-833-259 potential probe

<400> 339

tagcttggtg	tcttcgagtt	tttggtagag	ccttggtgctg	ggggtggcag	gaagagagag	60
gggacacagc	atggccagtg	ctatatagca	tggaatgctt	ttaacagaga	acaaagtgtt	120
tgtactaaaa	ggcaggaatc	tggggctcag	taggtgttga	gtaactgaat	tgctatgaat	180
gattttccgt	caaaatctaa	ataacattcc	agcctttgcc	agcttcatag	gggaattaga	240
tagtaggaat	gcactgagyt	tgtgctcctg	ggaagactcc	acgattgggg	gaaggaaggc	300
aacagaaatg	agggcagggg	tgttgtttat	ctccgtccaa	gcacaggagg	ccccgggtgg	360
gatgacaggt	gggatgacct	ccgtttactg	gtggcccaaa	agcacaccta	tgcttccagg	420
atgaagtgcg	ctctgctcct	cacccaaagg	tttatttctg	g		461



<210> 340  
 <211> 450  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 271  
 <223> 18-839-271 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 252..270  
 <223> 18-839-271.mis1

<220>  
 <221> misc\_binding  
 <222> 272..291  
 <223> 18-839-271.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 430..450  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 259..283  
 <223> 18-839-271 potential probe

<220>  
 <221> misc\_feature  
 <222> 434  
 <223> n=a, g, c or t

<400> 340	
ctacagcact tacacaagcc accaactggc acccacagca cttatcactc catgtgtctg	60
ctcaaccagc ctgggtaagg aaccctaccc tctctgtctc tgtccacctc caacaggcca	120
tggtgcaccc tgcattggggg ctgcctcatg ggggtctcca ggaacacctg ctgagtgaat	180
gcataaagag tccttggtctg ctgcacactg agctcacagt taactaaatg ctagaagatt	240
ttgtaatatg tccttttctg tcaccttacc kaagctcact ggtattttata cactcagttt	300
tccacattca aacatacac agctgtgtgt gtggaggagg cgggtgctgg gggcccttgg	360
ggcagcttgg agaattgctgc aatctgggtg tgtccgccag gaaaacaggg ccgagtcattg	420
ggttacagag tggnaagagt ggattcagag	450

<210> 341  
 <211> 496  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 194  
 <223> 18-770-194 : polymorphic base G or C

<220>  
 <221> misc\_binding

<222> 175..193  
 <223> 18-770-194.mis1

<220>  
 <221> misc\_binding  
 <222> 195..213  
 <223> 18-770-194.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 479..496  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 182..206  
 <223> 18-770-194 potential probe

<400> 341  
 ccaggtgata actaagtcac gaacgtttca gcaaacacct gctctagcct gggcactctg 60  
 cttgttgaca tgcaaggtga tgagagtcac actgtgacat gaattagcat caccgacaccc 120  
 tggcaaacct tttgtgatgc ctcccgtgaa agcacgtcat agttctcctt aaatgggatg 180  
 tcccttttct ctgsaggagc agcgtcttcc ccagaacagt tagcatcact tctccgatac 240  
 agaggataat gctgtccggg gtggagagag gagttcaggc ggctatcgtg aaaccacagg 300  
 ctgcctgctg tctgccatga gcccttttct cccccagctc acctgcagga ggacaggggc 360  
 agacgtgggc agcagaggcc caggtccaca ccggctggag ccacgtgcct gctgggtaca 420  
 agtcaggcca ttaatccgca cacctgaccc tcatcaaagg gcaagaagcg ctagggggct 480  
 gagtgagcaa ccgaag 496

<210> 342  
 <211> 481  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 302  
 <223> 18-771-302 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 283..301  
 <223> 18-771-302.mis1

<220>  
 <221> misc\_binding  
 <222> 303..321  
 <223> 18-771-302.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 461..481  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 290..314  
 <223> 18-771-302 potential probe

<400> 342  
 cttaaacaca cacttagagg gaaataattc aaactgtatc atgcttctat tatgagtcag 60  
 cagagaaagc cacctactag agactctgcc ttcttggcag agggaaaggt gagcattggg 120  
 ggtgaagcca ctggacagaa atgacctcac ctgcagacct gctgtgtcca aggtcaacag 180  
 agtgctgggc acccacagga aggacaagat taaaagagaa aaggcttcca ctcccacctg 240  
 ttttctccac cgcgtctata atcagtatag agtatagagt cctgtccact gtgctgcagc 300  
 crcatacaca gcccagaaag gatgtagaga tgggcactga ggtggcctcg cagagcgagg 360  
 gctgctcatg gtcaggctaa gggtcaggat gctctgggtc aaaagcccag gccaatggag 420  
 atgggtggca cagagctaca gaggaactgt gacacacttg ccaccaaatc ccatagtagt 480  
 t 481

<210> 343  
 <211> 449  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 53  
 <223> 18-827-53 : polymorphic base G or T

<220>  
 <221> misc\_binding  
 <222> 33..52  
 <223> 18-827-53.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 54..72  
 <223> 18-827-53.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 429..449  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 41..65  
 <223> 18-827-53 potential probe

<220>  
 <221> misc\_feature  
 <222> 431  
 <223> n=a, g, c or t

<400> 343  
 gtttgggatg gaaggcagta ggtattggca ggacagctat tgcacaaaat taktcattga 60  
 cctgaacatt ctcaattctt gtttctttgg aagttataaa ggcagatatt taacatgctt 120  
 taattaataa agttcttttg cactttcgaa gactattcga tggataaacac attccgtccc 180  
 ctgccttccc agcgtgggct gcctctggcc tagaaatgca aatgtttgct tggtcgtaaa 240  
 aaatgcgtag ccgagagctt caaaatgtga gcaagaacat catatttggt tgcaagtaac 300

tagcaaagca	gcagaaacat	tggctgactc	caataatctt	taatcattat	ccccttccct	360
gcagttttcct	tcagaaaccg	tttacctgta	atttgtagg	agacagctct	gagcttctca	420
ttatgagcct	ncactaattc	caccagctc				449

<210> 344  
 <211> 429  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 318  
 <223> 18-768-318 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 299..317  
 <223> 18-768-318.mis1

<220>  
 <221> misc\_binding  
 <222> 319..338  
 <223> 18-768-318.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 409..429  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 306..330  
 <223> 18-768-318 potential probe

<400> 344	
gtggaaatct	cattgcagtt catcactgcc ttgctctacc cgcagcctga tgatgtgctt 60
tccaggactg	aggccgggtg ccgcttgccc atggcacatc atcagagcat ggcttctgct 120
gcgctttctg	tggctggcat tgccagtttc ccagcaagct gggctcttaa ttctcccgct 180
aaccgcctct	tgccacctcc tgtcactcag ctcaggcagt ggctcggcgg ccgggggggtc 240
cttccaacag	ggtctgcctc cccaggccct tcctcttttc cctcctcatg gctgtggtcc 300
aggccctcac	tcctctcttc tcagcagctg ccacagcttc ctgcctgacc tcctgtagct 360
ggtcactcac	ctttccagaa cattctgtga actaccaaag tcacccttct gagacacaac 420
cttacctgc	
	429

<210> 345  
 <211> 450  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 26  
 <223> 18-769-26 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 6..25  
 <223> 18-769-26.mis1, potential

```

<220>
<221> misc_binding
<222> 27..45
<223> 18-769-26.mis2, complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 430..450
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 14..38
<223> 18-769-26 potential probe

<400> 345
agttatgctg agagcaccag gcacasgttg aacaccgcag tcttagaaac agcagaggga      60
agactgcctt ctcaggtccc cctcaggtga ggcagggaac gggccctcct cacctgagac      120
caagggggcc cagccttctc cctgcacagc tcaccccga ccagcccagg ctccagcagg      180
agagacaagt aaggcccaag tgtgcctgag tggaaaatgt ctgggacact gacctgtcaa      240
aactggcccc tggtcactg ggttcccatc aaatatagtg ggggatccat aacagagatt      300
cagagaggca ccgtggagtt ccagggtcat cggtcagcga ggaacaagga gggaaagggtg      360
tcttcctgcc ccttgatgct caactaagca tctgttcctt agaaatacat gtgtccaggt      420
cgtctccatg ggcttttctt tgcagatact                                     450

<210> 346
<211> 453
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 320
<223> 18-709-321 : polymorphic base C or T

<220>
<221> misc_binding
<222> 300..319
<223> 18-709-321.mis1, potential

<220>
<221> misc_binding
<222> 321..339
<223> 18-709-321.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 433..453
<223> downstream amplification primer, complement

<220>
<221> misc_binding

```

&lt;222&gt; 308..332

&lt;223&gt; 18-709-321 potential probe

&lt;400&gt; 346

ttagacgtgg	ctgcacttgg	ccaatgtgct	gtgaacccac	agtgagcggg	tccttgcgag	60
tgaagcttgg	tagaggagtg	tgtggctcct	tcaccacctc	ccctgccacg	gggtcccga	120
ggccatattg	agacaggctc	ctgtcagctg	gggccctgag	ggctcagagg	agcagacat	180
cctgatggat	acaggggccc	agatgggtggc	ttcggagata	agagacaaac	ctgctacctt	240
gctatccctg	caagcgaggg	gcacgccagg	ctgagggcgg	catggcaaag	gcggaggagg	300
tgttccccca	cagctctcty	gggaaacgac	acgtgcttcc	tgctaccagc	aggcagactc	360
ggatggaggt	ggaggggacg	agagtgtggc	aggcaggcga	ccaaaagtca	acgcagtttg	420
gtctctgatg	accccaaagt	aaaaaccagt	ccc			453

&lt;210&gt; 347

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 281

&lt;223&gt; 18-714-280 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 262..280

&lt;223&gt; 18-714-280.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 282..300

&lt;223&gt; 18-714-280.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..19

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 495..514

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 269..293

&lt;223&gt; 18-714-280 potential probe

&lt;400&gt; 347

acttgaagga	ctccgacagc	ctcatgggcg	actgtattaa	gccccagcaa	tcggagaggt	60
gggctccggg	gctgggtggg	tctcctctgc	caggtgggtc	tcctctgcct	gtgggtcccag	120
cagctcggca	gcaggggccc	gcccagatgg	ccgttggtca	cagagacagc	tgggctttgc	180
tgagtgcgtc	gtggtccagc	ctaggcccat	gccactgaag	cctttctcag	aggtgtgggg	240
tctgcaggga	ccggtcacat	gtgagcccag	gatcagggca	ytgggggaag	aaccagctga	300
ggacattccc	cagccccaaa	acaaaggcac	ggcagtcctc	gagcagggag	gagtgaggag	360
ccacatgtgg	gatcccgcct	ctctggcgctg	tgagctgtgg	atggcatctg	gtaccagccc	420
catgcccgtc	ggccgctggc	gagcttgacg	gctctgcagg	caaccggaac	agcatactgc	480
aggtgcacrc	gggkctcctc	tgccgagtgga	ttaa			514

&lt;210&gt; 348

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

```

<220>
<221> allele
<222> 271
<223> 18-843-271 : polymorphic base C or T

<220>
<221> misc_binding
<222> 252..270
<223> 18-843-271.mis1

<220>
<221> misc_binding
<222> 272..290
<223> 18-843-271.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 433..451
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 259..283
<223> 18-843-271 potential probe

<220>
<221> misc_feature
<222> 438
<223> n=a, g, c or t

<400> 348
ggagagacat ttgctttcag tggctcatca ataattcaca tagaaacgag catttctaaa      60
gcacagtgag gagacagagc tggaacagtt tcttgccagg acatatcatg ggcaactgga      120
acccaagtgtt aggcaagaca ggaaaaacca ccacctgcaa attatctttt ccctcaaattg      180
gataaacagg cgcaggggtgc ggtgaaagcc gtcattccgt tcagcagcag ccacgccgct      240
gagacggagc aacggccgag catacgcagc ygcactcacc accgctggta caggtagacc      300
agaaacacca cgtcgtcccg gaagcaggcc agccgggtgag acgtgggcat ggtgatgatg      360
aaggcaaaga cgtcatcaat gaaggtgttg aaagcctgca gggccagacg ggaggagggt      420
gaaccccgat tgctgggnct ggaatcctac t                                     451

<210> 349
<211> 460
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 265
<223> 18-850-265 : polymorphic base C or T

<220>
<221> misc_binding
<222> 246..264
<223> 18-850-265.mis1

<220>
<221> misc_binding

```

```

<222> 266..284
<223> 18-850-265.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 443..460
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 253..277
<223> 18-850-265 potential probe

<400> 349
gaagacatta ttgaatgctc ttagaagatt gtaarattgc tctctggaag tgtgggggaa      60
ggtggaagtg atatccatgc attgttagta gaaagccacg ctagagctca cacagccttg      120
cactttgata ggagtgggga ggggtgcagg ggaaggagar gcaaaccaga gtgtctgtct      180
tgaggcctcc atgggccagt gccccagccc tgtggtgagg gctggcactt cccagctccc      240
gtgccccagc tgtaccatct caggygctga gaacgcaccc atcccttccc agaggaatgc      300
ccgtgaatgc ctcggggctc tgccctccgc accaggatat tccctagccc tggctgctga      360
attgttgctg tcctgttgtg tgtttatttt tcatattggc tgaagaccaa gagggaagaa      420
gcacagaatt cctcaactcc cagtgtgccc atgagtaaga                               460

<210> 350
<211> 459
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 296
<223> 18-853-296 : polymorphic base C or T

<220>
<221> misc_binding
<222> 277..295
<223> 18-853-296.mis1

<220>
<221> misc_binding
<222> 297..315
<223> 18-853-296.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 440..459
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 284..308
<223> 18-853-296 potential probe

```



```

<220>
<221> misc_feature
<222> 441
<223> n=a, g, c or t

<400> 350
atgcccactg cacagatgag gagccgagggc caggaagggg tttgccagat gcctgggctg      60
gggccagggc tcaggaccac ccaactgaact gcctgctcgg cccaccctgg caagtgtgtg      120
caagggcccg gtggtgccga cgaggagggc catggggagg agatgttggt gtcctgagac      180
tcccagcccc acctgagggg gaagaggggt ggagagcaag gctgggagcc acccttgggg      240
gctgtgcatg tgccccctga cattggagga cacaggccac gccacacctg tgccayccag      300
ggagtgggaa ggaagcacgt ggccgtggag aggccagcag gtggcaggaa gggctgcaag      360
cccsaacca cggggtcaca cgtaggggac ccagcaccac atgcaggagc tggctgtgcc      420
ctgcatctgc acaggccggg ncatgaactg gcatcagca                               459

<210> 351
<211> 463
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 332
<223> 18-867-331 : polymorphic base A or C

<220>
<221> misc_binding
<222> 313..331
<223> 18-867-331.mis1

<220>
<221> misc_binding
<222> 333..352
<223> 18-867-331.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 445..463
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 320..344
<223> 18-867-331 potential probe

<220>
<221> misc_feature
<222> 424
<223> n=a, g, c or t

<400> 351
tgtgaactgc tctatgtctc cttgcagttc tatcagtttt tgccgaattc attatgaagc      60
tatgttatta ggtacataaa catttgtcct tttggtgaac tgatgctatc ataaaatgac      120
attgttttaga catgatctgt tttgaggatt cctatggcct gcatattagg tggcttgaag      180
tcccacagtt ctctgatgct tggttcattt ttttgtcttt tttctttatt tcattttgaa      240
cagtttgcac tgccatctat gtcttcaagt tcatgtatcc ttttctctcg agatgttgaa      300
tccaccctc ctctcaacca gtgcattttg cmtctgagac attgtggttt tcatctctag      360
aatttggtatt cgtgtctttt aaaaaatc tgatcatgtct ctattaaaca tattcagctc      420

```

cgcnttttggc tagctcttgg aatkgaggta acagttatga ttg

463

<210> 352

<211> 449

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 73

<223> 18-877-73 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 54..72

<223> 18-877-73.mis1

<220>

<221> misc\_binding

<222> 74..93

<223> 18-877-73.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 432..449

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 61..85

<223> 18-877-73 potential probe

<220>

<221> misc\_feature

<222> 377,402

<223> n=a, g, c or t

<400> 352

ctgataccac ccgaacacgc atttccttgc tctccacttg ttcaaagcct ttacacccac	60
tgccctgccat ccyacagctt ccagaacact gaggccatcg ggaacaagca cacaggcttc	120
cacagaagggt ctcaggtecc ggggctgaaa gcctttcctg agtgcgtgga ggcacatgga	180
cctcagacag ttcaggtcac tgcccggaaac tcacctcaat ggcggctcca acaccgccc	240
ggaccagcac cagcaggctc gtctgctcgt ccagcaggaa cagaaagatg accacgggtc	300
tgaagcagcg ccagagcact ggggacagga tggtcggggt gggaggggggt gcagggcaga	360
ccccacctgt gttcccncaa gtcacacaca taccctcagt cncctcatcc caaccacca	420
cgcccaagaa gcttcaggta ctccccagt	449

<210> 353

<211> 450

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 85

<223> 18-856-85 : polymorphic base C or T

<220>

```

<221> misc_binding
<222> 66..84
<223> 18-856-85.mis1

<220>
<221> misc_binding
<222> 86..104
<223> 18-856-85.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 430..450
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 73..97
<223> 18-856-85 potential probe

<400> 353
ctgcttcctc tctcaagaca gcacctctcg aatctggccc caagtgagac acagcaacag      60
cgacacatga gagagactgt gattyggggg aaaagctgct gtcggcacac gtgtctccat      120
aaccactgga acgcaggcca cactggcac agctgcgccg caaagcctgc cccgggcctc      180
taacaagaca gatctgcaga cagacacaca gggcagcctt ctgcagctgc ctgcccctgt      240
ccaccatctc ctgaatgcct gcaaggagtc agcggcatga ggcttcacaa gaggtgacca      300
cgagctgggtg ccacagctca cacagctctg tatggggcat ttagcagaa cttgctgtcc      360
tgaggtttgt cagcagcaca ccagcaaact ccagcaaaca gagaaagagg ttggaattgc      420
agggggccgac agagaaacta ctcagggata                                     450

<210> 354
<211> 480
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 101
<223> 18-861-101 : polymorphic base C or T

<220>
<221> misc_binding
<222> 82..100
<223> 18-861-101.mis1

<220>
<221> misc_binding
<222> 102..120
<223> 18-861-101.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 462..480
<223> downstream amplification primer, complement

```

```

<220>
<221> misc_binding
<222> 89..113
<223> 18-861-101 potential probe

<400> 354
ccctcaaattg gataaacagg cgcagggtgc ggtgaaagcc gtcattccgt tcagcagcag      60
ccacgccgct gagacggagc aacggccgag catacgcagc ygcactcacc accgctggta      120
caggtagacc agaaacacca cgtcgtcccg gaagcaggcc agccggtgag acgtgggcat      180
ggtgatgatg aaggcaaaga cgtcatcaat gaagggtgtg aaagcctgca gggccagacg      240
ggaggagggt gaaccccagt tgctggggct ggaatcctac tgtttttggt aacctaacca      300
agccaacggc ttttggcaga tgcttggaac taactggaac tcctcacagc aacaacaaaa      360
agagcagaaa gccggcaagt ggagatacgg agctctgttc cctcatgggc tccccacagc      420
tgctggcacc cgacacactg cgggtcttgc ccaggctccc acatcgggga accaaagaga      480

<210> 355
<211> 465
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 323
<223> 18-635-323 : polymorphic base A or G

<220>
<221> misc_binding
<222> 304..322
<223> 18-635-323.mis1

<220>
<221> misc_binding
<222> 324..343
<223> 18-635-323.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 445..465
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 311..335
<223> 18-635-323 potential probe

<220>
<221> misc_feature
<222> 81
<223> n=a, g, c or t

<400> 355
gataattgtc tcagggttaag cttgagcata acatgcacca tgacacatat gatataaggc      60
aatgaggcca sggagtgggtg nctcacgcct gtaatcccg cactttggga ggtcgaggca      120
gcactttggg attgcttgag cccaggagtt cgagataatg caatgcaaac atttttgtgg      180
ccaccagaaa gaaattgatc tacaccagtt ctttggaac tgaattatcc atggcaaaaa      240
aaaactatat tccatattca gttttcaatg ttgctgaaat tatctgagat ttccatccaa      300
gttgacatct taaaacttta tctgatcat cactcccttt actatgtagt cttatttgge      360

```

catatTTTgc ttacccttat caactaagga gccagtgtaa atctctgagt tgcagatctg 420  
 gaagtgatgt 'gaagaaatgt tatagaggga gtgtacttat cagtg 465

<210> 356  
 <211> 493  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 205  
 <223> 18-636-205 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 186..204  
 <223> 18-636-205.mis1

<220>  
 <221> misc\_binding  
 <222> 206..225  
 <223> 18-636-205.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 473..493  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 193..217  
 <223> 18-636-205 potential probe

<220>  
 <221> misc\_feature  
 <222> 36  
 <223> n=a, g, c or t

<400> 356  
 cgcccttagc ataagatgca tccatttget gggcctgtg ctgtaatcag agggccttag 60  
 cctggccttc cttctgctgc cctccacca aggaagtaag gagttggccg ggccaaggga 120  
 gcagctttgc tcccctctct aaactacatt ttgcatctgc tggaccccca cattctctgt 180  
 ccaaatggct ttgaaccac ttccyggcca cacaagcctc ttcctgggat gtgctgcagg 240  
 catacacacc cttaggccta aggagttaa ccaagaggca gcaatgagag gtgtgaagag 300  
 acttgtgtag gaggaacttg ggtaagcagg ctgcgggtcca gggctcacga cggctgctca 360  
 caggtcccctg gagatggaag gacatgggga aagaagaggg ccaaccata tccaaggagt 420  
 tcaagaattc taaattcaac ctgaccttc aggctgttat ggagggatat ctgtcaagg 480  
 aaaggagata gct 493

<210> 357  
 <211> 589  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 427  
 <223> 18-649-427 : polymorphic base G or T

```

<220>
<221> misc_binding
<222> 408..426
<223> 18-649-427.mis1

<220>
<221> misc_binding
<222> 428..447
<223> 18-649-427.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 570..589
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 415..439
<223> 18-649-427 potential probe

<220>
<221> misc_feature
<222> 536
<223> n=a, g, c or t

<400> 357
tctgtgtaat gcccaacgat ttttcattag ctgggagctg ttttagggac attttacagg      60
ttaatgactg tgggagagga gaataaaaatc aaaactgcaa gaaccattt ttgtcttcat      120
aagcattgca ttttaaaata cgagggcctg aagacttctc agaagagaca ctactactg      180
gagttaaagt tatatgaagt ccctgagccc ttaatcatcc aagactggac ctaagcagtc      240
ctcttcgttt gtagtctctt tcaatatctg cttatcaagg acaacgagaa tatcttagtc      300
tactaattaa tcttttttat caccatagtc taccaagaaa gaaagctgat aagataataa      360
agatgattca ttcctcagag taggaaaaaa taaaaagaaa aatttaaaaa gatgctaaat      420
atgagckctg agtctcaaca ctgtctcaag atgaggcaga tgtcaacttt cttgcctatt      480
ctgcttgcta tttaggcata tctcttgagc aaaaccagtc atttgtcttc tcattntycc      540
aaaaattaaa ttcaagaaca aattgttgag gaagggttatt agaatctca      589

<210> 358
<211> 432
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 316
<223> 18-1134-316 : polymorphic base A or G

<220>
<221> misc_binding
<222> 297..315
<223> 18-1134-316.mis1

<220>
<221> misc_binding
<222> 317..336
<223> 18-1134-316.mis2, potential complement

```

```

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..432
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 304..328
<223> 18-1134-316 potential probe

<400> 358
catcttggtg tctacgtttc tggggctgag aagatatttt gctccacacc tgccagcatg      60
ccctttccag ccctgaggtg caccagtgag tgtgtgtccc ttctccagct ttcctggggg      120
aaaagtacca cctttggatc aaggcttgct ggctgcggtc cagaggatct gcgcagagga      180
agcagtgtgt cctcaggaga tcctgaagga ggggaggggg gactcttcct acttgggaact      240
ctttgtttat tggttaatga aaggggcaaaa ataagtccct ttctaaaatt ttagttttaga      300
gtttaagttg gaaggraaaa aaaaagaaaa gaacacattt gaggattaac tattttattga      360
cttttctctg aagttctcaa ttgaaggtta aactcagggg ttttccaggc tggggtaaaa      420
ctcaaccaac tg                                     432

<210> 359
<211> 432
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 316
<223> 18-633-316 : polymorphic base A or G

<220>
<221> misc_binding
<222> 297..315
<223> 18-633-316.mis1

<220>
<221> misc_binding
<222> 317..336
<223> 18-633-316.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..432
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 304..328
<223> 18-633-316 potential probe

<400> 359
catcttggtg tctacgtttc tggggctgag aagatatttt gctccacacc tgccagcatg      60
ccctttccag ccctgaggtg caccagtgag tgtgtgtccc ttctccagct ttcctggggg      120

```

aaaagtacca	cctttggatc	aaggcttgct	ggctgcggct	cagaggatct	gcgcagagga	180
agcagtgtgt	cctcaggaga	tcctgaagga	ggggaggggg	gactcttcct	acttgggaact	240
cctttgtttat	tggttaatga	aagggcaaaa	ataagtcct	ttctaaaatt	ttagtttaga	300
gtttaagttg	gaaggraaaa	aaaaagaaaa	gaacacattt	gaggattaac	tattttattga	360
cctttctctg	aagttctcaa	ttgaaggtta	aactcagggg	ttttccaggc	tggggtaaaa	420
ctcaaccaac	tg					432

&lt;210&gt; 360

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 425

&lt;223&gt; 18-489-425 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 406..424

&lt;223&gt; 18-489-425.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 426..445

&lt;223&gt; 18-489-425.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..20

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 515..533

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 413..437

&lt;223&gt; 18-489-425 potential probe

&lt;400&gt; 360

tagcctctat	gctcacgctg	gtccctatct	tttccaccct	tcctggctgg	ccccagtggtg	60
tcctaacaca	gagctgccct	ctctgaatca	ccgaaccgcc	caccttgggg	ccctggggcg	120
gcactagttc	cctgagtcac	tccgtgagcc	cggtaacaca	tcctgtgccc	caggctgaag	180
ttcaagcggg	aggcggggccc	aggagaacct	gtctgactgg	tccccaggca	ggteccatgg	240
tggccagaac	agagttcaag	gggaactgca	ccaccgtcag	accctgtgag	tgtggggggcc	300
tgttgctcctg	gggcagcagg	cagcagggcc	tgcaggggtc	atcagggacc	ctggcaccct	360
gggactccag	aggagccccc	cagccctatc	tgggcatatc	ccagggttcc	cagcccccctg	420
gaaayggggt	gataacagct	tctcctgtaa	gggctttgat	gcctggctct	gggtccctgt	480
cccagagctg	agcacctgct	ggcccggacc	ccacctttct	tgctgcccac	ggt	533

&lt;210&gt; 361

&lt;211&gt; 485

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 212

&lt;223&gt; 18-492-212 : polymorphic base C or T



<220>  
 <221> misc\_binding  
 <222> 193..211  
 <223> 18-492-212.mis1

<220>  
 <221> misc\_binding  
 <222> 213..231  
 <223> 18-492-212.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 465..485  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 200..224  
 <223> 18-492-212 potential probe

<400> 361  
 agtcggggag acaagcatag agccacaggc gtgatgacaa acaggacaca gatggcagga 60  
 aggaggccag ttctaagcgt ttacacacgg ggcagctctg ctgggcacac aggtccccc 120  
 cgggggctgc agagggccct acctggggct tgctcaacag ggctggaaac cccagcaaa 180  
 ggctggaact gctgcaagaa gccctgccct tyggggctga tccggtgtga taaaggggga 240  
 ccaggattct ggcaggggat tcgactgcga tccagtaatc caggagagagc cagtacaggt 300  
 gcgtagagac aggccaggca gcaccaggta ggccacacgc ttgggcagcg cctgtggaca 360  
 ggctgagagg acacctggag gccagcctgg gagacccac aggctgcagc caggccccgc 420  
 gctcatctct ggaccagggt gctggccact cacctccatc cagcctctgg gaatctaaag 480  
 gaatg 485

<210> 362  
 <211> 570  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 156  
 <223> 18-488-156 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 137..155  
 <223> 18-488-156.mis1

<220>  
 <221> misc\_binding  
 <222> 157..175  
 <223> 18-488-156.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind

&lt;222&gt; 550..570

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 144..168

&lt;223&gt; 18-488-156 potential probe

&lt;400&gt; 362

tgtctagcct	cactcggggc	actcaggggc	ctcgccagtg	gggctgggtt	gggggvatgc	60
acaagatggg	gcctcaggag	gaagatctgc	aggagacaca	tgctttcttt	gcacgagcag	120
tggcttgctt	gggggagagc	aggctgggcc	cagagyggcc	cttccccacc	ccatctcctt	180
ggctcctgtgc	cgtttctgcc	ctgggtgtctg	gtctgggggtg	tgcacccac	ttctgccacc	240
cattttgcac	ctgcacaggc	agctggctcc	ccagttccca	acaggccacc	cagccaggcc	300
cctggcccag	ctccccaccc	atctccaccc	accacagggc	ctcctcagtc	ccccacactc	360
ccagacctca	ggtggtgcct	ccagagcgag	ctgtgtccac	acagggtctt	actggaatgc	420
ctggctcttt	ggagaggctg	aggctgactg	aatgggtctt	gggcagcagc	tggcacggat	480
gccatcctgg	ttggggctca	cctccaagag	aagcgtgtcc	ggcagggtacc	ggtccttcca	540
gtggtcgagg	aagaccatgt	ccagtgtgtc				570

&lt;210&gt; 363

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 266

&lt;223&gt; 18-491-266 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 247..265

&lt;223&gt; 18-491-266.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 267..285

&lt;223&gt; 18-491-266.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..20

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 430..450

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 254..278

&lt;223&gt; 18-491-266 potential probe

&lt;400&gt; 363

ggtagagcca	tacaatgagg	tatgattcag	ttattaaaat	gaataaagta	cagatgaatt	60
cacgggttc	caaaatggat	gaaccttctg	caccggctgc	ctggccatcg	gctcgcaagc	120
tcatgagacc	cccgtagggt	ccacattccc	tcctctgtga	aacggctgat	ggctttacct	180
ctccagacaca	gtagagggca	ggcatgatcg	tgcccacaca	gcacctgcac	atgcttgcca	240
catgcacgcc	acatgcagat	gcacgygtga	gggcattcctc	agtgcctcac	agtgcggcca	300
ggacacagggc	agctgggctt	gacacctctg	gctctaaaga	gcatgaagct	tctgggcctc	360
agtgccaggc	ctgcccgaagc	ttctctgccc	agcagtctgc	tgcagagcta	gagagtccat	420

cacctctgtc acctgktagc tattctctct

450

<210> 364

<211> 435

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 141

<223> 18-497-141 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 122..140

<223> 18-497-141.mis1

<220>

<221> misc\_binding

<222> 142..160

<223> 18-497-141.mis2, complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 416..435

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 129..153

<223> 18-497-141 potential probe

<400> 364

ctcatgttgt	cagtagttac	caagtaaaat	ctgttttttc	tgcatctaact	agtgtctcac	60
tgggctctgc	agggcagctc	ctacgggtccc	tcaggcttgg	agggtcactt	taaacaataa	120
aaagcaacag	gacacaaaaa	yccctggctg	gaaaaatcca	aaaagcaggt	ctgttagcag	180
ggcaggcccc	gagtgacttc	ccctttctct	aacattccca	cgtggtcctg	cacaccacac	240
atccccccga	ccctggggag	tcctggggcc	cttccctggg	gagcagcctc	tctcttgacg	300
ggaaaaggccc	tgggggtacc	caaggcctcc	aacagggagc	ctgttggaga	agtcaccaag	360
gccctctgag	tctggggctc	cacagaccct	ccccaggcc	tcctgcaact	ctccagctct	420
gagagtctga	tccca					435

<210> 365

<211> 475

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 174

<223> 18-503-174 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 155..173

<223> 18-503-174.mis1

<220>

<221> misc\_binding  
 <222> 175..194  
 <223> 18-503-174.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 455..475  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 162..186  
 <223> 18-503-174 potential probe

<220>  
 <221> misc\_feature  
 <222> 57,422  
 <223> n=a, g, c or t

<400> 365  
 agtgcgtgcat tctcttgggc cttgctatga gctctgggct cctgctcttt gctggcntgt 60  
 accaggcagt gggttcaaag aggagcagaa aattaatgga caatatgtca gaaggcagag 120  
 gcaagacaga cacttgctgg ggccaagccc tgcaggtgga gagggatgac ctgrctaaag 180  
 tgggtgaaag gcaagggttat gaggttctcc aggacactgg agtgcacagg tgggtgtgtcc 240  
 ccaggtaacg cctgccaccc agcccttcct ccacagaaac agcatctgcc ctaccacact 300  
 ttgagggtact ttggggtcct tccttcccag caggctaccc aagcccttcc aagtgtctaa 360  
 aggcagattt cctatgcttg caaacgactg ccctatgccg gtgtttatca gcccgagagg 420  
 gntcctgggt gtgcacaggg ggcgagcaag ctgcccaaga taagcacatc catac 475

<210> 366  
 <211> 501  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 95  
 <223> 18-490-95 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 75..94  
 <223> 18-490-95.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 96..114  
 <223> 18-490-95.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 481..501  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 83..107  
 <223> 18-490-95 potential probe

<220>  
 <221> misc\_feature  
 <222> 239  
 <223> n=a, g, c or t

<400> 366  
 tgtgaaccac aagaggaggg aaccactctg ctcaagttgt atttcccctg aagagtcctt 60  
 agtaccttgg aaatgatgtg taagaccaag ggctrgttta ycaagaacat acacaaacca 120  
 gtaagaaaaa gatgatgaga cagataggtc acagtggcca acatgcagct cacaggaaaa 180  
 ggccaaaggg cagagccccg agcagggtgat ggaacccggg gcagggctca gtgacagtng 240  
 ggggtgcccct gtccacagct gcaggagtgg gaatcgtgct gccttctgct gctacccttg 300  
 ggaaggggtcc caggcctgca gggaaacccg tggcccactg tgtttcccag cggggcagga 360  
 cgtgccatga cccacagggc tcgtggggaa aaaacaagag atgggtgcttc cctaaggaca 420  
 gtgtccttat tctggcagga agatgacagg gggaaccatg gtggagaggg accatgcaga 480  
 cctgaagcag ccagaacttt c 501

<210> 367  
 <211> 448  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 114  
 <223> 18-699-115 : polymorphic base G or C

<220>  
 <221> misc\_binding  
 <222> 95..113  
 <223> 18-699-115.mis1

<220>  
 <221> misc\_binding  
 <222> 115..134  
 <223> 18-699-115.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 428..448  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 102..126  
 <223> 18-699-115 potential probe

<400> 367  
 ccattcttct ctcataataa ctgagagtga gatgaacata ttctactaaa taaagatggg 60  
 atgagaattc ttaacttcat actttgctgt ttttccctta ccgacctec agcsaagaaa 120  
 actgtgttaa actgttcaga aaccagcaa atctggctgg aaagagaaca ttatgtccaa 180  
 gccacaggaa gcatgaaaag gaaataaaaag aatttctctg gaagtataaa gttagaagtg 240  
 ttaagatgcc ttggaagcca ggaacaattg aaatattttc aaagcacaaa gtttctgatt 300

tcctcaaagg caaaatattt gagtaagact taactatatt ctagcttcta atatattagc	360
ttattttatt ttcaccctgt atttggtga cttaggtgca gacattctag taataatgag	420
atatttggag tattagcatg gctattta	448

&lt;210&gt; 368

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 293

&lt;223&gt; 18-1099-293 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 274..292

&lt;223&gt; 18-1099-293.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 294..312

&lt;223&gt; 18-1099-293.mis2, complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..19

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 459..478

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 281..305

&lt;223&gt; 18-1099-293 potential probe

&lt;400&gt; 368

ttgatgtact cgcctaccc cggttcaact gctaagtac agcctcacag gggcagctgc	60
tggaaatcttg ggacaggaag gctggagagt gagagtctgt ccaagccctg ctgagatccc	120
aattgagagt gttggtacag acttggtccc ctctagatag gacaaaaacc ttgagactgg	180
aaattcttgg agaagatcaa aacgctggga taaagctatg aaccaaagca aggggaagat	240
ttttctgag gggacctgtg agtctccctg ccatctgggg agagaagaat gtygggcaga	300
gtcctgtcta cctgtgaatg tggaagaaga gcagtggatg tgagatacac aaactgtagt	360
gtctactatg acaatgaatc ttgcaataca catattcaat tttgaattaa gaatgttata	420
cgataaataa tggtttctaa aatagaaaag tcatgtaagg ggaaagactg ataaaatc	478

&lt;210&gt; 369

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 22

&lt;223&gt; 18-1105-22 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 3..21

&lt;223&gt; 18-1105-22.mis1

<220>  
<221> misc\_binding  
<222> 23..42  
<223> 18-1105-22.mis2, potential complement

<220>  
<221> primer\_bind  
<222> 1..18  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 456..476  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 10..34  
<223> 18-1105-22 potential probe

<400> 369  
ttctctcaag catagtggcc trtgccccag gaatgtagca taatgcatat ttacatctat 60  
ctctgtatag gcagggtgtag attaaattgc aacataattg gcacagcatt tgtctctatc 120  
ttaatgatga tacagatgga aaactaaaaa agatgagaga tttttcttct aaaaaaaact 180  
tttaaagtta tggagttaga acatatagtt actgtagacc caatcaccac aagtgttagc 240  
aattgtccat gtatatacag agacttaaag gcaaattgag aggcaagcag ttaattatct 300  
aaatgctgta gagctatgta gcagcccaga gataaagggt aacgggaaag ttttcaatca 360  
caactttatt atgtagggtat acaccataag ctaaacttaa ctcaaacata atccaccttc 420  
agacctctga gcagcaagtt atatagggaa ggaaggatga cacaagtttg aatgac 476

<210> 370  
<211> 495  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 418  
<223> 18-562-418 : polymorphic base C or T

<220>  
<221> misc\_binding  
<222> 399..417  
<223> 18-562-418.mis1

<220>  
<221> misc\_binding  
<222> 419..438  
<223> 18-562-418.mis2, potential complement

<220>  
<221> primer\_bind  
<222> 1..20  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 475..495  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding

&lt;222&gt; 406..430

&lt;223&gt; 18-562-418 potential probe

&lt;400&gt; 370

acttgcatg	tggatgaggg	gaagcacagg	cagaggtgag	cgctggggtg	ctggcgagggc	60
attttcctga	catcgctggt	ggggatggtg	gaccaagtgc	agagctgggg	tctgaggcac	120
gaggggaact	ttcttttcct	cttccttaag	cctggggatg	tggccagaac	cttggggagc	180
tgtggaggcc	actgtgagct	gcagacagag	tccaagaagc	gggtgaagac	cctgcggtcc	240
atctctttgc	tcctttccct	cttcccacat	ttaacaatta	gtttctccca	tggggggccc	300
atcaagtc	ctcctcaa	ctggccagtg	cttcatccac	tgctgcetta	tcttctcccc	360
agaaaatact	tcttccccaa	ctgtgaggat	tatgctccga	aactaccccc	cagcaccygg	420
tagactttca	cagctgagag	acattgacct	caaagtttag	gttgcaagt	agtccacaga	480
accacttccg	cacat					495

&lt;210&gt; 371

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 204

&lt;223&gt; 18-564-204 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 185..203

&lt;223&gt; 18-564-204.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 205..224

&lt;223&gt; 18-564-204.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..18

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 456..476

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 192..216

&lt;223&gt; 18-564-204 potential probe

&lt;400&gt; 371

tcacgcattg	ctttgaacac	agcaggtact	cactacatag	tggttgattg	ataccttggt	60
cacacctccc	tagaagtggg	cacctattgt	cttgccctgcc	aaacctatct	tccttctctg	120
gaagctgttc	cctgtctctc	taccccgctc	tcccccatcc	tcattgtaac	gatggaagac	180
ttccttctct	acagcccccg	cccygccatg	cagctctctc	tcagctccag	agaggaagct	240
acagtgtctc	accaagctct	tggaggagag	cagcagttac	agccaacatt	tattgaacat	300
gtgccagaga	ctgttccaga	tggtacataa	actcttaatt	caagctcatt	aaacctgac	360
aagatcccta	caaggcaggg	aatattttta	tcccattttt	acacaggagg	agaccaaggg	420
agaggcctcc	cggctgctgc	gtctcccatg	cagtacatag	gtttatcaca	ctccaa	476

&lt;210&gt; 372

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens



```

<220>
<221> allele
<222> 261
<223> 18-1032-262 : polymorphic base A or C

<220>
<221> misc_binding
<222> 242..260
<223> 18-1032-262.mis1

<220>
<221> misc_binding
<222> 262..281
<223> 18-1032-262.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 447..467
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 249..273
<223> 18-1032-262 potential probe

<400> 372
ccactcaaat tctgatagac atttttccct aacctaaaat atttttatat ttaaaagtct      60
ttactcatca aacacacgca catcaaaaat gtgtagaaaa ttgaagttaa tttttatttc      120
acgtcaccac tatgccctaa tagtttcata aaattatact ggattgagct attattagaa      180
ttattactag tatacaactg agaaaaatat tatgtataca gtataaatat taataatttt      240
aatatataaa tggtaaaaaac maaatccatg gggaaaacat gtctaacaaa atatgcagaa      300
gtttctcttt tttcccagtt ttctcatgtc catggataga tattgcctat tggtttaata      360
gttgagtatt cataatcgat tcctactctt ctttttatat cgtatgcact gagaaaactt      420
gtcacataaa ataggtaggt gggaaatggga agaggttttg tacagta                    467

<210> 373
<211> 466
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 412
<223> 18-1035-412 : polymorphic base A or C

<220>
<221> misc_binding
<222> 393..411
<223> 18-1035-412.mis1

<220>
<221> misc_binding
<222> 413..431
<223> 18-1035-412.mis2, complement

<220>
<221> primer_bind

```

```

<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 447..466
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 400..424
<223> 18-1035-412 potential probe

<400> 373
cagatatgat ccactggaaa caggatcatt aacgcctttg catctaataa ggtcagataa      60
ttgattccag aaaactcaga accaattgag aaaattcctc attaataattc agcttcccct      120
gggcactctc agggcagctg gttaagccat tctctgtaag gtttactgtc tttgaacctg      180
aagcctctag tccacaggtc agagcaagga cagctggaat ccacaatcat gagctacaga      240
gcaggataga ctgaaccagg tcagctcttg tctctgacct tgatgggtgtg gatgccctgc      300
catcagcctc cccactgagc ccagctcacc tagggggaga gggagcttct aaaatgcaaa      360
tcgcatacaga tcaactactct gcttaaactc ttcagcagct cccagtgtcc gmagacagtc      420
cagactcctt actggtatga ggatccctcc tcctccatt tctcct                        466

<210> 374
<211> 484
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 293
<223> 18-1036-293 : polymorphic base A or C

<220>
<221> misc_binding
<222> 274..292
<223> 18-1036-293.mis1

<220>
<221> misc_binding
<222> 294..313
<223> 18-1036-293.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 467..484
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 281..305
<223> 18-1036-293 potential probe

<220>
<221> misc_feature
<222> 463
<223> n=a, g, c or t

```

```

<400> 374
acaacacacc ttttctcctt aaattcatat ttccactcaa attctgatag acatttttcc      60
ctaaccataa atattttttat atttaaaagt ctttactcat caaacacacg cacatcaaaa      120
atgtgtagaa aattgaagtt tatttttatt tcacgtcacc aatatgccct aatagtttca      180
taaaattata ctggattgag ctattattag aattattact agtatacaac tgagaaaaat      240
attatgtata cagtataaat attaataatt ttaatatata aatggtaaaa acmaaatacca      300
tggggaaaac atgtctaaca aaatatgcag aagtttctct tttttcccag ttttctcatg      360
tccatggata gatattgcct attggtttaa tagttgagta ttcataatcg attcctactc      420
ttctttttat atcgtatgca ctgagaaaac ttgctcacat aantaggtag gttgggaatg      480
ggaa
484

```

<210> 375

<211> 484

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 95

<223> 18-1038-95 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 75..94

<223> 18-1038-95.mis1, potential

<220>

<221> misc\_binding

<222> 96..114

<223> 18-1038-95.mis2, complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 466..484

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 83..107

<223> 18-1038-95 potential probe

<400> 375

```

gccacaatga atgttgagga aaaagtctgg atatttaaga atgatcctta caatccagat      60
gtcaattctg taaactgtga atagcagttt gtcaytgata cttaagagtt gagaggctaa      120
ctccattgct tctagcaact aacaaaatgg ggattccatc tgaggaagta aattctgggt      180
gattatgaag tatgaggctt ggaatggaaa agggatggat gaatagcttc atgtcagctt      240
cccaatacta ttaggtgttt ttaaaccaag tatatgttgt ggtaacaaat atgaaatttt      300
taaaagaaaa caaaaataat caacatatac acatataaaa aatgacattt atgattttta      360
gataaacaag ttactacctg aaaggggtctc agagattgat gatttattag gagaactgag      420
aacggcaaat gatacttgaa gtgggttctat gttttcctaa acaaaggaaa agacagaagt      480
taga
484

```

<210> 376

<211> 455

<212> DNA

<213> Homo Sapiens

<220>

<221> allele  
 <222> 361  
 <223> 18-1040-361 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 342..360  
 <223> 18-1040-361.mis1

<220>  
 <221> misc\_binding  
 <222> 362..381  
 <223> 18-1040-361.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 437..455  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 349..373  
 <223> 18-1040-361 potential probe

<400> 376  
 ttcagacagg gggatcaact caagaaaaac cttgacagtt ggaaagtagc ctggtatatt 60  
 tgagggatct gagacagaat cagtttcatt agggttccct tttgaagtaa tgggaggtga 120  
 ggttgccag ataagggtat acctcaaatg cctgtaggta gtgaggggaac cttcttaatc 180  
 aaaggaataa cagagaaagt gctgcttcag ataaccaagg ccaaggctga gttttgaatg 240  
 ctgtctgggc ttagcttcca atgactgagg gagttatttc cctggatgaa ggtatgttct 300  
 tatttcaatt gattcttaaa gtacttttta ttaatattta ttaaggagag ttatccaact 360  
 rctcatgaag tttaggcggg tacactaggg caagatatgt ttccctcatc ttctcatcta 420  
 ccaccttctt gaagtcctgr aaatctaagg aatgg 455

<210> 377  
 <211> 403  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 356  
 <223> 18-748-356 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 336..355  
 <223> 18-748-356.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 357..375  
 <223> 18-748-356.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..20  
 <223> upstream amplification primer

```

<220>
<221> primer_bind
<222> 383..403
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 344..368
<223> 18-748-356 potential probe

<220>
<221> misc_feature
<222> 27
<223> n=a, g, c or t

<400> 377
gagctgggttc acattgatac tgaaagnaag acaacccatt agatgctgtt acaaaaaata      60
ctatcagaaa agaagagcca aaagaagagc caaagttatc catccacctg acctttttcc      120
catcctccat cttgtctttt tctcctctag ccaccagggg gcactttggg gctagctcct      180
tgaggacact ggagattctg agctttcaca agtacctcaa tattggcggg ggggtcagtg      240
gatggggatg gaatgaatca gaaagtagag ctaaaggaga aacctaggga ttctgtagag      300
cagaaagggtg agttcccaaa atcttcagct caaatatacc cctctaattc aatcaytaaa      360
tgctgaattc actaagaaac taccgagcc cgacagattt tta                          403

<210> 378
<211> 448
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 179
<223> 18-937-181 : polymorphic base A or C

<220>
<221> misc_binding
<222> 160..178
<223> 18-937-181.mis1

<220>
<221> misc_binding
<222> 180..198
<223> 18-937-181.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 428..448
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 167..191
<223> 18-937-181 potential probe

<400> 378
cccaatctct ctacccaac ccacttccaa catcctccca tgatagcaga atgatctctc      60
tgaagggttca atgacaataa tgaacatgaa aacacttcgt aatacggtac acaaatagca      120

```

acacctacct	atacacaaat	gtaccgatgt	ggcaggagag	acagaaatgc	tgtctttamt	180
cactgttgac	tatgcaggtg	taaagggcag	tgcattgcaa	gggaatgaaa	tcgatagact	240
aagaggaatg	tttctgggaa	ataatggctc	aagttggcac	acacagtatt	ggaaccctca	300
aacgagtcaa	aaaggcattc	aagggtggact	tgcctgcttg	gcaattgtat	gtcactgtga	360
taaacctgat	gagagatgta	agatgtagat	ctaattatgc	ctatTTTTca	ggtaactgag	420
gctgagagag	gcagtaattt	gcagaaga				448

&lt;210&gt; 379

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 175

&lt;223&gt; 18-942-175 : polymorphic base C or T

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 156..174

&lt;223&gt; 18-942-175.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 176..195

&lt;223&gt; 18-942-175.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..20

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 431..449

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 163..187

&lt;223&gt; 18-942-175 potential probe

&lt;400&gt; 379

gactcctgtg	tttctgagcc	ctggataatt	tcacacacat	gtctggtttg	gggctccaca	60
ttttcagaaa	aatatagaaa	tcttggagga	ggtccaggg	agaccaaggg	aaatgattaa	120
tgggttgaaa	gttggagttt	atgaagaaag	gttgtgagat	ctgatctttt	gctaygagaa	180
aagtctgagt	ggtgacttaa	taacataagg	aggttagtaa	gcagctgttc	tccatcttca	240
ctaagggtga	atgaaatgaa	ataagatata	aattgcaaca	ggaacaaaaa	tgcattacaa	300
gtgaggactt	ccaagcacca	gcattgctgg	attctagata	gctcccaaaa	agaaggatgt	360
gtagtctact	tccttggtct	gcaatgacag	gcctataaat	agtgagaaag	atgagataat	420
ctcttaagat	cccttctgga	cctatcttt				449

&lt;210&gt; 380

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 221

&lt;223&gt; 18-1213-221 : polymorphic base A or T

&lt;220&gt;

```

<221> misc_binding
<222> 202..220
<223> 18-1213-221.mis1

<220>
<221> misc_binding
<222> 222..241
<223> 18-1213-221.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 434..452
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 209..233
<223> 18-1213-221 potential probe

<220>
<221> misc_feature
<222> 403
<223> n=a, g, c or t

<400> 380
ctttcgggtt ctcatttgcc tgtagccaag acccttgaag agaacttata tggctagggt      60
ccagaggaca ttttcaatta tccatttgat gaactctgtc aaccgtctac ctgtgtttct      120
gctttaaagc tgaattttct ttcattagt tcaaccaatt tgtgcagacc ttaaaattta      180
gaataaagaa taagacagca gtaccgtact taacttggag wccctggacc tcctcggagc      240
ataaaaatca cctgggtgag tgttaaaatg aaggctccctc ctcttgaaat tgtgatttag      300
taggggtggg gcagggccca ggagttataa ttttaataaa taccacaagc aattcgaabg      360
cagacaatcb gaagtcacac tttgagaaac actctcttgg ggntacaaca ctgggtatca      420
gaggaatctc ccaccaagcc cacacccaaa tt                                452

<210> 381
<211> 448
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 145
<223> 18-937-147 : polymorphic base C or T

<220>
<221> misc_binding.
<222> 126..144
<223> 18-937-147.mis1

<220>
<221> misc_binding
<222> 146..165
<223> 18-937-147.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 428..448
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 133..157
<223> 18-937-147 potential probe

<400> 381
cccaatctct ctacccaac ccacttccaa catcctccca tgatagcaga atgatctctc      60
tgaagggttca atgacaataa tgaacatgaa aacacttcgt aatacgttac acaaatagca      120
acacctacct atacacaaat gtacygatgt ggcaggagag acagaaatgc tgtctttact      180
cactgttgac tatgcagggtg taaaggccag tgcattgcaa gggaatgaaa tcgatagact      240
aagaggaatg tttctgggaa ataatggtct aagttggcac acacagtatt ggaaccctca      300
aacgagtcaa aaaggcattc aaggtggact tgcctgcttg gcaattgtat gtcactgtga      360
taaacctgat gagagatgta agatgtagat ctaattatgc ctatttttca ggtaactgag      420
gctgagagag gcagtaattt gcagaaga                                     448

<210> 382
<211> 473
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 407
<223> 18-946-408 : polymorphic base C or T

<220>
<221> misc_binding
<222> 387..406
<223> 18-946-408.mis1, potential

<220>
<221> misc_binding
<222> 408..426
<223> 18-946-408.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 453..473
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 395..419
<223> 18-946-408 potential probe

<400> 382
aattagtttt tgtgtgcgga caagatggaa ggtaatggaa atttggcttg caaagtagtt      60
ctaactgatg ctacatccac aatctgggta taatgctata agaataattat gtgggaatag      120
tagttcaaat cagtatttag tatgaacata aagggacaaa caatgcaaag ctaacttaag      180
ttgtttacac ttggaactta tttaaattaa aaaggccagt ggatgggtcat atgtttggct      240
cattcttctc aaggccttca ggaaaacatg cctatgaaat aaaagatcct caatattaaa      300
cattttactg catttggggg acacatgaaa tctggtaata aaggaagtgt tggcttcat      360

```



ttttctaatt cagcatggaa actatcttga ggaaaactga ctatgggctt agtttgtgtc 420  
 tcagaaatat atttagtctg aatcatggcg tcgacatctg acttccaaaa ttg 473

<210> 383  
 <211> 497  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 133  
 <223> 18-787-133 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 113..132  
 <223> 18-787-133.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 134..152  
 <223> 18-787-133.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..21  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 480..497  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 121..145  
 <223> 18-787-133 potential probe

<400> 383  
 cactgtgaac tactttaata ctgcacatt ttccctaaag tcaattgcca tggatatcaat 60  
 gatgcttaaa aatagagtga aattttggtta tgtgactttc acctcaataa attattaata 120  
 aaaaataaag tgrgccataa gtaggtactt cccagatttt atttatattt atcaacactt 180  
 tattctgggt cctttacagg ctgtagaaga ttctgatagg catgaaaact acaacatatt 240  
 taaaaaaaaca ttgcttagga tatctccggc ctttcaagtt tgttctcaaa aataactttg 300  
 cttgatcaaa tgaactatat ttgggtttac taaagatggt ctcagaaaga agaatatgtg 360  
 tacatcaatg atttgtaatg cattttaaatt tcaatactat tttttaaaaa tttaagtatt 420  
 ataatggtac tatttatagc tagcagaagt agatataggg ccaagtttta atttgcttgg 480  
 aagggtgagg cattcct 497

<210> 384  
 <211> 552  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 239  
 <223> 18-1149-239 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 220..238  
 <223> 18-1149-239.mis1

```

<220>
<221> misc_binding
<222> 240..259
<223> 18-1149-239.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 532..552
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 227..251
<223> 18-1149-239 potential probe

<400> 384
ggggactaga gcaagagatt gaaaaaagaa tgaaaataag catacattca cacagaaaca      60
cacacatgca cacaacttga gatcaccaaa gccaaacttc tcttttgctc ttcttgcttg      120
ggacataccc aaagtgtggc agttcaacag taagctgtag ggataagtgc tcgagctctg      180
gagttagaga aaatgggttc tgaccctaatt tcatttcttt gtatctatat tacttgctrc      240
aagttactga atctttctga cccttaattt ccttcatctg caaaaaggga taataacact      300
tatttcttag gagtgttgtg aagattaaat aagatgatgt atactgagtg attggcacag      360
tgcctaatac ataataaatc aaattaaagg gcagtgaact tcagtataca tttgggagga      420
ctcttggttt ttaggaaaga agtcagaaga cccaagtcc ctcccatctc ctctgctgca      480
ttatttttct ggaacggatt agggaggggt tggcaagaaa gaacagatga tgtccctatg      540
ctattcacac tg                                     552

<210> 385
<211> 500
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 291
<223> 18-1159-291 : polymorphic base A or G

<220>
<221> misc_binding
<222> 272..290
<223> 18-1159-291.mis1

<220>
<221> misc_binding
<222> 292..311
<223> 18-1159-291.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 480..500
<223> downstream amplification primer, complement

```

```
<220>  
<221> misc_binding  
<222> 279..303  
<223> 18-1159-291 potential probe  
  
<400> 385  
atgtgtcttg tcaagtgaag caaacagcac ttttctctgc cttaaagtgt acagattctg      60  
acagaaaaat atcttaatta atcagacttt atcatgggca ttcaaagggtg attgaaacaa      120  
taggtgaagt tcaacttgaa ggtaatcaca aagggccatt tacagtgttt cttagagttg      180  
ggtaggtact gtcctcttgg ttagattcag aaatgctgcc tgctgtttct ttctgggttg      240  
aggatatctag tagccttgcc tgctcttatg tgacaagcac aaattactcc rctgtgatga      300  
atctcatggg atcacagaag gtagagggtga caaggagatc tatcacatca tatcagggtcc      360  
aaattcccag gtgccctgta ctgcatttcc tctgccttcc actgtatttc attttaacct      420  
gggttaaagt agcagcatct tccactgggc tgtactgttc ggaaatgggt ggctaccatg      480  
ggttgcttta ggattctaca                                     500  
  
<210> 386  
<211> 449  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 273  
<223> 18-1135-273 : polymorphic base C or T  
  
<220>  
<221> misc_binding  
<222> 254..272  
<223> 18-1135-273.mis1  
  
<220>  
<221> misc_binding  
<222> 274..293  
<223> 18-1135-273.mis2, potential complement  
  
<220>  
<221> primer_bind  
<222> 1..18  
<223> upstream amplification primer  
  
<220>  
<221> primer_bind  
<222> 429..449  
<223> downstream amplification primer, complement  
  
<220>  
<221> misc_binding  
<222> 261..285  
<223> 18-1135-273 potential probe  
  
<400> 386  
gcaagcgatg agctaaagtg gaagtgtagg agagggtgagt tgcttaggtc taaggagaaa      60  
gactgcttag gtgtgtgttc acccccagga cgaagaaagg aacctgggt gagattttgt      120  
tcaactacce atagttacca ccagatgggtg aaactgatcc cgggcctctt ggggtattgat      180  
cagtttatgg ggagatgggg agaagactat ctttcacttg ttaattcatt aatttccttc      240  
gcaaataattt tttcagtagc tgctaagtcc cayggactat gctaggagct gctgttaaaa      300  
tgacaaacca gataaggtca ctgcccttaa tcaacttaca gttgggtgag aagctatcag      360  
gtacaagtat ggccctagaa caaattagtc ttttctagtt aataatctta tgtgatgaga      420  
tttggcttct ctttgtgtga cttgcctca                                     449  
  
<210> 387  
<211> 450
```

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 108  
<223> 18-1136-108 : polymorphic base G or C

<220>  
<221> misc\_binding  
<222> 89..107  
<223> 18-1136-108.mis1

<220>  
<221> misc\_binding  
<222> 109..128  
<223> 18-1136-108.mis2, potential complement

<220>  
<221> primer\_bind  
<222> 1..21  
<223> upstream amplification primer

<220>  
<221> primer\_bind  
<222> 433..450  
<223> downstream amplification primer, complement

<220>  
<221> misc\_binding  
<222> 96..120  
<223> 18-1136-108 potential probe

<400> 387  
gtattactaa attcctcatc cctggttaaca tttccatggt agctgttttc tatttgtttt 60  
ttcttttcca caatggtgcg gcctagaaac agttaacctt cttcgggsta ttacatacct 120  
tagacatata aaaaagctat gagcattcaa cactgaaata atcatataaa ccaaatac 180  
tgcacactac ttcagggata ctctgaagcc catccttaga ccccagactc aaacaaaaca 240  
aaatacgaatg taaagaactg acacaaatca tcggagttaa gagaacaacg tgacgggcag 300  
cagaggagag gagagggttg aagcaaaactt ttttggtttt tttttcctaa gtagggctgg 360  
ttctggcttg tcttcttct cccactttg cttcttactc ttgggcttac aaactgcctg 420  
gtttcccttc tccaagtcag ggcttcgttt 450

<210> 388  
<211> 450  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 68  
<223> 18-1147-68 : polymorphic base A or G

<220>  
<221> misc\_binding  
<222> 49..67  
<223> 18-1147-68.mis1

<220>  
<221> misc\_binding  
<222> 69..88  
<223> 18-1147-68.mis2, potential complement

```

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 430..450
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 56..80
<223> 18-1147-68 potential probe

<400> 388
atctggattt aaagttctgg gaagggaag ttgaccttct agacagggca acacttgccc      60
ttgccctrty tatttacctc agtaagcaac aagctgtagc tgtaacctaa tgtgtggcca      120
aggaatggga atttcaatgg ttctactagg aatatttggg caaatgctga tgggtgtctg      180
tattaaagct aagctatgcy ttttctgata aatgtataaa ttattcttt cccttattaa      240
acaaatgttt attgagtacc tactgtgtac cagacacagt tccatgcact gagaatacat      300
cagctaaaaa cataatcaaa attcctagct ttcattggagt ttattatatt ctatttgggg      360
agtgggaatg aggtagcagt tggtgaaatg gaaacagaga ccatgactag tctgggttaac      420
agaaaactac agaaggacaa acactcagac                                     450

<210> 389
<211> 595
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 295
<223> 18-1157-295 : polymorphic base A or T

<220>
<221> misc_binding
<222> 276..294
<223> 18-1157-295.mis1

<220>
<221> misc_binding
<222> 296..315
<223> 18-1157-295.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 576..595
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 283..307
<223> 18-1157-295 potential probe

<220>
<221> misc_feature
<222> 568

```

<223> n=a, g, c or t

<400> 389

gagtcactag	agagtcctttt	gtggacacct	gctccttctg	aaacaattga	cttgtctact	60
ttcacaaaca	gcagtatttg	tattaaagaa	ccagttggca	tcaatgcca	agtcgaggtg	120
tcctaataata	taagatgggtg	cttcattcag	aaaactcaag	gtagagtaaa	ataaattatc	180
aacatcttgg	ctccatgctc	cattcacaaac	tgtaaatttt	acagggttat	gcttccatct	240
ctgagcagag	aactcctggc	agggacagct	gctcctgtgt	ctcacattgg	gctgwgtca	300
ttccagtagg	agtcatcaag	agcagcaggt	tagcgagaag	gtgatagtac	atcagagaaac	360
tgagcagtg	aggagggaga	aggatggggc	tctccaaagt	gcttttcatt	tactccttta	420
atctttgtgt	gtatatacat	gcattggttaa	ctaaggaaaa	aggaaaagtt	gacttgaatt	480
tgactgagaa	aattatcara	cctgctttta	cttgtacatg	tagctcattt	tcaaaaatac	540
ttttgtgtat	ccactggtat	gttgatgntc	ctatscagca	ataggtctgt	acgct	595

<210> 390

<211> 569

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 459

<223> 18-802-460 : polymorphic base A or G

<220>

<221> misc\_binding

<222> 440..458

<223> 18-802-460.mis1

<220>

<221> misc\_binding

<222> 460..479

<223> 18-802-460.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..21

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 549..569

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 447..471

<223> 18-802-460 potential probe

<400> 390

cctattagca	attcattggt	ctccaaaaga	attcattcaa	atagacatac	cagagcagag	60
aggttcagag	catgagtttc	agagcatgat	aaacctgggg	ttaaattccat	ggtctgtcaa	120
gtactgacca	tgtgaatttg	gacaacttac	taacctctta	taaacttgtc	ttctctttca	180
taaaatgggg	ttaatcatat	ttacttccta	gggctaatta	tttgataaaa	gaggatatct	240
aaaacctatt	agagtgccga	catgcagtaa	atgactatac	attaaatttt	ctattcagaa	300
tattattctt	ttatactaata	attcccaata	ttagtaagat	taaatgaatg	atattttatt	360
tcctagtcc	ctgttttgg	accctattta	ttctgattga	aagagtcttg	ttattgggtga	420
tgtcagaaga	agaaaggccc	tattaatatt	ttcagaacrt	ggaattttga	attaatataa	480
actggaagag	tcctttgaca	attgtaagct	attccaaagt	cacataaaga	ataacaatgg	540
acctctctgt	gcagcatttt	tatgatgcc				569

<210> 391

<211> 455

<212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 109  
 <223> 18-1064-110 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 89..108  
 <223> 18-1064-110.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 110..128  
 <223> 18-1064-110.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 438..455  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 97..121  
 <223> 18-1064-110 potential probe

<400> 391  
 tctgtgactg taaatcccaa ggattttaaata gaaaaataga aaaatgccca ctaattagtc 60  
 attcactttg ggcatttaac agaaattcct tgagtatat ttatatcayc tctattacaa 120  
 tcacactcct ttctaaagtc atagcttgcc ttccagcaag atattcaaga ctaattcatt 180  
 ctacagttacc acgagtcatt cctttgtggt tatatttccc ccagagtaat atatcctgcc 240  
 acttctttct ctgtcatatt gtcattattgt tagaatgatg aattctagca tacttcccaa 300  
 ataattattt tcagttaatc tgtctataaa atctctttat ttttaacaga gtcaacaaaa 360  
 tgtactgagt gggcacagtc agcaaacatc tctaccagc cagacacaga gcactcttac 420  
 agccccactg tataacacta tgggtgatttc tcagc 455

<210> 392  
 <211> 516  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 327  
 <223> 18-1068-327 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 307..326  
 <223> 18-1068-327.mis1, potential

<220>  
 <221> misc\_binding  
 <222> 328..346  
 <223> 18-1068-327.mis2, complement

```

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 496..516
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 315..339
<223> 18-1068-327 potential probe

<400> 392
ctactagatt ttgcacagga aaaatattca catataagta tcaagggttaa cgttaccaaa      60
tgatttttaaa tttggattaa ccaagatatt tactaaatgc taccatctgg gataaatcca      120
ttctcactta atctttcaca cagattgagc ttcacatggg acaagatatt tcccacgaag      180
tataccagag gataagagct tgggatttaa attccaacag gcagggttca ggtaccaccc      240
ttgctagtac tagcatcact gcacaactgc tatcttctaa gcttgagtct gcatgtgtgt      300
aaatgggaat aatgacaata acatctycct cacagggtcca ctgtgaggat taaatgagga      360
aaggcacgta ctcttagta gtcatcacat aatcatatat gtaaaccatt agtcaatggg      420
ggttactatt tataaaccag taaaatctct cccacatgct ccttagccat tagcacattt      480
ttttaaatga taaaagtga aagcatcttg tgaatg      516

<210> 393
<211> 472
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 365
<223> 18-1069-365 : polymorphic base A or G

<220>
<221> misc_binding
<222> 345..364
<223> 18-1069-365.mis1, potential

<220>
<221> misc_binding
<222> 366..384
<223> 18-1069-365.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 455..472
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 353..377
<223> 18-1069-365 potential probe

<400> 393
tcaggacagg cagataaggt agttgtcata tttcatttgt tattttttaa attgtaaacc      60

```



gattgattag	aaaacaataa	tttgatttct	taatcaaatt	ttttaatgtg	attttaatga	120
gatgctcact	gcagccaatg	ttcttaaatt	tgaaataaaa	acactgaatg	tattcattgt	180
ttaaagactt	cataattaaa	gggtaacaac	aaattttttt	tcttgtccaa	aaatatgcta	240
caaaatatta	tagaatacaa	attctgcagc	acactgttag	aaaagggtta	tgacaggctc	300
tgtgtcactg	tgaagctttt	gtcttttcaa	tatagatgct	agagaatttc	catgtagtaa	360
cagtrgttag	ggtagcttac	cttttttaag	tttgttaaat	gctcaaaaata	tattatctca	420
aatagtcatt	tattaaaaga	aaatgtatgt	gaggcctcct	tttatttccc	ag	472

&lt;210&gt; 394

&lt;211&gt; 458

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 367

&lt;223&gt; 18-1073-367 : polymorphic base A or G

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 348..366

&lt;223&gt; 18-1073-367.mis1

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 368..387

&lt;223&gt; 18-1073-367.mis2, potential complement

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 1..20

&lt;223&gt; upstream amplification primer

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; 441..458

&lt;223&gt; downstream amplification primer, complement

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; 355..379

&lt;223&gt; 18-1073-367 potential probe

&lt;400&gt; 394

agagagacga	ctttcacggg	gcactcatat	caaaatctaa	cctgaggagg	aagctcactc	60
acagattggt	ggaaatcgct	agacctcagc	ctgagtttac	aaggatggac	agggcagctg	120
aaaacatgga	gccctgggtt	tagagacaat	ggtcattaca	gacctacggg	gtctagactg	180
acagatacta	aggctgcaag	gtcagggtta	cctcagcact	ataaactcat	tcccatcacc	240
ccaagcgact	tgaattcttt	ataatcatgc	attgttttta	caaaaatggt	agtcatatgt	300
gttaggtaat	gtccctcctc	ccccccataa	aacaaaaaat	ccatttcatt	tccttctcgt	360
aaacaargtc	atgggttggc	tccctctctc	ctggctagt	agagcttaga	gactaaaaca	420
caattttcac	taccacagta	ctctttgtcc	tctctctc			458

&lt;210&gt; 395

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; 272

&lt;223&gt; 18-1070-272 : polymorphic base A or T

<220>  
 <221> misc\_binding  
 <222> 253..271  
 <223> 18-1070-272.mis1

<220>  
 <221> misc\_binding  
 <222> 273..292  
 <223> 18-1070-272.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..19  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 455..475  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 260..284  
 <223> 18-1070-272 potential probe

<400> 395  
 atcagacatt tctactaggt ccattgacaa atttatttga ccggagtacc tcattttctt 60  
 catatattac cctgtataaa atccagaatt gttacagcag tacatttcac cattagctat 120  
 tagatacctt gtttaatcac ctttttcatt atttttaaat gtgtctcatc tgctaatact 180  
 gacattatct taaagattct ttgtatttga atcctcaaat tctatagcat actgtctaaa 240  
 aattgagata cacacacaca cacacacaca cwcacacaaa tttgtgtgta tctataactt 300  
 ttgtaagagt ggatggcctt tcagcgagag ttgagaaaaa ctagacttgg agaattcatt 360  
 tcaagccttg ttttaaaacc aagttcatat gacattgacc attaggccac tctagtctgg 420  
 tacttagaaa gatgtaggct gtatataata gataacctaca attagtattt gaagc 475

<210> 396  
 <211> 469  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 35  
 <223> 18-1057-35 : polymorphic base C or T

<220>  
 <221> misc\_binding  
 <222> 16..34  
 <223> 18-1057-35.mis1

<220>  
 <221> misc\_binding  
 <222> 36..54  
 <223> 18-1057-35.mis2, complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 449..469

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 23..47

<223> 18-1057-35 potential probe

<400> 396

caagcagtc	attacacctc	tcataaattt	attayacacc	tgcatTTTTa	taactattat	60
gctTTTTaat	tggtggccac	cattTTTTagt	gcttctgaat	tggtatgggt	ctcaagcagc	120
agttgtcacc	ttggttttga	attaatgctg	tgacgcttgc	ttccaggacc	cctatgggtg	180
agccgtgggt	ggaactgtgg	ggcactgcct	gtgcacggga	ttggcagtaa	ttggaggaag	240
aatgatagca	cagaaaatct	ctgtcagaac	tggttaagtct	tgaaaattac	aaatcagata	300
acattttaga	atcactgaga	gattaaaggg	tggttagcttt	gattatttaa	atttctgctg	360
ctgaagtata	cttggttttt	ctaattacct	accatctctt	ataataagag	gtattaawcc	420
tggtatwgca	aatacggact	tttttcacct	gtgtagaagt	tagcaaaat		469

<210> 397

<211> 577

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 415

<223> 18-1062-415 : polymorphic base C or T

<220>

<221> misc\_binding

<222> 396..414

<223> 18-1062-415.mis1

<220>

<221> misc\_binding

<222> 416..435

<223> 18-1062-415.mis2, potential complement

<220>

<221> primer\_bind

<222> 1..18

<223> upstream amplification primer

<220>

<221> primer\_bind

<222> 557..577

<223> downstream amplification primer, complement

<220>

<221> misc\_binding

<222> 403..427

<223> 18-1062-415 potential probe

<400> 397

acagcacaag	tacctagcaa	attagataca	tctaacaaat	gactgtttta	taaagtagat	60
aatttatctt	tatattta	aatttttaaa	gaaacataga	aattttttcc	agtttgagtg	120
tccaattggg	taacaatggg	gaaaattaga	atgtttaatt	ttcccttatt	aaatacagta	180
aagttttatt	tataaattaa	taacaatata	ttgccaggtc	tcacttttgc	ataaaatata	240
gctttatggc	ataatgggag	tccaggattt	attataacaa	ataagatggg	atttcaatat	300
acactgaaat	agattacaga	tttttaatat	ggtcacaatt	tcattttata	tatattttta	360
tattgaaaaa	ggaccataata	gggcatatgg	agtaatgctg	tattttaaga	agtcygtatt	420
tttcataaac	ttgcataaagg	atagtgtctac	tgaatacaac	atttgacttt	tttgtaaca	480
gctactactt	acatttttaa	tattctgggg	ttaatgaatc	actttccagc	agatgagtag	540
agagtatttt	ataaacctct	gaatgttccc	cttctggt			577

<210> 398  
 <211> 453  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 165  
 <223> 18-1082-165 : polymorphic base A or G

<220>  
 <221> misc\_binding  
 <222> 146..164  
 <223> 18-1082-165.mis1

<220>  
 <221> misc\_binding  
 <222> 166..185  
 <223> 18-1082-165.mis2, potential complement

<220>  
 <221> primer\_bind  
 <222> 1..18  
 <223> upstream amplification primer

<220>  
 <221> primer\_bind  
 <222> 433..453  
 <223> downstream amplification primer, complement

<220>  
 <221> misc\_binding  
 <222> 153..177  
 <223> 18-1082-165 potential probe

<220>  
 <221> misc\_feature  
 <222> 50  
 <223> n=a, g, c or t

<400> 398  
 cctcatTTTT tcatggcgct tcagtcgtca ccctcgtttg agtatatttn gatttgacta 60  
 ctacttcacc caagtagcat aacagctgct ttctctcagc cttttatatt ctagaatcat 120  
 atgcagtaac attcccatta atagcctcac taaattgaag gacarttcta cagaaacatc 180  
 catgttattt gtgtgaggta taataggaga cccagagcaa ttcagggtta tgagctacta 240  
 caaagggtcca caatgtagtc tgcaatttga agagattgtg aaagaaccca gttaatcatc 300  
 cagcactgta ggatgcagca attgtcctac atggtaactc tgtgaggaag atgatagcta 360  
 ctactgtgga gatcttaaga ggagttttca gcttaaatac caagttagaa gtagcacatg 420  
 ttggtaaaaa aggtcatatt tgtagttttc tgc 453

<210> 399  
 <211> 494  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 363  
 <223> 18-1080-361 : polymorphic base C or T

<220>  
 <221> misc\_binding

```

<222> 343..362
<223> 18-1080-361.mis1, potential

<220>
<221> misc_binding
<222> 364..382
<223> 18-1080-361.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 475..494
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 351..375
<223> 18-1080-361 potential probe

<220>
<221> misc_feature
<222> 342
<223> n=a, g, c or t

<400> 399
ttatcgacc taaggctgca actttgcctt catatztatg atgcttttaa ataattattaa 60
tatttaattt ttattaagaa cccaatgtgg taggcactgt tattcctatt ttctaaagaa 120
agaaactgag gccagagaa gtaaacagct tgaccaagtc acacatgtgg taagtagggc 180
agcccaagtt tgaaccattc agtctacctc agggcccacc acgctcctgg ccacttaact 240
gtgccgctct aaccagctga gcgaacctgt gtgcagaagg cattgtctgt ctggcctcag 300
agtatttggt tttcatatag tcataactat gctcaaattt tntaatttaa aatatgggtc 360
ttyaggacat aaagtgaaag aacgtgtgtg atttggctca agatatagat tgctttctat 420
accataaaat ctgtagctca gattccttta aaaaatgaaa ctctctcata cttyagaaag 480
agggaagccc ataa 494

<210> 400
<211> 511
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 297
<223> 18-506-297 : polymorphic base G or T

<220>
<221> misc_binding
<222> 278..296
<223> 18-506-297.mis1

<220>
<221> misc_binding
<222> 298..317
<223> 18-506-297.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

```

```

<220>
<221> primer_bind
<222> 491..511
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 285..309
<223> 18-506-297 potential probe

<220>
<221> misc_feature
<222> 46,100..101,104,123,166
<223> n=a, g, c or t

<400> 400
atctccacct tgccgtgttg gaacaccccc acgcaggagt aggtgntgcc caggtcgatg      60
ccgatcgccg cggctttggc catgccggtk ccctgctctn ngtnngctcs gctctgagay      120
ysngggctgg aaacggmrsc ckggatccgc gasaagagct crgtcnttcs gracgccgga      180
aactcracrc gccgggtgcct gcagccgcac aggttcgctc tggaaagcct tgggaccgcg      240
ggagtcactc tcgaaagacg aagcggaccc tcgcagcagc tcctcaggct ggccgkwtc      300
cggaccgcky gccctsggc ttttataagt cgtcryggag acccgccttt ycccttctga      360
gccaatcacc ragctcgatg aggctgccag gtcgggaata ttccaggggt ttcgcctccc      420
gtcctgcccc ccagccttcc ttggaccaat cagaggscag rgtgccgccc yctgctcaga      480
astctccaga gtcttctggg attcactgga g                                     511

<210> 401
<211> 400
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 38
<223> 18-570-38 : polymorphic base A or G

<220>
<221> misc_binding
<222> 19..37
<223> 18-570-38.mis1

<220>
<221> misc_binding
<222> 39..58
<223> 18-570-38.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 380..400
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 26..50
<223> 18-570-38 potential probe

<400> 401

```

gaagaactgc ttcattcggg gctcagtggt ccgatacrtg cagytgccag cagaygaggt 60  
 csacamacag ttgctacagg atgcrzcaag gaaggaascc ctgcagcaga aacagtgatg 120  
 gctcctcctc ctcttcccct ycctctttca ttggtgaccc ataaccccaa gtcccagccc 180  
 agaacccta accccaata cttgaagggg ttttgttttt ttactaatga tggttttgtg 240  
 ggtttttttt aagggatgag tggatgagag gagtaatagg gaacagctat cctctcttga 300  
 gaaggggagg ataagtaggc tgggaaactt caaagccttc ccagtcccca gcacctgcct 360  
 ttctcactac ttctctggag atggtaggag agtttcctag 400

<210> 402  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 24  
 <223> 18-473-362 : polymorphic base C or T

<400> 402  
 ttcttagggc taagaaatca gaaygtgcct ttagaaataa taagtat 47

<210> 403  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 24  
 <223> 99-12361-88 : polymorphic base C or T

<400> 403  
 acctggcatt atttggaatg cttyatttcc tctgtacctg gccttca 47

<210> 404  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 24  
 <223> 99-12368-335 : polymorphic base A or C

<400> 404  
 ggtgacagta atacctacca ctamggtggt gtgagaatta aatgagg 47

<210> 405  
 <211> 47  
 <212> DNA  
 <213> Homo Sapiens

<220>  
 <221> allele  
 <222> 24  
 <223> 99-12370-67 : polymorphic base A or G

<400> 405  
 tttaaaagga aaagcagagt tcartgcaaa ttctagaaat agttgtc 47

<210> 406  
 <211> 47  
 <212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-32148-315 : polymorphic base G or C

<400> 406

gtgggttctct ggaaaccgag gctsgttgca aaccctaaa aagtact

47

<210> 407

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 19-46-322 : polymorphic base C or T

<400> 407

ggccctggct gttccctgct gtgyactgcc caaggctaga catcaca

47

<210> 408

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 19-47-315 : polymorphic base C or T

<400> 408

cgctgttttg ggggaagtct ctcycacttt gggatcctgc tgaagct

47

<210> 409

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 19-51-347 : polymorphic base A or G

<400> 409

gtgtttctct ttcacttact tggrrgatca accttggggg gtgtgat

47

<210> 410

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-32052-262 : polymorphic base C or T

<400> 410

cctatTTTTT ataacgtatt aacyttatta ttttcttatt attttaa

47

<210> 411



<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 10-213-292 : polymorphic base G or C

<400> 411  
tcatcatgac ccaaagtact ggasagagcc tgagaagttc ctccctg

47

<210> 412  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-419-135 : polymorphic base C or T

<400> 412  
cacttccctt ctgttggggc aaaytcagtt ttttttgtga aaatgtt

47

<210> 413  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-424-419 : polymorphic base G or C

<400> 413  
atttccaagg gtaaaaggta gagsaggggg tgtggagggtt tggatat

47

<210> 414  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-429-289 : polymorphic base A or C

<400> 414  
aggtaaagcg tcttttttcc cttmaactag cccatttgaa actcttc

47

<210> 415  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-246-256 : polymorphic base C or T

<400> 415  
tgggggtggca gtgaccgttc caayatggat gagtgagaag cagggttc

47

<210> 416  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-355-67 : polymorphic base C or T

<220>  
<221> misc\_feature  
<222> 7  
<223> n=a, g, c or t

<400> 416  
gactagntcc cctagagctg aggyctgtct tgaaggactc actgggg

47

<210> 417  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-353-267 : polymorphic base C or T

<400> 417  
tggcctctag gggatctgca gttygggcgg tgggcggttc tgattgg

47

<210> 418  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-338-305 : polymorphic base A or G

<400> 418  
cctgcagcag ttctttggct tctrccact cctggggttg gggagga

47

<210> 419  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 24-243-346 : polymorphic base C or T

<400> 419  
ttccaggagg aagccactgc aaayagggcc tgcagctgcc ctctctc

47

<210> 420  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-62531-351 : polymorphic base C or T

<400> 420  
ccctagaggc agttgactta cccyctgcag ccctccctgc cgctca 47

<210> 421  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-54279-152 : polymorphic base C or G

<220>  
<221> misc\_feature  
<222> 9  
<223> n=a, g, c or t

<400> 421  
acccggcang ggctctataa atasagatgg aaagagggag gtgggcg 47

<210> 422  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-168-245 : polymorphic base A or T

<400> 422  
caagctatatt gcatataggg aagwttccca gtctgcccct gttctcc 47

<210> 423  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-171-291 : polymorphic base C or T

<400> 423  
ctgcagagac tgtcacagga ataytgaaga aagcatcatt cctagaa 47

<210> 424  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-172-346 : polymorphic base C or T

<400> 424

ccatccagtc aagccccact cagyatagat gtcctctgcg taccccc

47

<210> 425

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-177-406 : polymorphic base C or T

<220>

<221> misc\_feature

<222> 34

<223> n=a, g, c or t

<400> 425

ccccggaggt gcaatgaata gctyaccgaa gggnscaact tcattca

47

<210> 426

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-298-338 : polymorphic base A or G

<400> 426

ttcccacatc tgcctcagac tggrgggggc tcagctcctg gggatgat

47

<210> 427

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-298-110 : polymorphic base C or T

<400> 427

ggaacttcca gattcagaga atsygattta gggaaackgt ggcagat

47

<210> 428

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-299-105 : polymorphic base A or C

<400> 428

taaacagtcc tggggagatg tccmgctcct gtagcccat catgggt

47

<210> 429

<211> 47

<212> DNA

<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-884-30 : polymorphic base G or C

<400> 429  
gcttttcctta ctcttcagat agtsataaag gacattaaac ctaagca 47

<210> 430  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-299-343 : polymorphic base C or T

<400> 430  
tgtgtatgta caggaattgc tgaayggaagt ccaacaggct ctcttag 47

<210> 431  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-61513-139 : polymorphic base A or G

<400> 431  
gcctcttcac atcttctttc cacracatag tctggacttt gtacatg 47

<210> 432  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-61514-179 : polymorphic base A or G

<400> 432  
tacgaattca gtaaatactt ggaraataag tgaataattt caattca 47

<210> 433  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-61516-323 : polymorphic base C or T

<400> 433  
accaggtgct cttgggcagg agayggcttc aaatgcagac cggagtc 47

<210> 434  
<211> 47

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-204-70 : polymorphic base C or T

<400> 434  
ctcagagata actataggat tttyaatttg gataataaga agatggt 47

<210> 435  
<211> 46  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-207-441 : polymorphic base C or T

<220>  
<221> misc\_feature  
<222> 31  
<223> n=a, g, c or t

<400> 435  
aaatggaaat gtttgaatt cttygatgtg ntacaaacct gaaact 46

<210> 436  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-210-65 : polymorphic base A or G

<400> 436  
agacaacttg tttttctctc tcarttaca aagtagacta caaatat 47

<210> 437  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-212-200 : polymorphic base C or T

<400> 437  
catactctga tacttgtgga ggyatatcc tgataaagca gcgattt 47

<210> 438  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24

<223> 18-229-334 : polymorphic base C or T

<400> 438  
agaccagttg gactgttgga ataytgtagg ccagaactga gatattt 47

<210> 439  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-230-332 : polymorphic base C or T

<400> 439  
gttcaaaatt cttgacataa agayaaagat gttgagttcc agaaaga 47

<210> 440  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-966-378 : polymorphic base A or C

<400> 440  
ctaggaatgt tccaagctat gctmcaggat gttgagtttc tcaggga 47

<210> 441  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-987-308 : polymorphic base A or C

<400> 441  
gctacagggtt tttaaaaaat taamttttta tttaaagcaa ctcaaca 47

<210> 442  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1169-118 : polymorphic base G or C

<400> 442  
ggccatgttg aaccacttt ccastgggga gcagttcett taattac 47

<210> 443  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>

<221> allele  
<222> 24  
<223> 18-1172-138 : polymorphic base G or C

<400> 443  
aagagtagga aggggtttct cagsttgtaa aactttcaat gctaaca 47

<210> 444  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1173-92 : polymorphic base C or T

<400> 444  
tgaaacttca gagggccaag attycccctt ggctcccaca ctgtagt 47

<210> 445  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1174-387 : polymorphic base C or T

<400> 445  
ttatctaagc ccttgggcta cacyaaatag tttaagctaa gaaagtg 47

<210> 446  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1175-416 : polymorphic base G or C

<220>  
<221> misc\_feature  
<222> 36  
<223> n=a, g, c or t

<400> 446  
aagagtagga aggggtttct cagsttgtaa aactbncaat gctaaca 47

<210> 447  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-542-146 : polymorphic base A or G

<400> 447  
caactgcttt ttgttgatt gtgraaagta ttacaattaa ttttaaa 47



<210> 448  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 8-42-211 : polymorphic base C or G  
  
<400> 448  
ggaagaagac cgagtgtgtc ttcsttttta aaaagctacc tccgttc 47  
  
<210> 449  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 8-45-389 : polymorphic base A or G  
  
<400> 449  
agaccggcgg caacactact ggtrtctcgg acgtgaccgt cagctac 47  
  
<210> 450  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-994-270 : polymorphic base C or T  
  
<400> 450  
gtaaattgtgt agcaattact gaayctgtgg tataacaatt ttctcca 47  
  
<210> 451  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-912-165 : polymorphic base C or T  
  
<400> 451  
ttgggttttt actgaacttt aaayatttta ttaggactta caaattt 47  
  
<210> 452  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-991-124 : polymorphic base C or T

<400> 452  
tagcagaaga caaagccttt tcaygtttac cgatgaagct gcaaaaag 47

<210> 453  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-920-219 : polymorphic base C or T

<400> 453  
gcatagataa aaactgcccc acaycccca gtaaaagtct gctctct 47

<210> 454  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-911-312 : polymorphic base A or G

<400> 454  
tcagtaataa aaacaattca gccrtagttt ggggataatg gacaaac 47

<210> 455  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-65963-368 : polymorphic base A or G

<400> 455  
atttgtgtct ttacagaat tgtrtgacaa tgacttttgg acatttg 47

<210> 456  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 99-65966-225 : polymorphic base C or T

<400> 456  
gccaccctgt tgcaactctt taaygggttaa tgattctctc ctcattc 47

<210> 457  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24

<223> 99-65968-75 : polymorphic base C or T

<400> 457

atcattctga caccagaaag cagyagaatg aacaaacata acaacag

47

<210> 458

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-5069-331 : polymorphic base C or T

<400> 458

accccggaag accgctcgga cccygacgca tgcaccatta gcaagga

47

<210> 459

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 99-5070-176 : polymorphic base G or T

<400> 459

ggttctctat gggcgcatat tcckagtgcg cgcttccgca tccgcaa

47

<210> 460

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-511-348 : polymorphic base C or T

<400> 460

agaagggttac tacttgtaaa attycctgct agaccagttg gtaaatt

47

<210> 461

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-523-352 : polymorphic base A or G

<400> 461

gacattgggg aggtggtaat gttrggctct gtgatgtaaa atcaacc

47

<210> 462

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele  
<222> 24  
<223> 18-545-478 : polymorphic base A or G

<400> 462  
aggaagcaag acctggcaaa cccragacga tgcgctctta cttgtgt 47

<210> 463  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-522-194 : polymorphic base G or C

<400> 463  
ttttttcaaa gaacaagttt tcasaaatac actggattca acaattt 47

<210> 464  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-524-284 : polymorphic base A or G

<400> 464  
gcattgcaat gagaacataa attrcaatga ctttgcattc taatggg 47

<210> 465  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-626-52 : polymorphic base C or T

<400> 465  
ggaaagttgg tttggttgag cagygagggga taaattgagg gggtaga 47

<210> 466  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-629-189 : polymorphic base C or T

<400> 466  
taagatgatt gcctttttcc cttygaacca aatgaaaaga tgagaag 47

<210> 467  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1131-71 : polymorphic base C or T

<400> 467  
gcatcatttc cttgtgtgcg gttyagggtta aaaataacct ctaatcc 47

<210> 468  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-534-126 : polymorphic base C or T

<400> 468  
tggacataaaa aaaaaataaaa aaayccttaa gataattata tttataa 47

<210> 469  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-596-59 : polymorphic base A or G

<400> 469  
tttctaatta tggttacttt tctrtttctct tcacttttct gtttaac 47

<210> 470  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-597-27 : polymorphic base G or C

<400> 470  
tgggagcttg cgttctgtca agasctgaca ccaaacagtt attgggc 47

<210> 471  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-730-203 : polymorphic base A or C

<400> 471  
gaatcgtact ttacagttta caamgatgtg agcatccagg atcacga 47

<210> 472  
<211> 47

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-734-89 : polymorphic base A or G

<400> 472  
ggaagagaag gagagatgca gggrrggagga tataggggtc ctctggg 47

<210> 473  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-895-321 : polymorphic base A or C

<400> 473  
aacatcccca attaggaag aagmtaacac aaggcgctct tgccctg 47

<210> 474  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-896-69 : polymorphic base A or G

<400> 474  
catgcgtcta tttcccctta tgcraacagc aacagaaaag cattctt 47

<210> 475  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-903-58 : polymorphic base A or G

<400> 475  
tggaaaacat ggacaggcac cacrttggtt tatgaggctc tgagtct 47

<210> 476  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-590-216 : polymorphic base G or T

<400> 476  
ggcatggcag gcaggagacc agckcagcct ccaggccgtc catcctc 47

<210> 477  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-817-436 : polymorphic base G or C

<400> 477  
gactccaatc cctgaagtag aggsatTTTT gcatagtcac gttcctg

47

<210> 478  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-829-85 : polymorphic base G or T

<400> 478  
tgccctgcag tgcccagcac agakcagtgt ctgttgaatg cgtgagt

47

<210> 479  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-832-387 : polymorphic base A or G

<400> 479  
aaacaggggc agagggttgag gtttrtcagaa cctggaagct gggagga

47

<210> 480  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-833-259 : polymorphic base C or T

<400> 480  
ttagatagta ggaatgcact gagyttgtgc tcctgggaag actccac

47

<210> 481  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-839-271 : polymorphic base G or T

<400> 481

atgtcctttt gtgtcacctt atckaagctc actggtattt atacact 47

<210> 482  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-770-194 : polymorphic base G or C

<400> 482  
aaatgggatg tcccttttct ctgsaggagc agcgtcttcc ccagaac 47

<210> 483  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-771-302 : polymorphic base A or G

<400> 483  
gtcctgtcca ctgtgctgca gccrcataca cagcccagaa aggatgt 47

<210> 484  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-827-53 : polymorphic base G or T

<400> 484  
aggacagcta ttgcacaaaa ttaktcattg acctgaacat tctcaat 47

<210> 485  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-768-318 : polymorphic base A or G

<400> 485  
tgggtccaggc cctcaactct ctcrtctcag cagctgccac agcttcc 47

<210> 486  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-769-26 : polymorphic base G or C



<400> 486  
ttatgctgag agcaccaggc acasgttgaa caccgcagtc ttagaaa 47

<210> 487  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-709-321 : polymorphic base C or T

<400> 487  
gaggtgttcc cccacagctc tctygggaaa cgacacgtgc ttcctgc 47

<210> 488  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-714-280 : polymorphic base C or T

<400> 488  
catgtgagcc caggatcagg gcaytggggg aagaaccagc tgaggac 47

<210> 489  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-843-271 : polymorphic base C or T

<400> 489  
agcaacggcc gagcatagc agcygcactc accaccgctg gtacagg 47

<210> 490  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-850-265 : polymorphic base C or T

<400> 490  
tgccccagct gtaccatctc aggygctgag aacgcacca tcccttc 47

<210> 491  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele

<222> 24  
<223> 18-853-296 : polymorphic base C or T

<400> 491  
caggccacgc cacacctgtg ccayccaggg agtgggaagg aagcacg 47

<210> 492  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-867-331 : polymorphic base A or C

<400> 492  
tcctctcaac cagtgcattt tgcmtctgag acattgtggt tttcatc 47

<210> 493  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-877-73 : polymorphic base C or T

<400> 493  
tttacacca ctgcctgcc tccyacagct tccagaacac tgaggcc 47

<210> 494  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-856-85 : polymorphic base C or T

<400> 494  
gacacatgag agagactgtg attyggggga aaagctgctg tcggcac 47

<210> 495  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-861-101 : polymorphic base C or T

<400> 495  
agcaacggcc gagcatacgc agcygcactc accaccgctg gtacagg 47

<210> 496  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-635-323 : polymorphic base A or G

<400> 496  
agttgacatc ttaaaacttt atcrtgatca tcactccctt tactatg 47

<210> 497  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-636-205 : polymorphic base C or T

<400> 497  
caaattggctt tgaaccctt tccyggccac acaagcctct tcttggg 47

<210> 498  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-649-427 : polymorphic base G or T

<400> 498  
ttaaaaaagat gctaaatatg agckctgagt ctcaacactg tctcaag 47

<210> 499  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1134-316 : polymorphic base A or G

<400> 499  
agtttagagt ttaagttgga aggraaaaaa aaagaaaaga acacatt 47

<210> 500  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-633-316 : polymorphic base A or G

<400> 500  
agtttagagt ttaagttgga aggraaaaaa aaagaaaaga acacatt 47

<210> 501  
<211> 47  
<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-489-425 : polymorphic base C or T

<400> 501

cagggttccc agccccctgg aaayggggtg ataacagctt ctccctgt

47

<210> 502

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-492-212 : polymorphic base C or T

<400> 502

ctgctgcaag aagccctgcc cttyggggct gatccggtgt gataaag

47

<210> 503

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-488-156 : polymorphic base C or T

<400> 503

gggagagcag gctgggccca gagyggccct tccccacccc atctcct

47

<210> 504

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-491-266 : polymorphic base C or T

<400> 504

tgcaagccac atgcagatgc acgygtgagg gcatactcag tgccetca

47

<210> 505

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 24

<223> 18-497-141 : polymorphic base C or T

<400> 505

taaaaagcaa caggacacaa aaayccctgg ctggaaaaat ccaaaaa

47

<210> 506

<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-503-174 : polymorphic base A or G

<400> 506  
tgcagggtgga gaggggtatgc ctgrctaaag tgggtgaaag gcaaggt

47

<210> 507  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-490-95 : polymorphic base A or G

<400> 507  
aatgatgtgt aagaccaagg gctrgtttay caagaacata cacaaac

47

<210> 508  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-699-115 : polymorphic base G or C

<400> 508  
ttttccctta ccgaccctcc agcsaagaaa actgtgttaa actgttc

47

<210> 509  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1099-293 : polymorphic base C or T

<400> 509  
gccatctggg gagagaagaa tgtygggcag agtcctgtct acctgtg

47

<210> 510  
<211> 45  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 22  
<223> 18-1105-22 : polymorphic base A or G

<400> 510  
ttctctcaag catagtggcc trtgccccag gaatgtagca taatg

45

<210> 511  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-562-418 : polymorphic base C or T  
  
<400> 511  
ctccgaaact accccccagc accyggtaga ctttcacagc tgagaga 47  
  
<210> 512  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-564-204 : polymorphic base C or T  
  
<400> 512  
ttccttctct acagcccccg cccygccatg cacgtctctc tcagctc 47  
  
<210> 513  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-1032-262 : polymorphic base A or C  
  
<400> 513  
tttaatatat aaatggtaaa aacmaaatacc atggggaaaa catgtct 47  
  
<210> 514  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-1035-412 : polymorphic base A or C  
  
<400> 514  
tcttcagcag ctcccagtc ccmagacag tccagactcc ttactgg 47  
  
<210> 515  
<211> 47  
<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> allele  
<222> 24  
<223> 18-1036-293 : polymorphic base A or C

<400> 515  
tttaatatat aaatggtaaa aacmaaattcc atggggaaaa catgtct 47

<210> 516  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1038-95 : polymorphic base C or T

<400> 516  
aaactgtgaa tagcagtttg tcaytgatac ttaagagttg agaggct 47

<210> 517  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1040-361 : polymorphic base A or G

<400> 517  
ttattaagga gagttatcca actretcatg aagtttaggc gggtaca 47

<210> 518  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-748-356 : polymorphic base C or T

<400> 518  
aatataccccc tctaattctaa tcaytaaattg ctgaattcac taagaaa 47

<210> 519  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-937-181 : polymorphic base A or C

<400> 519  
gagagacaga aatgctgtct ttamtcaactg ttgactatgc aggtgta 47

<210> 520  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24

<223> 18-942-175 : polymorphic base C or T

<400> 520  
ttgtgagatc tgatcttttg ctaygagaaa agtctgagtg gtgactt 47

<210> 521  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1213-221 : polymorphic base A or T

<400> 521  
gcagtaccgt acttaacttg gagwccctgg acctctctcg agcataa 47

<210> 522  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-937-147 : polymorphic base C or T

<400> 522  
cacctaccta tacacaaatg tacygatgtg gcaggagaga cagaaat 47

<210> 523  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-946-408 : polymorphic base C or T

<400> 523  
atcttgagga aaactgacta tggycctagt ttgtgtctca gaaatat 47

<210> 524  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-787-133 : polymorphic base A or G

<400> 524  
aattattaat aaaaaataaa gtgrgccata agtaggtact tcccaga 47

<210> 525  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>



<221> allele  
<222> 24  
<223> 18-1149-239 : polymorphic base A or G

<400> 525  
tctttgtatc tatattactt gctrcaagtt actgaatctt tctgacc 47

<210> 526  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1159-291 : polymorphic base A or G

<400> 526  
atgtgacaag cacaaattac tccrctgtga tgaatctcat gggatca 47

<210> 527  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1135-273 : polymorphic base C or T

<400> 527  
ttttcagtac ctgctaagtc ccayggacta tgctaggagc tgctggt 47

<210> 528  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1136-108 : polymorphic base G or C

<400> 528  
agaaacagtt aaccttcttc gggstattac ataccttaga catataa 47

<210> 529  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1147-68 : polymorphic base A or G

<400> 529  
agggcaacac ttgcccttgc cctrtgtatt tacctcagta agcaaca 47

<210> 530  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1157-295 : polymorphic base A or T

<400> 530  
ctcctgtgtc tcacattggg ctgwgctcat cccagtagga gtcatca 47

<210> 531  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-802-460 : polymorphic base A or G

<400> 531  
ggccctatta atatatttcag aacrtggaat tttgaattaa tataaac 47

<210> 532  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1064-110 : polymorphic base C or T

<400> 532  
ttcttttgagt atatatttata tcayctctat tacaatcaca ctccctt 47

<210> 533  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1068-327 : polymorphic base C or T

<400> 533  
tggaataat gacaataaca tctycctcac aggtccactg tgaggat 47

<210> 534  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1069-365 : polymorphic base A or G

<400> 534  
gagaatttcc atgtagtaac agtrgttagg gtagcttacc tttttta 47

<210> 535  
<211> 47

<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1073-367 : polymorphic base A or G

<400> 535  
tttcatttcc ttctcgtaaa caargtcatg gtttggtccc cctcttc

47

<210> 536  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1070-272 : polymorphic base A or T

<400> 536  
tacacacaca cacacacaca cacwcacaca aatttggtg tatctat

47

<210> 537  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1057-35 : polymorphic base C or T

<400> 537  
ttacacctct cataaattta ttayacacct gcatttttat aactatt

47

<210> 538  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1062-415 : polymorphic base C or T

<400> 538  
gtaatgctgt atttaaagaa gtcygtatgt ttcataaact tgcaaaa

47

<210> 539  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1082-165 : polymorphic base A or G

<400> 539  
tagcctcact aaattgaagg acarttctac agaaacatcc atgttat

47

<210> 540  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-1080-361 : polymorphic base C or T

<220>  
<221> misc\_feature  
<222> 3  
<223> n=a, g, c or t

<400> 540  
ttntaattta aaatatgggt cttyaggaca taaagtgaag gaacgtg

47

<210> 541  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-506-297 : polymorphic base G or T

<400> 541  
cagcagctcc tcaggctggc cgtkwtccgg accgckygcc cctsggc

47

<210> 542  
<211> 47  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> allele  
<222> 24  
<223> 18-570-38 : polymorphic base A or G

<400> 542  
ttcgggggctc agtggtccga tacrtgcagy tgccagcaga ygaggtc

47

<210> 543  
<211> 123219  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 53695..55695  
<223> 5'regulatory region

<220>  
<221> exon  
<222> 55696..55860  
<223> exon 1

<220>  
<221> exon  
<222> 63298..63534  
<223> exon 2

<220>  
<221> exon  
<222> 72940..73022  
<223> exon 3

<220>  
<221> exon  
<222> 74834..74978  
<223> exon 4

<220>  
<221> exon  
<222> 77044..77214  
<223> exon 5

<220>  
<221> exon  
<222> 77764..77844  
<223> exon 6

<220>  
<221> exon  
<222> 80888..81036  
<223> exon 7

<220>  
<221> exon  
<222> 86504..89112  
<223> exon 8

<220>  
<221> misc\_feature  
<222> 89113..123219  
<223> 3'regulatory region

<220>  
<221> allele  
<222> 68753  
<223> 24-243-346 : polymorphic base A or G

<220>  
<221> allele  
<222> 108366  
<223> 99-62531-351 : polymorphic base A or G

<220>  
<221> primer\_bind  
<222> 68583..68603  
<223> 24-243.rp

<220>  
<221> primer\_bind  
<222> 69081..69098  
<223> 24-243.pu complement

<220>  
<221> primer\_bind  
<222> 108259..108276  
<223> 99-62531.rp

<220>  
<221> primer\_bind

<222> 108699..108716  
 <223> 99-62531.pu complement

<220>  
 <221> primer\_bind  
 <222> 68734..68752  
 <223> 24-243-346.mis

<220>  
 <221> primer\_bind  
 <222> 68754..68772  
 <223> 24-243-346.mis complement

<220>  
 <221> primer\_bind  
 <222> 108347..108365  
 <223> 99-62531-351.mis

<220>  
 <221> primer\_bind  
 <222> 108367..108385  
 <223> 99-62531-351.mis complement

<220>  
 <221> misc\_binding  
 <222> 68741..68765  
 <223> 24-243-346.probe

<220>  
 <221> misc\_binding  
 <222> 108354..108378  
 <223> 99-62531-351.probe

<400> 543  
 aggacagggg tttgagacca gcctgggaaa cataatgaga ccccatcttct ataaaaaaaa 60  
 aaataaaaaa ggtagccagg tgtggtggtg catgcctgta gtcccagcta cctgggaggc 120  
 tgaggctgga ggatcacttg tgcccaggag ttcaaggctg caatgagtta tggtcacccc 180  
 agtgcactct agccttggca acagagtggag actttgtctc taaaataata atgataataa 240  
 tatagtcaat attttccttt gtgatgtgag ctttttgtgt tttgttaaag aaatgcttcc 300  
 tttctttgag gcaataaaat attctcccat attccctttt aaatgttttt aagttttact 360  
 gcttggtttg agaataaatg cttctggaat tgtgttttat gtacaatggg acctagagag 420  
 tctattttatt ttttctctca tggcaacaac cagttgccta accagttgtc ctggcattac 480  
 ttatttagaa ctccatcctt tttcaattca acctgtgaca tatattaagc ttccatgaat 540  
 gcatggcctg cttattttat tccattcgct tatttccatg ctaatatcac actggcataa 600  
 ttccttttagc tttatagcaa gtcttgatat ctgtcacagt aagttccccc aacttgttca 660  
 tcttcttcag agcaattaag ctattcttag ttcttttctc ttttatataa aatttggaac 720  
 tagcttggca acttttgcaa agaaccctgt tgggattttg attggaattg tattgaaccc 780  
 atcacacaat ttggagaggc atgacatctt ataagactga gttccctcat ttatgaatcc 840  
 tcctattttat gtaggtcttc ttaaaccatct ttctatatgg aagtataatt ttctgtgcaa 900  
 aggtcttgca catatgccaa tagatttatt ttcatgaaat ttattttcac tattgtaaat 960  
 ggtatcatte ttaaaattat gcgttcttta tgtgagaggc agaggattct gcatgtgctc 1020  
 attaaatcaa gaatattaat tgtgttggtc aaatcttttc tattcttacc aatttttctt 1080  
 ttttactctt tggcctgtca atgaaagacg tatgttgaaa catcacaccc attaggatgg 1140  
 ctgctatgat ttgaatgtgt cctcccaaaa tttatatgtt gaaacagaat cccaatgtg 1200  
 atagtattaa gaggtgaggc cctgtgggag gtgattaagt attgaggtgg gaccttcatg 1260  
 aatgagatta ataagaggcc caaaggagtc tgttttctca ttctggcatg taaagacaat 1320  
 gccagaaggc accatctatg aagcaaagaa caaacctca ccagacacag aatttgctgg 1380  
 tgagttaatc ttgtactttc cagcctccag aactgtgagc aataaatttc tacggcttat 1440  
 aaattaccga gtctatagtg cttttttata gcagcccaaa cagactgatg caatgactat 1500  
 tattgtttta aaaaaacaaa aaaaaagta ggaagtgttg gtgagcatat ggaggaatta 1560  
 gaaccctcat atgctgttga tagggatcta aaatagttaa gtcactgttg aaagcaacat 1620  
 ggctatttcg caaaaaaaaa aaaaaaaaaa aaaaagcata aaattaacat acaattctgc 1680  
 tgtgccactt ctgggtatag ctaaaagtag tgaaagcaga gacttgaaca aatatttgca 1740

cactcatgtt	catagcagca	ttagccacaa	cagcggaaag	gtggaggcaa	cccagggtgc	1800
gtccatcaac	agatgaatga	gaatatgatg	tggcagggtac	ctgcaatgga	atgttattca	1860
cccttaaaaa	ggaagacatt	ctgacacata	ttataacatg	gattacatta	tgctaagtgg	1920
cataagccag	ttacaaagaa	ccaatatttt	atgattccat	tgatatgagg	ttcctagagt	1980
agtcaaattc	atagatacaa	tgtaacatgc	tgggtgccaa	gggggtggaga	gagaggtaat	2040
gggagtcagt	gtttaatggg	tacagagttt	ctgttttgga	tgacttaaaa	gttaaggaga	2100
taggtagtgg	tgatgggtgc	acaacaatgc	gaatgtactt	cataccactg	aacttataac	2160
cactgaaaaa	tggttaaaat	ggcagatttt	atgttacgta	tattttacca	caataaaaaa	2220
aatttaagtg	atatgttaaa	atgctccact	aaagaatgaa	attgtcaatt	tatcctttta	2280
gttctctcaa	tcttcatttt	atgtattttt	gtttcatata	cagcatcatg	catgaagtcc	2340
tagaattggg	atctcttcat	ggtgaattta	ttatttggtg	gtaaacctct	ttatcctaata	2400
tattacttaa	tctaattctta	atcgaatgat	tttgttcaat	attcagagct	gcagcagcta	2460
tcttttactt	cacgtgcctt	tttccatcct	ttgactttca	acatttctgt	gtcctcctcg	2520
tgctctgggt	acatctcttg	aaaacagcat	acagttgggt	tctgcatttt	tagccaacct	2580
gataaccagc	cagcgtattc	acctaacacg	actataatta	cagatatttt	tgaggttccct	2640
tctacccatc	tgatttttga	tttttatttg	tcttgctttt	tctttacttc	cttttctccc	2700
tcttttccct	cttcttttgg	attgcttgag	cttttttccct	tatttctttt	tcctctactg	2760
tcttaaagtt	atacagttta	cttccatatt	ttcagtgact	aaaatagaca	ttttaccata	2820
ttatttttatg	gtaaaaataa	tcaaatccta	aaggaatcaa	aatctcaatt	gtcatctcaa	2880
acaataaatg	ctttaacctc	aatttctttt	ctcacagaag	catgtgtaaa	acacatgcta	2940
tgacatgaat	tatattatgc	taagtgagat	aagccagtta	caaaggacaa	atattttatg	3000
attccattga	tatgaagctc	ctagagtaat	caaatttata	ggtacaatgt	agaatagtgg	3060
ttgccaaggg	gtggagggag	gggtaatcgg	catctgtgtt	tttggtccag	ttttttagtt	3120
ttaacatcta	cattttttaac	atacaaatta	gaccactaat	tttatatgca	caatacgtat	3180
tatcattcac	tcttaaatat	gttattatat	ttcccctttt	ttcaatcatt	cttttgattt	3240
cttccttgac	ccatgtatta	tttaagggtg	ttttacttaa	tttcctaata	tttgaggagt	3300
tttgtagaca	tctcattggt	actaaactcc	aattttccaac	tactatcatc	aaagaataat	3360
ttgaaaaagt	tcacattttc	atgtttcatt	tgtctaataa	tctttaatgg	aagctggaca	3420
ttgtgaacat	tatgccgttg	agtgtttagt	tttgttttct	tcctttaaag	aatgtttggc	3480
tttcttctgt	ccaacattta	atttacttgc	agatcagttt	gatgcctttg	cagtttagtt	3540
ttaatTTTTg	ttagggttg	tcttaggggt	gcttttacat	gagcacttgg	tcagcccttt	3600
acctaagtea	tgaccattct	gggctctcta	ctgaatgcca	agggaaattta	gcaagatctt	3660
tccactctga	ctgattagaa	ctcaaagtgc	tcccagcctt	gtgagagatc	cagtagttag	3720
tcaattttca	gctcccttgt	agcttgtctt	tgccataaat	caaaaaagtt	catctgttat	3780
atgtttggct	tagtattcat	tcagagactc	aagaggaccc	aaatgtggcg	tttttagagct	3840
ctttatgtgc	atggctccct	cttgtctgat	attctacctc	tcaaacccca	gcttccttgg	3900
gtttctctgc	cttctacctc	tcctcagctc	agcaaatgca	ccatgctctg	cttcagttcc	3960
tcttcttaca	ttacagttga	caaagtgccca	agtcgtcata	gagttcacct	tatttgcttc	4020
tcttctctca	gagattactg	ttgtgctctg	tttggtgcc	aagatctgaa	aacaaaattt	4080
tttgcatata	gtttgtccaa	ttttcctcat	ggataggaac	agaaatctca	actcttcatt	4140
ttctctcagc	atcttgaata	tattagttct	atgtcttttg	ctttctattg	ttgctgttga	4200
caactctgtg	gccagtttac	cacatttcat	tcataaatgt	tcataagata	ccactgaata	4260
tgcaatccat	cattatttta	ttgacagtaa	gagataaaaa	actgccaat	ataattgtaa	4320
gactccatca	atgataagat	tagtcccaat	ttcaaactg	ttaaattgtg	ggaaaaataca	4380
tatcttgga	ttgatgaaat	acggctcact	ttattttttg	tagagtatct	tttctgtttt	4440
tgttgcttct	tgatttatct	tgatgtcttc	ttatttcata	tgaaattatt	atatgtagat	4500
tatttttctt	tacactgctt	gatatacttc	gtttttccta	gatttgaaat	ttgtcatctt	4560
tgaacagttg	tgaaaaaattc	ttaggcacta	tctcttcaaa	tattgcctct	cctcagcttt	4620
ctctatttta	gtcttctgga	actccaatta	ggcaagtgtt	agactttcat	attttatcat	4680
gcatgtcttc	aaacctctct	tatttctctt	ttcttgctac	tttgcatgct	attctcggtg	4740
atatcttcag	atctgtcctc	tggttatctc	tgtcttcagg	caatctgatc	tgctatataa	4800
cacaacaatt	gagggttcaa	tttcaatcat	taaatttctt	tgtttgtttg	tttctttgtt	4860
tgtttgtttt	aaagacagag	tctcactatg	ttgcctaggg	tggtctcaaa	ccccggcact	4920
caacagatcc	tctgcttca	gcctcttgag	tagctgggac	aatagggtatg	tgccaccatg	4980
cctagcacat	tcactatatt	tcttactaca	agatgcttta	gttggttctt	tctcaattct	5040
tccgggtcat	tttggttgac	ttttgtctct	tgaactttta	aattccattt	ttaatctctt	5100
aacacagttt	atgtttatgc	atgattattt	ttgtctctctg	aattagatgt	ctactatcag	5160
aaatgcttga	ggacctaaat	acattgttta	ttattcagct	gcttcttgct	tacattgagc	5220
catttcgccc	tgtgttggtg	aatttttatt	atgagctcag	gcaggatattg	tggtgatggg	5280
actagactga	ggatgctttt	ctccagacag	cactggcatt	tgcttcttct	aggctccagg	5340
aggcactacc	aatctgtaac	tataatattt	taatttcggt	gcccgggtga	tgtttcttga	5400
cattaggggc	agtataaatt	tgaacctcag	tcacacgaca	gagcagtcct	ctggctacaa	5460
aagttcagga	aagactctct	agctttgtgt	acatgtttcc	accagagggc	agcagagatg	5520

gctgtgttca	tctgtcctct	atatccgtat	gaatccctcc	agcttgaagt	tctgtgtgca	5580
ggtgcctgta	cccattgggg	cctggatttc	cattttcata	gccactctag	tttgggctga	5640
ttattcctgt	tttttgtgaa	gaggcataat	ctttgggcat	ttctctggat	tctcctgtga	5700
gttttagcagg	gcatttttgag	tttgttgtaa	atagtttccc	atctccatat	tttagtctgt	5760
gaagggtgtt	cagttgacat	tttcagatga	gcataccatt	gggatcccaa	agccttcttg	5820
caaatttttt	attgtttact	ttattacatt	taagtattta	atctgtctaa	aatttacttt	5880
tgtatttggc	ataatgccag	agtccatttt	cccctttcca	atggctagcc	cgttaccagc	5940
aataatttat	attaatttat	tcctttttac	tgaatttaac	cattagattt	gtcgtaaact	6000
agcttagcac	atgttctaga	tttaattcta	gttccatctt	ctgtttgact	catctatttg	6060
tccattccta	tatcaacacc	aattactgat	tagattccag	tggctctttg	tatcctctga	6120
tgtaggaaca	ctcgagtctc	acttgaatgt	tcttacattt	tgtaattttt	taactattct	6180
caaagattta	gtttcagaga	ctattttgta	ctcactttgt	taaggaggcg	gtctcagcat	6240
gtatttgcta	cacttaattg	gactaaattg	agaagcttca	tggggaggta	gacagaattt	6300
cacttgga	agccacttac	cctcttccag	actcagtttc	tggcactaag	gaaggatggg	6360
ctagtgccct	agacctctgg	gctccttgcc	ggctctagaa	tcccagcccg	gattggcttc	6420
tccttaagca	ctggacaaca	tgcagtgata	agaacagctg	tttgtatgtg	tgtatttttg	6480
tttgttttag	agacaaagtc	gtgctctgtt	gaccaggctg	gagtgaatg	gtgccgagat	6540
agctcactgt	aacatcaaaa	ctcctggact	caagtgatcc	tcctgcctaa	gcctcccaag	6600
ctggctactac	aggcatgcac	caccattctg	agtaattttt	ttaaaaagag	atggggctct	6660
gctatgctag	ccatgctgtt	ctcaaacccc	tgaactcaag	tgattcttcc	caccttagct	6720
tcccaagtg	ttgggattac	aggtgtgagc	caccacaccc	agcttttttg	tgttcttatt	6780
ggccaggtaa	cgcatgtcag	gcgtcctgct	cagccagtta	tgtacattca	cccctcagca	6840
totcatttaa	tcctcaggca	tcctcgggag	gcagggtgcta	ttcatactat	ctccattcta	6900
tagagcaagg	aactaaagaa	tacagcgcta	tagtgactta	tttgcgaag	atattgggtg	6960
agtaaaaaag	gaaacaaggg	aatggagtg	cgagctttgg	gggagtatgc	aaagaccaa	7020
ttatgttatt	acataattag	tgcacattgt	tcttgataca	tgaagaagcc	ctcagtaata	7080
atagcttact	cgtttattga	gtgcttccta	tgtacttttag	gaatattaaa	tcattaatcc	7140
cacaaccttc	ttagctaata	ggcactatta	ttatctccag	tgtacggacc	acgagattga	7200
gccccaggta	tgtgaagtca	ccagcccacc	ggcaccacgc	agagggtggc	gatggcccca	7260
gaccgctagg	ctccagggac	tgtgccgtct	ctaggcaacc	gcaaaaatta	ccaccacag	7320
atatggcgaa	ccctgtgatt	gtcaccagct	cacctgtctc	gggtgggaag	gggatgtgca	7380
aacatggaag	cgttgccatt	ggaaggagg	atggagctcg	tggccatttc	taatgtttaa	7440
aactatcggt	ttaaattatac	tttgaatgtt	tttatgtaaa	ggaggtgcac	caaagggtta	7500
acagggtggt	gactctggaa	aggactcccc	gagagcagct	gctctgaatt	ttctaatttc	7560
gctacactgg	tgatgtatca	tgtattcctg	tgtgattcga	aaatgttaaa	agtcataata	7620
taatgtagaa	gacgaccctt	cgcgagcgag	gccccccacc	tctggccact	gagggcactt	7680
acgtaactgc	ggggcgggcg	caggcctcca	ctgggtgagc	ggcaggcg	ggcggggctg	7740
cccgagcg	cgccccgcc	caccctctc	ccccgccac	tgtccccgc	cagccccggg	7800
ctgctcgga	aggccggagt	ccggagcaca	gcaacgcgcg	gagcgcccg	gccccctgg	7860
tggtcccgcc	cacgcgaccc	ggcgcgagcg	gcggcgcccg	gacagctgcc	ccggcgggcg	7920
aacgacatgc	agcggaaccg	cgggaggctg	cggttcggtg	gctggacttg	cgccccccac	7980
ctcctctgtc	gcgcgtgccc	tgtccccag	tgagggcgtc	cctgggatgg	gatctggg	8040
cccggcgcag	cgcggtgac	aacagccgag	cggttcggt	gcgctggc	gtggctcg	8100
cctgcccccc	cggcctggcc	gctccccgc	gcgttccccg	gtgcaggtgc	ctggcccg	8160
ccccgccatc	tccgcccggc	gccgcctgtg	ctgaaggagc	cacgccccgg	gctccggagc	8220
ctgcctctgc	aaagtccagg	cccgcggcgc	gcaggtcagg	gccgctgctc	cgggcgagc	8280
gggacgcgcg	gtcacaggca	actcctgtcc	taagggcaag	tgagacagga	tcagggctgg	8340
tatgaaggca	tctccattag	cagggaacca	gacaccttcc	atctgactgc	tctgctatcc	8400
ttcgcatgct	gcctcatggt	ccaaagtggc	tgctgagcac	cagccttcgt	gtctgcatcc	8460
tagccagcag	gaacgaggtg	agagtgaata	aagatgccat	ttctttatga	atatgtccca	8520
gcagttcatg	tagatcacia	gaagccagtc	cactttacag	gcagaggtgg	actccaaaag	8580
gtctgatgac	tctcagaagg	taatgtgtgc	agcgggggag	caggattcaa	atgtaagtgg	8640
actgccatcc	gtacaatagc	agccaaccgg	agggcttcc	gcagtcagc	acctatccag	8700
cgcttaccta	gtcgtttaat	cctcacagct	agtgaagaaa	gagctggtta	ccctattgta	8760
cagaggaggt	cactgaggct	cagagagggg	aggtgatgtg	ctcaagactt	cagagccagt	8820
acatggagag	gttgggactc	caatccgggc	agtctgctcc	agaatccaca	ctttgaccac	8880
caccctccac	tgtcgctcag	ccttgtaaac	tctcccttg	gaatcctgtc	tgcaaacctg	8940
gttcaagttg	agatgagaaa	tgaggcaagg	gagggccatt	ggtgtctaac	agtcctgtg	9000
tcaaaaaata	taaagtacag	cgtgggaac	atagtaagac	caccgtctct	acaaaaata	9060
aaaattaact	gggcgtcatg	gtgtgtgcct	tagtgcctag	ctacttggga	ggctgaggtg	9120
agaggatcgc	ttgaacctgg	aagattgagg	ctgcagttag	ccaagttcac	accactgcac	9180
tccagcctgg	gtgactgagt	gagaccctgt	ctcaaaaata	acaataataa	taataataaa	9240
gtacttcttt	tgcactgtat	tcgtcacctt	ggcctgccat	aacaatatgc	catagacgga	9300



gtggctgaaa	caacagaaat	ttccccagct	tctagaggct	ggaagtcccta	gatcaagggtg	9360
ccagcagggt	ccagttctgg	taacgaacta	tccctggctt	gctggctgcc	tcgctatgtc	9420
ctcacatggg	ggagagaaa	atttctctgc	tttcttctta	gaagggtgaca	gtcctattgg	9480
attagggctc	cacctcatg	atctcattta	tccttaaata	ccttctaaag	accctatcta	9540
cagatacagc	catattgggg	gttagggctt	aaacatctga	atgtgtgggg	gctgagtggg	9600
ggatgcaatt	cagtcacag	cacagggtta	gtttacttca	gaaataaatg	aactagaatt	9660
tcaaagtcag	gactacagta	tcaaaagggtg	agaaccagc	ctttaacagt	ttacttttc	9720
tcatggtgtc	tagaacaatg	taatcaacat	tcccactgtt	cagatgggga	gagtgtgtgag	9780
tgcccttgac	aaagtctctg	ggaatagcca	ggatctagac	tttgctaggg	cagttgtttg	9840
taaaccacaca	gaggccatgg	gccatttctt	gacagtaact	gtaatcatct	tccgagcttg	9900
ggctctgggtc	ccaaatgata	cattgcataa	actaaaatgc	ttttcccttt	gaggcttgct	9960
cagcaagctg	cagaatctgg	ttgatcggtt	tgtacttgag	ttttttccct	tactggtaaa	10020
gagagagagg	gaaggcatgt	gctgagttcg	gccatgtgcc	aagccctttg	caaacattag	10080
ctccccgacc	ccaccactgc	tccttggttg	ttcccagtta	gcagcttggg	ggtaaaggag	10140
ctctcagggt	cacaccatgt	cagagctggg	ggtagccca	gagctgtcat	tcaagccctt	10200
gtttgtcttt	gtcctgtctg	acccccaaag	gagcttctct	tcgtaaaaca	aaattctttt	10260
taaaaaaacc	taaatatcca	aaattcacca	tctgttgcaa	tctcaatgta	ttacgttggt	10320
gcaaaagtaa	ttgcagtttt	caaagtaatt	gaaattggca	ttgaaagtaa	tggctaaagc	10380
tgaaaatact	tttgaccaa	cctaataaaa	gggtgtgtct	ggtgaaaact	cctgttgga	10440
tggttttttc	cccttggaat	cttgccaatc	aattaatttg	cagctctgct	actggccttt	10500
ctaaaacttg	aacctgggag	gttgaggctg	cagtgagcca	agatcacacc	actgcactcc	10560
aacctgggtg	acagaggggag	accctgtctc	aaaataatag	gtttttcagc	cttcccttgg	10620
tgggccatgc	tctcttctc	tgtttctctc	gtagctgaca	cattactgtg	tgtgggcaat	10680
gttctccacg	tagtaacacc	ctgtactaat	gatgagtgcg	ctgtctacgt	gactctattt	10740
agggcaaggc	aatttggtgt	aaatcctgca	tgaggagttc	aacaagaaca	aaaagcttca	10800
gaggaaaaca	tcctgcagcc	ttcccccttg	tctcagtaac	tatggtttct	gggcaaatta	10860
agaaaacact	caagaagggt	ttcttttttt	ttaattggagc	tgaagcacag	agcctcagat	10920
gggcacaaaa	tgatgaacac	atttattttg	attttttact	tataatacta	gcataatagag	10980
aagtacggta	aataataat	tccttccaat	taacaacaac	aacaacaaaa	aaccttctct	11040
gcgccagagc	agggaggctg	accaagaaaa	gagtagaaga	tggccactgt	gctccagggc	11100
agaggatacc	tggccacct	tcctctgacc	ccagagagtt	gtggggcctc	tgtcaggagg	11160
caccggctct	aacaagagct	gtgggtgtgc	tctgggcttt	ctgcttggca	ctgctgtcca	11220
gtgatcaaac	cacatcatcc	ttctgagtgt	cttcttgtga	cataacgttg	atgatatttg	11280
cttcaaccag	aaaagggtgag	actcagattc	agggttttgt	gtgtatttga	attagagccg	11340
accaggggcc	ttgggagctc	tcgggggtgc	tgaaggatg	gtcctcaaac	tccaaggatc	11400
agcatagtct	gtgcatagga	gtgagccagt	gagaatgtca	ttcattgagc	acctactgtg	11460
tgccctggcgc	ctggcttctt	cattatctctg	ttaacacata	tggttgctat	caggctgttt	11520
gcctctgcct	ggcctcagct	tggccctcct	gctctgaag	tcccagtg	cagccgtctg	11580
accaacatgt	gtgtggcctg	accgcctctg	tcccttgggtc	tgtacaacaa	ctggcttgcc	11640
tgtggcagtg	ccaccagcc	agcctgctgg	gccaccgact	tgctttgtat	cttctggcct	11700
tggaaaggct	gacttgggct	tgtttgtgag	ggagattgga	aaactggaag	gtgaggttct	11760
taaggctcag	tcttgattat	tctctaccat	ttttgtcatg	tgtgtttggg	tcaggaaaat	11820
ttgaaactga	accgtgagga	caggggcatt	caggctatca	tcctataacc	ccactccctt	11880
gtgctggact	gttacaatta	tttctataaa	atcagcctcc	ccatggcact	gtgagccact	11940
tgagggcaga	gcctgtgcct	tatccagccc	tctagcttct	gagcctggca	taggctcctg	12000
ataatagtgg	gagctcagtc	accattgatg	aaccagata	tgaatggat	ggaagggtga	12060
gcccacaact	tggatttctg	tcttgagagc	tggcgtctgt	gggagagggg	tctgtacaca	12120
gtcacgccag	cctctgcact	cactgagcac	ttgctgggct	tctggctctg	ctctcaaaac	12180
tgcataaata	tcaacatttc	caatcctcac	tgaacccac	gatataggga	ctatgatcct	12240
cattttacaa	atggggaaac	tgagtcaaa	agctatgcat	aacttgccaa	ataccacaca	12300
gcaggctcag	tgcagggtg	agatgagaac	cccagcggag	ttgccatctc	agctgtcaac	12360
cctctgcacc	accggtcctg	gtgccaaggc	ttcatcccat	cccccatgga	cctagtaact	12420
aaaacttttg	gtgacttact	tgatttgtgcc	cagtgaccgt	cacgcagctt	ggatgggagg	12480
gaaggctcctg	gtccccacac	tgctggggcg	tgctggggcg	aatcactgca	tctttccata	12540
cttcagttcc	ctcaacttca	gggggaggct	cactcctacc	atggaactgc	tgggagggtca	12600
taggccatct	gtgtgaagcc	cagggccctg	tgggtggcatg	attgtatgct	gtgatctgaa	12660
tatgatcatg	cgttattgat	ggctctgagg	ttttccctg	tggattttct	ttttcagaaa	12720
aggaaagggg	gctggcctaa	aggcaagaag	agaaaccccc	cgagggaacct	agtggttccg	12780
tgttcctacg	acagggttaag	atgcaggggag	attactctga	cccaacgttg	aagtaactctg	12840
cagggctcac	catgtggcct	ggggccacatg	gcggggttgg	tacgatccca	tctcagcctt	12900
tacctgttct	tttaggggtg	ttggtttagct	agggggcctg	acaccactgg	gagtgtgggg	12960
tgggctgctt	agttctttaa	gctgtaatga	ggctcctggc	ctggaggaga	gaggacagaa	13020
gaaccagggt	tgggttccag	acaggaaaa	gggtaggtgt	gggcttggtg	ggtctgcttt	13080

ccatcccagg	cttgaagaca	tgggcgctct	gtggccttgg	gtaagctggg	taaccttcag	13140
ggggctcaag	ccacccttct	cagcacctgg	gaccttgtcc	ctttcccatg	aatcttgccg	13200
catagaagaa	aggtcccacg	ccagctgctg	accagagctc	tgaggggtcac	cttgccccat	13260
ctagaagctt	gtacacttta	tcctcagggg	tcacacgggt	ctaacgctga	ggggcttcct	13320
tcagtattcc	tgtggctcac	atggatgaaa	ctggtttggc	cacagccttt	ctccctcccc	13380
ttcaaaagaa	gtccttgagc	aggaggggga	ggggcctgca	cctggagtat	tagggccacac	13440
ctgtgagcag	gtggcattat	gttcattata	caaaggggga	aacggagggt	cagatgggtt	13500
acatggtttg	tccacataat	gcagcatggc	tatttgaacg	tgtcccctgc	cagacacagc	13560
caccagcct	tcatacacct	cttgccctgt	ggggagcccc	tcttctcatt	cctaggcctt	13620
ttacgagact	ctgggttaac	aagccactgg	agggtgtgcc	cctcttagcc	ttcagttctc	13680
tgggttagact	gaacaagatg	ggcaaaccag	tgactcgttg	tgaaaaccgg	aaagtggaa	13740
gagctgcccc	tggccggctc	ccttccccac	cggttctcag	agccagggtt	gtcccttctg	13800
tggcacaggt	acatgatatt	cctgaatgag	cagagaagtc	agctgagggc	cacacacccc	13860
gatctgcctt	tcacagaaat	catgaagatg	ctggctgttc	agtgggccc	gctgtctcag	13920
gataaaaagg	ggtaagtcct	gttctatgtg	gtgaatacaa	agcgagtccc	cccgtagat	13980
ggggcctggg	cagcccgag	ccaccgccag	gggcccgttc	ctcctaatac	atttcttaca	14040
ccacagccag	agggaaacct	ctagagtgc	gacatgagat	gccactcact	caccatttta	14100
gagcaattaa	tgggtcccct	tgcttttggc	agcatctcct	aaactgggtc	aggcagaatg	14160
gcccattccag	gaatcatggg	ccggctgtca	aataagtcta	ggaaattctg	gaggaaatca	14220
agatcgtaga	tttctccctc	agcaggacat	ttttggcgaa	tctacaatat	atttgtgtag	14280
cacttgttat	gcctggcacc	acgctaggtg	ctggggatac	agccacaagc	acggccaatg	14340
ggggccctgc	tgtcctggag	tgaggctgcg	gaggaagaga	ccgagccaag	catgtaaagg	14400
ggcatgagag	tctctacgtg	tgagcgctgg	tgtgcggtgt	ttctcaaact	aatttacc	14460
ggagcctctt	tttcacagag	cacctgttaa	cctcctacag	aggcatgttc	tgggggccag	14520
gggaggaatg	ccaaattatg	gcataaggtc	aaagcccatt	tcgcatgaaa	tactgttaca	14580
ttccaatatc	acttctgcca	ccccagctg	tacctccag	ccacactgaa	caaactgttc	14640
attttctgtt	caagccatgc	ctgcctcagt	gccacctcct	acaataagcc	ctcccacacc	14700
cctaagaata	tctgacctca	aagcccatac	tttctccaga	acagcaccc	gcctccagag	14760
tgtcatttcc	ttgagtcaaa	tacaaagacc	ctgacgtgaa	cttctttaaa	cctctacaat	14820
ttcatcttgc	tttagtcata	gaaaactcct	gtttaacaat	tgacaaaatc	ctaattggggg	14880
gctcagttag	taacatccct	ctccttcc	cccagtttc	caaccaacta	ggaactatcc	14940
agtagccagt	cagatggaga	ttaaatgtca	gctgtattca	cgcaaagcga	gggggagggt	15000
gtctttggat	cagtggctcc	agctgctggc	agtgcgggac	aattcctggc	actaggtcag	15060
agcaggcccc	tgagcatgtg	gccaaagaca	gtgcagagcc	ttcgctgcct	gccagcggat	15120
ggcaggggca	aagagagagg	gaggggctct	actcagcatc	ccaaggcctg	gggttggatc	15180
tgattcgtct	gtcactagt	cccagcccag	gacctgtgc	agggaaaagt	gctgatgttt	15240
gcatgaagga	tcattgaaga	gaagtctaag	gttccccctg	gcaggagctg	ataatgctgc	15300
ccttctctgc	agtcatcaga	ccaaacctgg	agaatggtag	tggccacagc	aaggcagatg	15360
ccagttgatg	ggaaggaaaa	cagtgccatt	caaacaagga	atgaacttgc	ttggaggtag	15420
tgaggctccc	gtccctggag	gtgtgcaagc	agaagctgag	tagtagcttc	ttgggatcat	15480
cctaagagc	cccaggagg	ttggacaaga	ggatgccac	cctccatccc	cctcccaacc	15540
ccaaatctgg	agcgctcag	aatctctgtg	ctcctctc	cagaggtag	tgtctcaggt	15600
ggacgaggac	aagtagggt	atgtctgcga	gctacaggcc	ttccagagct	ctgaggccta	15660
ccgagcttcc	ctgcagaggt	gtgcagccca	caaggcgctg	tgtgggatgc	aggagtggac	15720
tggagttcac	ctctcccaag	ccggggctctg	ggatgtttac	gcagcagaaa	gtacgctggg	15780
aaagcccttg	gtgttactcc	acctccttca	gcgctcacac	cagtgccttc	gattgaagag	15840
ccaaagcagt	tggacatcca	gtctcttcc	tttcagccca	tcctggaccg	gttaaagatt	15900
aaagataaga	ggcagcttgt	tcctctctac	ctgggagggg	cagtggacat	tcagggagtg	15960
ctgaggcagc	ggttactttg	tagtgtttag	aaaagggaaa	ggaatcacag	tgacaggcct	16020
ggcacttctc	aaattccagc	atgcacacgg	tcaccgaggg	tcttgctggg	aggcagggtc	16080
tgtccagca	tggtcagggg	ggggcctggg	agtctgcatt	tctgacatgc	ccatgggcca	16140
tggctgctgc	gtgtccagg	cccacactga	ctatgtgcga	gggtgggttc	tcgagcactc	16200
accactccta	catgccgcgg	cacctcccca	cagcccagca	tctctgccgt	gggcttttct	16260
cagatggcca	tggggccaca	tgtgcagggc	agagctagca	aactgagcat	ctatgtaaac	16320
ccacgcagac	agctttccac	caccaccgcc	atggtgagac	aaatcccagg	tgggttccat	16380
accccagaga	gttcccatgg	gactgagccc	cattcctgta	atggccctgc	ccagccagct	16440
gactcacttc	cagccctact	ggtgcttcc	gagatcaata	cccaaacaaa	ccattgacac	16500
caaaatcctc	atctgggggg	cctggctctg	tccccagagt	ctgaggcaga	ggagggaacc	16560
ctatccattg	tctactcact	atgccttcac	catggaggac	actttccact	catttttctt	16620
tttccctctt	tttgaaagta	ttctcaatcg	cagagcccat	cagcagcact	tttacattga	16680
gaccacagc	gcggccaccg	gccaccagga	ttccagctct	ctctgagggg	cacaggcctg	16740
cagggcagca	ttgaagtgtc	cttgtcagtg	ggggctccagg	cgccagctct	tggccccacc	16800
agtggctgcc	ccagggcaga	ggtaggcttc	tcccagtggt	cctgggtcca	cccccggttc	16860

ccctgcatgt	tcctgccctg	cacgctccat	ggtcagggct	ggcccgcgct	cctaggacgt	16920
cacagcaagg	cctgcctatc	tttcacgttg	ctgcctctcc	ggctgagcac	cggaggaagc	16980
atgcatcagg	ggctctgcca	tccacgagac	tccaggacca	gccacgtgtg	ttccatgtct	17040
ccaccgggac	tggtctgagag	agctgccttc	ctgggtgacca	gggtgtgggc	tccagagtcc	17100
aagtgccag	gttggaatgg	cagctctacc	actcgggtggc	tctgtggcct	tgcacaaatt	17160
gctggaacac	tcactgcctc	agtttcttca	tctgaaaaat	ggggctgtca	caggcccttc	17220
tcctcagggc	tcagtgagga	tgaatgagct	aaaccacaga	gaggttggtg	ctcagcgcct	17280
ggtacatggc	aagtgttcac	acttgcggtg	agtgttcaca	cttagtgccc	ctccctgtgc	17340
gctggggcat	ggcccccacc	ctagcttcc	ccaaagcagg	ggtcagcaaa	ctttttctgg	17400
aaagggatag	atagcaactg	tcataggctt	tgtggggccac	gtggcctcca	tgcagtcac	17460
tcaactctat	gctttagca	ggaaagcagc	catagacaa	atgttcacaa	agggccgtgt	17520
ctgcatgcca	ataaaacttt	atttataaaa	acatacagaa	ggctgagttg	gtccacaggt	17580
aggtctactc	tggcccatcg	tacttattgg	gtttccacgt	aacctttgtt	ttcaatcaag	17640
tgctgtaga	taaaaataat	caactggaaa	atctctgtgt	tggtcatagaa	ctagcagata	17700
taccacgca	tggtggcgct	tctgatgggt	ccaggggagc	tgcaaggcct	ctggctctca	17760
tcataaatgt	cagatctctt	ggtaccagag	ttaagcagag	ggtgcctgag	aacagctgtc	17820
attctgtctc	ctgggtttct	cccaaatgc	catttgctca	agcttagcag	agaacagctt	17880
gtcttgctga	attcttcatt	catgctgagg	ccctgcggcc	ttctccttat	ttgggggatt	17940
gtttgtaaat	tgctgtcatg	caaaaacctg	gtgtgttaca	aggaaagggt	actccaacac	18000
agcagcctcg	tctttaaaaca	aataaaatat	atcactgcct	tattttaaaac	atagtaattt	18060
taagagtttg	ctgtataaaa	ataaattagt	agtcaatatc	cattttaaaa	gtatcaccta	18120
gaatctgcca	tgctaaaaaa	tgaagtttcc	attttctctc	gtttctccct	catcttcatt	18180
ccatcacctg	caggtgctt	atacattgac	atcagaggta	cctgggtgtt	ctctctggct	18240
cattgggggt	ttcagacctc	agattaaatt	gaaccgcatt	gatcctcctc	cagcaggtaa	18300
catgaagacc	cctcgagatg	atgtttgcaa	tcaaagaagg	cacctctgac	cctctgattg	18360
gtgtcccca	aatagggctg	agccctttcc	tgagacaaat	tctgaaaacg	cacctctatc	18420
tactgaggac	ctagcacttt	ctctctcacc	ggatgacaga	ggtcttgaga	tgaattgaaa	18480
ttctcatctg	tgctcagaaa	ggtgtcacac	ctagcaagga	aatttacagt	ggggaaaggg	18540
agttgcaggg	cccagccctg	tccacacaaa	gcccgtgtgt	ctttttcagc	tgattttatg	18600
ttcagagaag	gctggatcac	ctgcgcctcc	tccctgtctc	cctgaaaacc	tttctgtcct	18660
cagggagatg	aactcaatga	cctctactgc	gggacctcca	ggcagctctt	cagctccctg	18720
tgcaacaaga	aggaacctgc	tgcaaaggca	gcacctgcag	cgctctcag	gtaaccagcc	18780
tggggccagg	ggctcagccg	caaacgctgg	ccttgactcc	acctgcgcca	gaggtcacca	18840
acaggcggcc	cacgtgacac	ctcttggtat	taaaatgcaa	ttttaagaca	gactctagtc	18900
aagcccactt	accaccaggt	gggtgtttag	gacagggtag	gtcttccact	atatctgttt	18960
tcctcttagt	tcgccaggcc	cgctgtctct	gggccacgca	ggacacggac	gtcagcttct	19020
cctggagcgc	tcgctcactt	tattccatct	ctacgagctc	ctcaagtatc	ccagagcatc	19080
cccaggcctg	tggccacctc	gggtctggat	gccgcattct	ctgacctgtg	gcacattctg	19140
ggtgcccatg	attatgatga	ggttctgtgc	ccatgtggcc	tcagggctct	tgagaccacc	19200
cttcaaccag	gtctttgtct	acctgtctcc	tgcccaggga	cgccacccag	gtcaccgggt	19260
caaacctcca	gcccctgccc	gtttctctcc	atgagtgcac	tgccacctcg	cagcctcttc	19320
cacttgtctc	ttcctgggtg	tattgcctgt	ctcccactgg	aagagaaggc	cctcaggttc	19380
agcaactgtt	ttgcctgttt	tgttcactgt	gggtgaaccc	gggcctagaa	ccacgcctgg	19440
cactcccagt	aggtgtctca	taagtatcca	atgagtggac	aaatgaatgg	atgtgttcaa	19500
caaatagacc	tagagcgtgt	attccttcca	gggacagagc	gaggtactgg	ggacacagga	19560
aggacgaggc	agagctccgc	gctgacgaaa	ccaagggcca	agcgtgcgag	tgaatacgaa	19620
catcctggcg	ttaaaacgtc	ttgcattcta	gtgaaatgag	accatttggg	cacagagaag	19680
ccccaccaca	attgcatctg	tgtaaaatcg	agagaaaagat	cgtgaaaaca	gccatggcag	19740
gtgctggact	aaggggtgac	attgggtttt	ctcttcccac	ctatccttta	gggttggttaa	19800
aacagaaata	gatctcacgt	aggccctgc	tctgcaccct	gcttgcctgag	tcacgcaggg	19860
ccagttacgc	agctaccgtg	tgcttaccgc	gcctcatctg	taaaataagg	atgacactgc	19920
ctgcctggca	gggctctcct	gagaatacac	agtgccctgt	gcagggccca	gtgcagcaga	19980
gaggtcacct	cctccaggaa	gactttcctg	acctgggctt	ggggttgggc	ctccccaggg	20040
ctcctaaggc	ttccccacat	acctttcact	ttgcaatgat	catccctgt	tactgtccca	20100
caacacacat	tacacacaac	accatacaaa	cacatgcatt	ctacacacac	acaacataca	20160
catgcactac	atataacaca	cattatacac	attacaaaca	caacacatac	cccacacttc	20220
acactcatat	acacacatac	accaccacaa	tacactccaa	acactccgca	cacatacaaa	20280
cacatactac	atacaacaca	ctcataccac	acacatgcac	acacgggtct	ggagggcggt	20340
gctgtgtggg	gctccaggcg	catccctgat	ccatagcaga	tactgaatat	ttgctgaagg	20400
aatatccagg	agacttgtgc	tacgtctggt	gtttgaaagg	aaatgaactg	ttcttggttaa	20460
tgtcttgggt	aggggtgaata	atggcactga	agacagaaaa	tgcatcttat	cacctgtctc	20520
ggagcaaaac	atgtgtgctt	ggatgcatag	agttattcta	tgtaaatatc	ccaccagaga	20580
gaattcaggc	atgtttcaaa	atctataaaa	ccgtgtgctg	ggggaccatg	aaaagttgta	20640

gatgcacgtg	gccgtgaacc	actgtaaactc	tctggggggcc	tgcgtgaccg	tttaaaagga	20700
aacagacatg	ggcaaaccctc	gtttcatctt	ctctctaaat	cacctacaat	tttacagtag	20760
cagtcgggct	cttgagagct	ttcccatttc	cacttttctt	ggtggatctt	gctggaaatc	20820
agtgtttttg	gcagctgcag	tctctgaggg	ggggccctga	ttggggatgg	ggtgttaacc	20880
ttgcattctt	tggggttcag	gtctcaaagt	gctctttag	ccctgggatc	tgaggagcga	20940
gaccaggact	cagctatctc	caccccgga	gaaccttccc	tgctcttcca	catccagccc	21000
aggcctcggc	ttcctcgtct	gcaaaacgag	ggtgctgaga	agatgggagc	aggggtccag	21060
cgttttctac	agcagggctg	ttgagatgta	attcccatgc	catagtcccc	actgggtgaa	21120
agtctatata	gttcagtggg	ttctagtgt	ttttcagata	tatgcagcca	tactgtggt	21180
ggacttttaga	acatctctgt	caccccaaag	agcaaccccg	tttccattgg	tgtcactccc	21240
ggggctccgc	attcccagcc	cagcagccta	ggacaagttt	tctgcctctg	caggaagccc	21300
ccaagtttca	gatcttgatg	tctcctttct	gtggggagtc	cagcaggcat	ctccacctta	21360
gggacagctt	agtggacagt	gctgtgtcac	catcaagggc	ctgaatcccc	gctctgtcac	21420
ctactacctc	ttttaccttg	ggcaaattct	tcaccttttg	ccttggtttc	cttaggtgaa	21480
aatgggatca	tctgtctgac	ctcaagggca	gctgtaggat	tcatgttcc	tcatgtcacg	21540
gtctctaaac	gtgtggcaca	ttctgggtgc	ccatgggtac	gatgatgggt	ttgggggctg	21600
gagggatcag	tgactttctg	cctccacccc	ctctctagga	acggcaggct	gctaaggaac	21660
cccacaggca	catgctgtgt	ggctccctgc	acgctgtcct	tctcctgccg	tggtttttca	21720
cctttgtgtg	ccagtcttgc	tctgttcat	gcctcaaaat	cccacaaaa	agacaataac	21780
aggtgctggc	aagcatgtag	agaaactgaa	gccctgtgc	tctggtgggtg	acagagggga	21840
cactgcattg	gagaatggtc	tgacagctcc	tcaaaagggt	aaacgtagag	ttgccgtgtg	21900
accagccat	tccgtccgg	tggccaatct	gaggtttcag	tccaggctgt	ctggttccaa	21960
ggactctgtt	ctttaccact	ttctatgtgt	acacccaaag	aactgcaa	gtatgatcaa	22020
ccaaaaatat	gaacatgaac	gctcatcgcg	gcacagttcg	taatagccaa	aaagtggaaa	22080
caaaccaaac	gcccatacag	ggttgaatgg	ataaaccaaa	cgtggcccat	ccttacaaca	22140
gcgtaacctt	gggccgtaca	gaggagtga	gtatgatatg	caccacgatg	cggaggaaac	22200
ttgagaacat	agtaagtga	agaaaccaga	cacaaaggac	cacacacggg	gtgattccat	22260
tcacaccaga	tgtccagagc	aggagatctg	tagaggcaga	aaggagattg	ctggttgtct	22320
agggctgggt	ttcggggagga	taagggagtg	atagccaaag	gctgcgagtt	tctttataaa	22380
ggatgaaaat	gtcctaaaa	tggggtgatg	gttgcatgtc	tgtgaacct	ctaaaaacca	22440
ctgaatcaca	cacttacttt	atttttattt	ctttatttat	attttattat	ttattttattg	22500
agtcaagggtc	tactctgtc	gtccaggctg	gagtcagtg	gtacaatcac	aactcactgc	22560
agcctcaacc	ttccagggtc	agctgactct	cccactcag	cctcctgagt	agctgggact	22620
gctggcggtg	gtcaccatgc	ctggctaatt	attttgtaga	gatgggtttt	acgccacgtt	22680
accagcatg	gtttcgaact	cctggactca	aggggtctgt	ccacctcggc	cacccaaagt	22740
gctgagatta	caggcgtgag	ccactgcacc	caaccatgat	atgtgaacta	gatctcaata	22800
aagggtgtag	gcaaaaaaca	aaacaaaaca	aaaaaacacc	atctcaatca	aggaccctta	22860
ctccaggagg	cctcctctgc	tggcctctgc	ccctgcctgg	tcctggcggtg	ctctgcttgt	22920
ctgtctctct	gtccaccaaa	caggggaccc	tgaggcagag	gctgggtcgc	ccacatgtgg	22980
acagagggcc	agggctggaa	gtgctgctaa	ttctctgtc	gtgggtgac	ctctgtgaca	23040
ggatttcttt	gcttttttagg	ggaatttaaa	aaagatcctg	ccacgtactc	aaagcactctg	23100
gagcctctgg	aggaagagag	ggacaaatga	ggtcaagtca	gaggaggaag	ctgagggccc	23160
cgagtcctct	ctgctcagat	gtccgcaccc	agagaggagt	tctgcttctc	tcaacctgtg	23220
tttcttgcaa	gagtttatct	ataaattgct	gaaaaatggg	taatcaagtt	cagcaactcc	23280
ctggcatctg	tgatgacct	tggtttgtaa	tcctagtcag	aatcacctac	atagaggata	23340
taatattaat	cagaacaaaa	cagaaaagtc	gctagaggaa	taacaatagt	aaaatttaca	23400
atcagatgaa	gaataaagtt	ttcaatgagg	cacagttcta	agcacttcat	acaaataacc	23460
tgtcttaatt	ctcataaaag	tactgcaagg	caggtgataa	tatcatctcc	ttctaaagat	23520
aaaatgcagc	acagagaggt	taagtaactt	gtccaatggt	gaacagctag	tgagtgggtca	23580
atctgagatt	taaatccagg	ctgtctgggt	ccaagaactc	tgttcttcac	tacttctcaa	23640
caacatcaac	tatgtaaaat	gacacacata	cataaaccca	catcaatggt	aatgggtggt	23700
atctctggcc	ggcaagatga	aagaagatgt	tatgcaattc	ttcagtcctt	tctgtgtctg	23760
ccacattttc	cccaatggat	agatgtcact	taaattatca	gaggaagaaa	caaactctat	23820
taaaagggaat	ttcaaggggc	gggcaagatg	gatcacacct	gtaatcccag	cactttggga	23880
ggccgaggtg	ggcggatcac	ctgaggtcag	cagttcgaga	ccagcctggc	caacatggcg	23940
aaacctgtc	tctactaaac	atacaaaaaa	attagccggg	catggtggca	catgcctgta	24000
atcccaacta	cttgggaagc	tgaggcagga	gaatcacttg	aatctgggag	gtggaggttg	24060
cagtgaacca	agatcgcacc	actgcactca	agcctggggc	acagagcaag	gcttcatctc	24120
aaaaataata	aataaaataa	aattattggt	ttattctgct	tataaaatta	gcatattcat	24180
tgaagctagg	cacagtgggt	cctgcctgta	atcgcagccc	tttgggagac	cagggcgggt	24240
agatcacttg	aggccaggag	ttcgagacca	gcctggccaa	catggtgaaa	ccccgtctct	24300
aatgaaaata	caaaaattag	ctgggtttgg	tggcaggcac	ctgtaatccc	agctactcag	24360
gaggctgagg	cacgagaatc	gcttgaacct	aagaggcgga	tggtgcagtg	agctgaggtt	24420

gcaccactgc	actccaacct	gggtgacaga	gagagactct	gtctcaaaat	aaataaaaata	24480
aaataaacat	attaattgaa	gaaaattttg	aaatttcaga	aaagtatatg	aagaaaatgt	24540
aaacactatc	agtagagaag	tggttgtagc	atttcagtgc	agtgtttcta	gtcttatttt	24600
ctataaatat	ctgaatctac	ccgcctatatt	ctctatctct	ctacctaaat	atatctgcat	24660
gttattttgta	tatctgcata	tttatcttat	atttatctaa	ataaatatat	ctaactatat	24720
ctctatatag	agatagagat	agaaagatgg	agagaaagag	agatagagag	atggacatga	24780
aggtaaaatc	cgtcctgcag	ctcccatttg	cagaagagcg	tgagcatttt	cacatctcct	24840
tcaacgtttct	tttaggcata	gccccctctg	gctgcataat	atttcatcat	atgcbtgagc	24900
cgcactggct	gcccagttcc	tcactgtgtc	gttgtttgtt	tgtttgtttg	ttttgaaaca	24960
gagtctcact	ctgtcgccca	ggctggagta	cctgtggcatg	atcttggttc	actgcaaact	25020
ccgcctcctg	agttcaagtg	atttccggct	aatttttgta	tttttagtcg	ggatgggggtt	25080
tcaccacatt	aaccaggctg	gtgttgaact	tctgacctca	agtgatccgc	cctcctcggc	25140
ctcccaaagt	gctaggatta	caggcgtgag	ccaccgtgcc	tggccattat	gactgtacgt	25200
tttggtgaca	cctggttctt	acgttagaaa	tcaggctgct	gaacgttctg	ctctgtgtgt	25260
gtctttgtgc	ccattcttgt	tggcttcctt	agagggattt	ctggaagttc	aatgattatg	25320
taaaaagcac	aagccttgct	gggacctgg	agtggcgttg	gagtctctcg	tggttaggag	25380
cccaggccct	ggcctggcca	tcgggggctg	gaatcctggc	tgtgtcctcc	gtagccatgt	25440
gccccaggca	gctttcctca	ccgcctgcct	gtcctcagg	gatgcaggta	ggctctgtct	25500
catgggggtg	tcatggcgat	cacagagact	tgtccgtgtg	gaccacctag	agcagttacc	25560
agcagggcac	ctggcgccct	gggggtcacct	tggatcaggg	ttgcagctga	cccactccca	25620
tccctcccaa	aggcccttca	gcccagactt	ttgtgcaccc	caaattccat	caaaatcctt	25680
tttcccttga	gagtaacttt	attcatttcc	ctgcagctta	ttaaagaatt	ctgaagaaca	25740
gtgggtgtta	aattttttaa	aagaaagaaa	acattccagt	aatccaaagc	catcacgcaa	25800
tagcccaccc	gacagaggtc	cctgaaaaac	agcccacagg	ggtccttggg	gtttgcgtcc	25860
acgaccctct	aagcaagggt	cctcacctgg	cggagctcct	gaagacggga	gctcctgaag	25920
acaggcgccc	cctcctagga	tgccaaagg	cagaggccgc	agtgggagag	gcctggctga	25980
cagcttgat	tccagtgggc	tagagcctcc	agagccctca	ccactggatt	gccccttctc	26040
ttggctgggc	gggacctgat	ttccacctgc	acagccctgg	tgaagccacg	caaaaggaac	26100
ctgggaaagg	ctcaggtcca	gaattggatg	gacacaattg	tggaaactcag	ccctcctccc	26160
cggtcggggg	acctctggac	aggtccctga	gccccttggg	acttcgcttc	cccagcctat	26220
aaaatgaggc	aggcatgcct	ctctgaggg	ctgggtgagct	cttgagctcc	tgcaaacggc	26280
ccagagtga	gtaataggag	tttttgagct	gaattctcag	tctgttgcct	aggctggagc	26340
acagtgggtg	aatcgtaggt	cactgcaacc	tccacttccc	aggttcaagt	gattcttctg	26400
cctcagcctc	ctgagtagct	aattttttct	acttttagta	gagacagggc	ttcaccatgt	26460
tggccaggct	ggtctcaaac	tccctggcctc	aagtgatctg	cccatctcga	cctcccaaag	26520
tgctgggact	acaggcatga	gccactgcac	ccggccagaa	gtcataggat	tttaacgagt	26580
ggagacagtg	tgggtggggc	cattattcca	cttctggag	aggaagagag	atcctggcaa	26640
tgtctataga	tctcaggtgc	tctgcagggc	ttagtgttat	ttattttacat	atttacttac	26700
ttgcttattt	atttattcac	ctatttattt	acttatgtac	ttattttacat	atttactttt	26760
gatttgctga	catatgtatt	tacttattca	tttacttata	tatgtattta	tgtacttcat	26820
tccctttctt	atttactctt	tcacttggtg	cccgtctatt	catgacatct	gagtgtctct	26880
ctcccagtag	aggccagggc	atgcacctct	catgttctct	tcagaaccag	cagtagaggc	26940
tggaggtgga	gctggcaggg	ctgaagacct	atggggggga	cctggaggag	tttgagaccc	27000
tcagcatggt	gctgatgctg	tcccacttca	gcccgcgaagt	gatggacacc	gggtgagccg	27060
ggcgtggag	ggcgtcgtc	gccccctcca	ctctcccttc	tcccctctcc	cctgcctcat	27120
gctccttccg	gtctcacta	ggccatacag	ccaaggccct	gggacactcc	tgtctgtcca	27180
ttgacttatt	cgtacatgct	tcactctttt	cttcactcaa	caaacattcc	tgtgtgtcag	27240
cgcacccag	ctatgctgtg	tgtggaggga	tggggagata	gacaatgact	ccggtcatcc	27300
ctaaccagc	cccatgggta	ccaggccctg	agctgggcac	tgggcagagg	aatgcagaga	27360
tgaaggagcc	cctggtaagg	agcctgtcag	gggacagggg	cagggggctg	gggagtctgc	27420
ctccatggac	aagggtccgt	tggcactcag	gtgggaggca	acgagttatg	cagcaggggtg	27480
gctcagcgaa	gggccagata	gaggccagag	ccttcacagc	gggcccaggg	ggacagttac	27540
aaactccttc	atcaaagggg	acaccggcac	gcaggcaggg	aaacctgtgt	gtgcaaaggg	27600
aaggagattg	gaaatgcaga	ggaaggagg	gagggaggag	agcagtagat	gatgcacctt	27660
tgtgcaggat	cggaggatac	acgctttttt	tttttttttt	tttgacgcag	tctcactctg	27720
ttgcccaggc	tggagtgcag	tggcgtggct	tctgctcact	gcaagctccg	cctcctgggt	27780
tcacgccatt	ttcctgcctc	agcctcccga	gtagctggga	ctacaggcgc	ccaccaccaa	27840
gcccggctaa	tttttttttt	gtatttttag	ttagagacag	gtttcactgt	gttagccagg	27900
atggtctcga	tctcctgacc	tcgtgatccg	ctgcctcgg	cctcccaaag	tgtgtgagatt	27960
acaggcgtga	gccaccatgc	ccagccggat	acactctttt	ctttaagaa	aaactcatga	28020
atgccatttc	gtcctaaaat	attcagacgc	aatccttttg	acagtacaga	actggggcca	28080
ttccccttcc	tctccctgga	agttttcgtc	gttaacattt	tcatgtgcat	ctttccttcc	28140
aggcattttt	ctatttatga	atgaatgggt	tgatagttga	atagttgaaa	actggcactt	28200

ctcaggacac	caccagcaag	caggctttgt	ccttgaggca	gggtccctgg	gggtcatgtg	28260
ctgagccagg	tttcagcacc	ttagatgggtg	gatgggtctgg	gggacatttg	ccaaacagac	28320
ctgatgtggc	cccactagt	cgtttctgac	cagccgtcag	caccatacaa	acactagcag	28380
agaagctcgc	ctgtcagcag	ctgtattcct	atttcttacc	catgggaggg	cactgttcat	28440
attgttcttg	gtgtgctgtt	ctgcgcctga	ccttagcactc	cttcccatct	acatgtagtc	28500
ccctttgttg	tcacctgtgt	atggtgtgat	gcagccaacc	ccagcaccct	gtccccgctg	28560
atggacactg	cagtggggac	agcctacggg	tacaccagca	cacgatgggtg	cagtgactcc	28620
tagggcacac	cacggctgga	cacaggctgg	agcactcctg	ctctcaaaca	gtgaagctcc	28680
gacccaggcc	cctggcatga	gaggggtggg	tgggtcctgc	tgctgcagaa	gcttgagag	28740
acccttcccc	tccatgcccc	tccattcccc	ctaaccttga	gtgagagcat	tggccttggg	28800
gtgatttcca	tgtgaaattt	tacacatata	cctagttagga	ttggacaaaa	gtggtcaggc	28860
tcgagkgcta	ctaaggaaga	aggaataggc	agacttgggt	cttaccagat	gcagggagca	28920
ggtaggaggg	acactcttta	gtgttaataa	gcccaccagc	ccccattctt	tcttccttga	28980
cactcagatg	caattcctgc	agtcatgaya	ttggctgctt	tgggaagcag	ctgcagaatg	29040
ctgtgggctg	ttgggcagt	gggggctggc	taacgtcagg	tgtgttcaca	tgagcgtcct	29100
cacagggaac	gtgtgatgga	aggtgctgga	gctggtacct	gggcagtgtg	atgagaaagg	29160
aacgtggctt	tcagaaagca	gagttacaaa	tgcattctagc	atcaagtaat	gtccagaaag	29220
cagttttgcc	agattcagct	ccttcctggc	tccagccact	ctctctactt	cctgcagttc	29280
ccactccagt	ccgctcacta	agttcattcc	ttccagaaga	catcttctga	gcacctactg	29340
tatgacaagc	cctgggcttg	gtgctggaag	tccagaaatt	agagatgttt	tatgacttca	29400
cagggtctcg	agtcctcagaa	gtgtggcaca	ggggtagtga	atcaggggta	ctgggtgtgt	29460
caaggcatcg	gggtgacctt	gagtcagtga	caccaggggt	actgggggtg	ccaaggtggg	29520
gagcagagct	tcagccttca	agacccagtc	ccagggcaaa	gtgaacctcc	gagttctttc	29580
ccagggcccag	taggtctcca	ggagggttta	agaggagagt	gaatgaatta	agatcaagt	29640
agactgggtc	tccccagct	ttgtcctggc	agtaactctt	cctctccctt	ccctactctg	29700
cagcataagg	ccatgtcctg	cccagggacc	agcctccagg	acccctccca	ggtgctcaag	29760
tgtagctccc	atagcagcaa	aggaaggatg	caaagtctca	gggctttgca	ggtggacagt	29820
cagacagctt	tgctgaccaa	ggagaaaata	agtttgtgtg	tgtgtgtctg	tgtgtgtgtt	29880
catgagtgtg	catgtgtgtg	catgcatgtg	catgtatgtg	tgacagtgtg	agtctgtgtg	29940
agcaaccagc	tcagtctgtg	tctgtgtctg	gggctcagca	gagcatctgc	tctgtaagt	30000
ttcctactgt	ggactataac	ctgggcagca	tgattttggg	aagatttttg	taacatggct	30060
ccatctttcc	acacctgaca	tccttagag	ggacatgtac	acacccactc	tgacctagt	30120
cacaggcgcc	aagcagccat	ggggaccaga	gcgcttacgg	tcttggcctc	tggagccctg	30180
attttgagcc	cattgctacc	tcctgtgggc	caccacgggtg	acttggggca	cagttgggtt	30240
tctccattga	ggagacaacc	aacaacatta	ggtcaataat	cgctacttgt	cagccttaaa	30300
tgggtggggg	aagatggagt	aaggcaatca	acttgtccaa	gtttcggtcc	ccaagaaacc	30360
aaccccaaga	tcagcatttg	cctgcaagcg	ggttatctgg	gaggtaatcc	caggtagggg	30420
atgttataaa	taaattttca	tggcactcgg	acataaattt	aattttctca	gcaaggcaat	30480
tttacttcta	tagaagggtg	tgattcgtgg	atggagcaat	ggcaaaagca	cacctgaaca	30540
agggagggga	aggggttttt	atttctgact	caagcagccc	ctcctgctgt	gtcattcccc	30600
tattggctag	tgttgactg	cacagtctaa	gctaattcca	actggccatt	tcaaagagag	30660
caggggtacg	agctggagt	gcggggtgag	tagtttggca	ggaaagatgg	ttacagaaca	30720
ggtgactcag	gatgactcag	gtcagagcag	gtgaccaggg	gtaactcggg	acagagctgg	30780
tgatagaggg	aaggaggggg	ttgtttactg	aaactagggg	caaggagacg	aaaaaaacga	30840
ggaagttaaa	ctttaaaacg	aagaacaaag	aacaggggag	ctgaacatac	tgatacatta	30900
gttattttgga	gaggatctca	gaacccattg	tactcaacaa	tttacaggct	aaaacctttg	30960
aagaggaatt	tattatatgc	tatagggagt	tagggaagag	aaactgggaa	gggaagacag	31020
ctttgtgagt	taggggggtta	tcctagccac	tggagctggg	aaagccagaa	gccagcgag	31080
cgcgtgcac	tgagagtcaa	cacgtgatgg	cgaggaagcc	aggggttttg	tgacgagct	31140
ccctccagtc	tgacaggaga	ccgcttccag	gaggacttcc	ggcctgctgc	accagtggca	31200
acctgagcac	agaaggccag	aagagccctc	gggcagggag	tgcggtgctc	ccccgtggag	31260
gctgtgccct	gggtgctcgg	gtgtgggggt	gccccgcgct	cctgggagcc	gagcaagggc	31320
gcgacccccg	cagtggggaga	ggggcttcc	gcgacgcg	ggaggagctt	ccaggacggg	31380
agctgtctgg	ggcagagccc	tggctacggg	ggcctcgcag	cacagcgaaa	gcacagggac	31440
tgcgagctcg	ggaggcgctt	gctctcgtg	cagacccccg	ggtgcgcggc	cgcagtgctt	31500
gcagccatcg	ccctacgggg	cctcgcgact	cgggcatcgc	ccctgctctc	caggcaggac	31560
tagagcttcc	agaaagtccc	agggcacccc	tcgcgcaccc	caggggagcc	gcggggcgtg	31620
caaagcctgc	tgggaggtgt	agttttcgct	gaagacgggg	ctgccagag	ccaaagcagg	31680
gtgggctcca	gagcaagaag	ccatcgtgga	cgcggcgtct	gcgggaggaa	agcagctcct	31740
tctggcttcg	cgaaggccgc	ctagtccagg	agccccagcg	cccttctccc	agccaggtgg	31800
atgacagttc	ccagcgctc	gaaggcctgc	tctgtgcgcg	gcgccttga	cacacgattg	31860
catttctctgc	acgcagcccc	ccggcggggc	aggtcgagcc	gtttacggat	gggaagagag	31920
agccccacac	cttggtggag	gcgcgcgtcag	caaaggcgag	ggcttctttt	ccatcctgac	31980



tgtgtctgtt	ctctgctctg	accgcggggc	ctgcagggct	gttagcccca	tttgaggag	32040
gaagggcacc	cttttctttc	cagaccagtc	tctccctccg	ggcagttacc	acctcctccc	32100
taccggccct	gccctccac	tttaccctcc	ccccacggt	tccggcattc	tccctgcttc	32160
ccctctgggc	tgggagctct	tccagagccc	ggacctgggt	gccagctggg	ccaaccttga	32220
tgagtgatta	acagtcagat	tctccaaatt	agactatgaa	taggattcac	agataaagca	32280
gataaaaata	cagacaccac	cagctaaatc	tcaatttcag	atagacaact	ttcagtgtaa	32340
gtcttacagt	aggtaggtag	tcagacagga	gcagggcagg	agagccacca	ccgcccccca	32400
tgcagccagt	gccagggaaa	gttgggtctcc	cactccgtag	aaacactgga	agctgggtgat	32460
cagcagcttt	ccgaatagat	cgcaggagtt	gggcagggtg	gctcaagcat	tcacgctaag	32520
aggcaaaatg	gtggagttaa	actgggtctgt	aaccttctag	gagaactcca	ctggtaaggg	32580
aagcagcgct	caagagagca	tgcgtacaac	tctggtaaac	acaccgcaat	gcagcccctc	32640
ccaagtactg	gcaggccact	gtgaatacac	acagcccacc	ccaaaggaag	aatcagggag	32700
aaggggacaca	accccgaaga	agcatgccaa	catataaaac	ccaaggtcaa	agggtgaaac	32760
gcacacttga	tctctcaagt	caccacagtg	gccctcttcc	aagtgtactt	tacatccttt	32820
ccttcctgct	ctaaaacttt	ttaataaact	gtcacattag	ctctaaaact	tgctcgggtc	32880
tcaaactctg	tcttatgccc	ctaggttgaa	ttatttcttc	tgaggatgca	aagaattgag	32940
gttgctgcag	acccatatgg	atttgccact	gtaacgtaa	gtatatccct	tgcaatattt	33000
gggatatact	tatataaaag	ttatccgttg	tttatgtgaa	attcaaactc	aactggatgt	33060
attagtctgg	gttctgtaga	gggacagaag	taataggata	gatctatata	taaggagaat	33120
ttattaagta	ttaactcaca	tgatcagaag	gtcccacaat	aggccaaatg	caagctgagg	33180
agcaaggaga	gccagtccga	gtcccaaaac	tgaagaactt	ggagtctgat	gtttgagggc	33240
aggaagcatc	cagcgtggga	gaaagatgga	ggctggggag	ctaagccagt	ctctcctttc	33300
acatgtttct	gcctgcttta	tcttctagcc	tactctggcag	ctgatcagat	ggtgcctacc	33360
cagatgaagg	tggggtctgc	ctttcccagt	tactgtactc	aaatgttaat	ctcctttggc	33420
aacacccccca	cagacacatc	caggatcaat	actttgtatc	cttcaatcaa	gttgacactt	33480
agtattaacc	atcacactgg	gcactcctga	ttttatctgg	caaccctaac	actgactatg	33540
tagctcaattt	agctcagccc	cttcctgtca	ccataggaaa	tacaggtgcc	cagaggggga	33600
aaggggtcct	cccagacaca	cagcaaattg	gtagtagcta	tccccaggca	cctggaactg	33660
agacagggct	tttccacaga	ataaactaa	agtggcagtt	tccaagttag	gagggagcag	33720
tgccatgggc	caggaggtgc	agtgcgtgtc	ttgggcagca	agaggaagga	ttacctgca	33780
gatggtgggc	agggttaatt	ctggccttgg	tgctacctcc	agaagcctgc	aggacctgaa	33840
gcccaccctc	tcgccttttt	tcccactgc	cacaagcgag	ttagaatagc	tgggggatct	33900
aatacttcca	gtctcgatgt	cagcagacac	gcccagtcoc	cacactcaat	cttatctcca	33960
ccttagctca	ggtggggcac	tgagcagggc	actccctctc	tcagcctcag	gtttcagatg	34020
tataaaatgg	gatatcaata	cctgacgggg	ttactgcaag	gatgaaagca	gatgcatttt	34080
tttaaagtgc	cctgtgtgat	gcttgatctc	tgacagggct	ctagacctag	ttattcatgt	34140
tgttattgac	agtcactctc	ccaggatcaa	tgctgggaga	tgacagtata	acaaaaccca	34200
gatggactgc	ctggcatgtg	ccatgcctgg	gtgcactgtc	tcgtgtaatc	cctgtggttg	34260
agccttattg	ctaaagtgat	tccattcaca	gtgcaccttg	gggttcaggt	cgggccttgg	34320
gtttctagtc	tggccagcaa	gcaagcccc	cagctgaggc	gcccacacat	ctccacccaa	34380
tgagcccgcg	cttacaggac	ctagggccac	cattctgggt	cattggggat	gaaacagcca	34440
aacctggggc	ttcagcattg	cgggtgaggt	cgaggagcag	agaggagtga	agacacagca	34500
cattggtgca	catgcgcccc	ctcctagtgg	ctcgggctcg	cgatgccagc	ctggectgca	34560
cctggagctt	gggtcccaag	cctcagcagg	acattcttct	ctggccaaat	ttaaagtgcc	34620
ccaggaaacc	aaatcactag	gggtaacaga	gcaagcagag	ctgtggcatc	acagtctcag	34680
tcacctgtct	gggacaggag	gcatggtaag	aaatgaattt	tacatatggc	ccagcacaca	34740
gatataacta	agaccaagcc	cttgcccaac	aatatttact	ccacttcaga	ggtgcgctct	34800
gaccctttgt	tttcttttct	atttcatatg	ttttagctac	tgacacacagc	ccactgaatt	34860
gctttcagga	cttcttaata	aagcatggga	tgacgcttta	aaatcttaga	caatcctcat	34920
cacagaccct	ttaaatttga	cgaccacctt	ttatggccag	acaagttgaa	gtcgtgagcc	34980
gtgaactatt	tctctctctc	acgcccggaa	gtgcctagac	cacagtgggg	ggccggccag	35040
cccttccatc	ccaagagcca	gcccctgtgg	ctcctcggc	ccctgcataa	atatggaact	35100
ctcaggccag	gatgggaact	gccagggctc	aagcagtaaa	ctttataagt	tattacaaaa	35160
cagaagtgtg	cacagggaca	ctgtaataaa	gcgtattggg	agttacggga	actctccaac	35220
aagtttagaa	tctctggttt	caaaaactat	tgcaacatta	taataaacia	atatccaaaa	35280
gcttagaaat	agaaattaaa	gataaagatg	gtcacgtttg	acaaaaagaa	caatattttc	35340
gtactgagct	ttgatgatac	aattattaat	gaggaagatg	attttaaaat	taaattcccc	35400
ttgtaattca	agatacagtg	atacaaggca	taaacgggca	attacgctat	agtgcatcca	35460
atccttaaag	ccaccgctgg	ttttctgtat	aacccccaca	gggtgcagga	aggctagcca	35520
tgaaacatta	aaataccact	gtctgtctac	attttaaaat	aaattcagat	tcacataaaa	35580
atgatattga	taaagagtta	aatattttta	gaaaaattgt	tctgcaagaa	tcacagctc	35640
tagatatacc	aacatttgta	tttcaaaatt	ataaaaaatg	tatctcaaag	ttattatagc	35700
ctataagata	ctcttaatat	ctccaataaa	aaatgcatca	gcagaaaggt	ccttcttaaa	35760

atggaaagtg	tcctaaaatg	atttgtgagc	ttgtatttgc	caacagcaac	tgatgtcaca	35820
ttcaattata	tcgattgaaa	acaaagtgtc	taaaagtgtg	agctttgata	acctaataaa	35880
tgaatttgca	gaaaagtggag	ccagggaag	cttctaatac	agttatcaca	taaagtatta	35940
tttgttttat	tgtataaata	atcacacca	aatattatt	ttgacaaatt	tgtaagttta	36000
tgttgttact	catgcatcac	tattatccct	attacattgc	ataagtaata	aatttttcaa	36060
gggaaaagct	ttctatttca	cccctgtaac	tgcactttcc	tcctgctttt	tgaataaggg	36120
gcctgaattt	ttattttgca	ctgggctttt	caaattatgc	agcaagggat	gatccagcag	36180
gtggagagct	ctgagctccg	agtggactgt	gccgtgctgt	ctgtgatata	tgctaacata	36240
gaatgtcttc	cgatatgtta	ctgtgcatgt	ggggagtact	ggctttgaat	caaaagatcc	36300
ttggtgaaaa	cccctgcctc	accactatgc	gtccttgggg	aagtcacctc	tgcacctttt	36360
ctttgacgtc	aggtagtggag	atggcacagg	gaagcgcctc	ctgtggggac	ctgcatagag	36420
gggaagctag	gtggctctta	agtgtgtaac	ctcttccgca	cgcaaaagtg	tgctctaagc	36480
accagccgca	tcgacatcac	ctgggaactg	gttacaatg	ccgaatctag	agctcgcccc	36540
agacctattg	agaaagaatc	agcattttta	taatattcca	agatgatctg	taggcctggg	36600
agtgtctaag	aagcgtggcc	ctagacaaac	ggcttgggga	ttacctgagt	actttgccgt	36660
ttaaatttag	tcctaactat	tgtatttcaa	agagtgaaca	ctagagggca	caagagtcaa	36720
gtgattagtt	gtttgatttg	ccaaccagga	gcttggaag	agaaaaataa	aatgtcacaa	36780
acagggtctg	gagttacctc	caagagtcaa	atcttctctc	acacccccga	tccccacccc	36840
aaagacaaga	gctttctgct	gacctcctca	aaagcatggg	tttttttttg	gagggccaag	36900
gtgaggggtg	ggttttttgt	ttgtttgggg	ggttttgttt	ttgttttttt	gaggcagagt	36960
cttgctctgt	cactcaggat	ggggtgcagt	ggcatgatca	tagctcactg	cagcctcaac	37020
ctcccaggct	gaagcaatcc	tccccatcag	cttcccaagt	aactgaaacc	acagggtgtg	37080
accacaatgc	ccagctaatt	tttttatttt	cttttttgta	gagacatggt	ctcactatat	37140
tgctcaggct	ggtctcgaac	tcctgagctc	aagtgatcct	cccacatcag	cctcccaaag	37200
tgcttgggta	acaggtgcga	gcttccgtgt	ccggcctcaa	aggcatgttt	aatcggaat	37260
gtgcattggc	catgggcctc	cagatctgag	gtcggaggac	tgatttccac	agcggaggcc	37320
ctacagttga	gccagcctgc	agggatgtgg	gaaccacagga	ctgggggggt	tggggcttgc	37380
acggcactca	ctgccaccag	gtgaccttgg	gcaagtcact	tctctcctgg	cccgcgtgcc	37440
tctatcctta	aagtgcaggc	agttggcgcg	cgagattccc	gggggtccctc	tcggttttta	37500
agcctaggct	tgcatagtat	gggtcttttc	ctgttgacgc	tttctgggtt	gtgcccacga	37560
atgttcagg	gaaatagaac	caagcccaac	gcttctgtct	ccagagataa	gatggccttc	37620
tcttcctgtc	atttaaggcc	ctgggaggcc	ctagaatttg	gagtgctgtg	caggcctgga	37680
ctgttaaggt	gcccagcatt	ccagaggcga	tggcacattt	gtctgtgtca	aggaggctct	37740
gggcatgggt	agggaggtgc	gaggtaagag	agggcagagc	tgagggcaca	aatccagcca	37800
tttcacagat	ggggaaacca	aggttcagag	gaggacatgg	ctatagccca	ggtccctgta	37860
gcccggagtc	agtgggtggag	ccaggacttg	aactcaagta	ttggagtgc	aaaggcagca	37920
gccccaatgc	tgacggcatc	ctagcgaggg	ctctgagccc	tggagtcgag	tgggtgcttg	37980
ttgectgggt	ctctggggga	gctcgcactc	cctggcattc	tcatgggcac	ctcctgcccc	38040
aggcagagct	ccaagccttg	gccagcagag	caggacaggc	ctgcaggggc	tgcccacgga	38100
cctagtgttc	tcgggggttc	tgccaaggta	acaagagcag	ggagggctcc	ctccccacgc	38160
tggatctctc	ccagtcctct	gcttggctcc	aggggcacta	actgggaccc	tcaagcctgc	38220
tggggcacag	tggtagggcca	taccatccca	gagcatggct	ctgaccaggc	cactcccctg	38280
cttaaagcct	ctaggggccc	ggcacagtgg	ctcaagcctg	taatctcagc	actttgggag	38340
gccgaggcgt	gcggatcaca	aggccaggag	ttcgagacca	gcctggccaa	tatggtgaaa	38400
ccccatctct	actaaaaata	caaaaattag	ccaggcgtgg	tgggtgcccac	ctgtaatccc	38460
agctactcgg	gaggcaggaa	aatcgcttga	acccaggagg	cagaggttgc	agtgaactga	38520
gatcccacca	ctgccctcca	gcctggggcga	caagagcaag	acttcatctt	gggggaaaga	38580
aaaagccttt	agaggctccc	tattgcctgg	gtgatacagc	aggtggcatc	ctcactcctc	38640
agcctgggtg	tcaatgcctt	tggcttggga	cccaccctcc	ttggccatgc	acaccaagct	38700
gtccttgccc	agggcatctc	ttgctgggcc	cacctaaagg	cacgcagtgc	cgcccacctc	38760
cctctttcca	tcttatttta	tagagccctc	gccgggtgcc	aggcagtgtc	taggcactc	38820
gggggcaatg	gtgagcaaac	ggagccctcc	ctctttggac	tcatgttcta	atgggaggca	38880
ggcgaagaaa	tcaacagcta	agcttatggc	acccagcagg	gaggaaggaa	gggggacggg	38940
atgggagggc	tgagtggtcc	cctagggtgg	ccaggggagg	tgtctgagaa	ggtggcacat	39000
gtgttgggat	catgaactct	gggcgtggct	gtgtagcatc	caggcagagg	gaacagcaag	39060
tgtaaggacc	tgaggcagga	gtaggctcag	catgttccag	gaccagcaag	gccagcttga	39120
ggccagtgg	caaaaaaaca	gtggaggtgg	gagatggggc	ccacgggtga	caccgccagg	39180
ccacgcaagg	ccttgggggc	attggaagga	ctttggcttt	tacattgaga	agacagagct	39240
cctggagggc	tttgtccaag	gactgatgag	cccagacatc	actggctgct	ccggtgagcc	39300
tggaggggc	acaggggagg	aagtggggag	accatggagg	gtgacccgtt	tccgtaaaac	39360
tgaacccctg	cagatgccat	tccatctacc	ttagccctcc	cctgcaagct	gtgttccggag	39420
aacgcctata	tgttcacgaa	agctaagctc	aaatgccacg	tgcttgctcc	ttcctgcacc	39480
ccaggtagaa	acacccctcg	ttgcctctca	attccactt	tctttgagca	ctgtttttga	39540



aagcacctgc	tttgtagacc	cctacagaaa	ttctcacttg	tgagcatctc	ctgctctggg	39600
accagatgct	gagcccttgc	aagagagcag	ggagctgggc	tgggttttgc	atcatggagc	39660
agtgcactcg	gccttctgca	caggccccc	agccaccag	cagggccttc	tgggtagcct	39720
caccagagcc	aacggaatca	aaatctgtgt	tgggggtggg	ggcttgagct	tctgtcttta	39780
aaattcttcc	aggggtttgg	gttaattttg	ctccctgggg	ctttgtgtta	atttgtctcg	39840
ctgggagtag	gggcccagcg	agatcgctct	aaattcaa	cctgcagcag	ccataggtag	39900
ctgtgggatg	tggctactta	atctcgctga	gcctcggtcc	ctcttctata	gccccaggtg	39960
cccagcaggg	cgacagaggg	tgtggccgcc	tctcccacct	ctttgaattg	ggctgagaga	40020
cagacgcgca	ccttccggag	aggaccgtca	ggctgaagaa	gacacagcta	gtgtctaacg	40080
ggagggttag	ttctaaggaa	gtgaagattt	atgagagaaa	tgagttagtg	tgatcatgtg	40140
tctcatacca	cagcgtgtga	gtccgtgcaa	acgccatgtc	tgtcccctct	caggagaacc	40200
ctctctcaga	gctatgaaaa	tccttaccat	tgcctcattc	agactctcaa	agtctgaact	40260
ctgtcacttt	agagcacagg	actcaaattg	gactgtgctc	aggaatcaga	tgggggttgg	40320
gttaacatgc	acattcccat	gggcaggtcc	agggcagggc	ccaagattgc	atttctagct	40380
catccttggg	gatgctggca	ccactgggtcc	acagatggca	ctttgagcag	caagattgca	40440
gcccctaagc	cctactgaca	tagaatctgc	aatgtaacac	tatctccaag	agatgcgttt	40500
gcacactaat	gtttgagaat	taccagtga	gagacttggg	agaatgctta	ttttgggggt	40560
cagcatgccc	tagagagagg	ccaagaatac	gtttgtcatt	ctggctcctc	ttcaataact	40620
gtgagtgcct	cttgggtttat	tgttagacat	tgagtatttc	agataattcc	tagtcagctc	40680
cacaaaagcc	ctatgtgagt	gtgtgcagtc	atgtctggcc	cccagtggag	gagtggcaga	40740
gggtgtgtgg	tggcccggga	aaggtgtggg	ttctgcagag	agggaaatta	actttgggtt	40800
aggctgctta	ctgggtgcca	gctttttgtg	ctgatactg	cgctggatt	agttmccgta	40860
tgtactcttc	acagcagcct	ttggaggcag	atattactac	tgtgttacag	atggggaaac	40920
caaggttggg	aggaggaaag	gcacttgccc	aaggcaagct	ggctagcaga	gggtgagacc	40980
gggattgaag	tcaggcttgt	ctgtgtgtca	gatggggcaa	agctagctgc	ggcaacaaat	41040
caaccccaga	ttgcaggagc	ttggcaaaca	gaagttcatt	tttgttccct	aacagtgcaa	41100
gctgggtactc	ctgggtgatg	ggccaccttc	ctccacatgg	tgactcaggg	atccaacctg	41160
catccagcct	gtgggtatcac	tctcccaggg	gcctcggaga	gcccactcsg	tggctggcag	41220
ttggaggatg	actgtgtaga	gacggtagag	tcttctttta	acccatagcg	cagaagtggg	41280
actcatcatt	tcccaggcct	cccattgggtg	agaagcagtc	acatagtcac	acgcacgggtg	41340
agggcactgg	gagctgtcac	ccaggctgga	gtgcagtggt	gcaatcatag	ctcactgtag	41400
ccttgaactc	ctgggtccca	gtgatcctcc	agcctcagtc	tctagagtag	ctgggactac	41460
agggttgggc	accatgctg	gctaattaat	tatttatgta	tttatatttt	ttgtagagac	41520
gggtgatatgg	ttaggccttg	tgtccccacc	caaattctcat	cttgaactgt	aatctccata	41580
atcgtcacat	gtcgagggag	agaccagggg	gggtgattgga	tcatggggac	cgtttcccc	41640
atgctgttct	cgtcacgggtg	agtgagttct	ttgagatctg	atgggttctat	agggggctct	41700
tctcccttcg	ctcagtgtct	ctccttctctg	ctgccttgtg	aagaaggtgc	cttgccttccc	41760
cttcaccttc	caccgtgatt	gtaggcctct	ccggccatgc	tgaactgtga	gtcaattaaa	41820
cctatttctc	ttataaatta	cccagccttg	ggcaattctt	tacagtagtg	tgaaaatgga	41880
ctaatacaga	cgtgggtctca	ttgtgttgct	cagggtagtc	tgaaactctt	gggtcaagc	41940
gatacctccca	gcttggcttc	caaagcact	gggattacag	gtgtgagcca	ccgtacctgg	42000
ctgggttctg	gatgttgaaa	aatcacacag	ccttggagcg	agaaaggctc	tgaggttctg	42060
ttcatccatc	cggcacctga	agggtgctctg	caagactggc	aagatgatca	tccagccctc	42120
gccagacatg	aggccacagc	cggcccagtg	acctggagtc	acctctgggt	aaggctgctg	42180
ccctgggacc	tgcgtttctg	ggatgctgct	gacctctgcc	ctccaggtcg	acccgaggct	42240
gaccgggaag	cccagtgggt	cgagaaacaa	ggaaagggtg	gagtgcgggc	cctcccagtc	42300
acctctcacc	ctcctcaggt	cacagtgatt	atctgattca	ttcattgatc	aatcaataga	42360
taccctggac	tgggtgctag	ggacagtagg	tgtactagtt	gaatggcccc	ctaaatccat	42420
gcccacttag	agcctcagaa	tatgacctca	tttggaaata	gggtcttggg	agaggtaagc	42480
aagggaagat	gagttcatta	tgtgaccggc	ggcaataacc	tgacattcct	agtgggttgg	42540
ggaagccttc	tctgcctctg	ctcatgtctg	tctcaccacc	tgtagcagct	aggagggggc	42600
ctactctgag	gactgtgtgc	cttttaagaa	gaggaggcgg	gcacagtagc	tcacgcctat	42660
aatcccagca	ctttcagagg	ctaaggcagg	ctgaggtcgg	gagttcaaga	cagccttggc	42720
caacatggtg	aaaaccctac	tctactaaaa	atagaaaaac	tagccaggcg	tgggtggcgg	42780
tgctgtaat	cccagctact	caggaggtctg	aggcaggaga	attgcttgaa	cccaggaggc	42840
ggaggtcgca	gtgagccaag	attgcggcac	tgcactccag	cctgagagac	agagcgagat	42900
tctgtctcag	aaaaaaaaaa	aataaaaaa	gaagaggaaa	ctggatacag	acacagagaa	42960
gctaattgcc	tataaacaga	gacaagggaag	actgtggaac	aacggagacg	cgatgggagc	43020
gatgctgcc	caaagaccgc	cagcaaccag	cgaagccagg	agagaagcaa	ggaccagga	43080
aggagccaac	cccgccca	cctgggttgc	agactcctga	ccctaggact	gtttggggaga	43140
gtgcatttct	gttggccgaa	gccactcatt	gtggcgctt	gttacggcag	ccagggcacc	43200
accagcgagg	ggcagaaacc	agcgggtgag	tcatgtgcag	gccaggaacg	gagaaagagg	43260
aagaggcaat	tcacaggcaa	agacacgaac	aaaacacaaa	caaggagagac	caagagcgcc	43320

tgcatgtgagc	aggggtggga	gggtgcggtg	gagggcagca	ggagaggacg	ctgtgtgagg	43380
gtggggaagg	agggctgaga	gtgggcgcct	tcgtgaagca	gggactctgg	gcagagagaa	43440
tagcatggac	gaaggctctg	ggctgggaaa	gagcttggtg	tggtcagggg	acaggaagga	43500
ggccggtgtg	gctgagtggg	tgggaggggc	agagaggggc	ctgagctcag	cggggagggt	43560
cactctcgga	ggccacagga	aggagtgggc	atcttcttct	aagtgcacac	ggaagtcttt	43620
ggaggggttt	aagcaagaga	gtgacatgat	gggattgatg	tcatttggac	tgctgtgtgg	43680
aggatgtgaa	agcattcatt	cattcattca	ttcattccct	catttcaaca	agtaataata	43740
caacaaccc	caggaccgtg	accaggcctg	tggacaaaag	aaatggcaga	gagatcacag	43800
ccttggggag	tcagggtctg	cagagaattc	ccctctaaga	tgacctggag	caggggcctg	43860
gaacagccat	aggagggctg	gggaagggtg	ctccagggtg	cgagtgagc	acaaaggcca	43920
gctggtggct	cacaccctg	caagccatct	ctccctcagg	ctggagtcgg	tgcttccac	43980
agttacttct	cacgactttc	tcattttgtg	agaaattcct	gataatgatg	ctctcagctt	44040
tctgacaaag	agctcaattg	ttcctcaggc	ggtaaccaatc	ttaatcgta	tagtcaagaa	44100
gttttataag	cactttttta	tttatttttt	tttaattttt	tgagacagag	tcttgctttc	44160
tcaccagtc	tggagtgcag	tggtaaaagc	tcactgcagt	ctcctcctcc	caggttcaag	44220
caattctcat	gcctcagcct	ctcgagttag	tgggactaca	agcgtgtgcc	actatgccc	44280
gctgattttt	gtaatttttag	tagagatggg	tatcaccatg	ttggccaggc	tggtctcgaa	44340
ctcccagcct	caagtgtatc	tcccgccttg	gcctcccaaa	gtgctgggac	tacagggtgcg	44400
catcaccatg	cctagttaat	ttttgtattt	ttagtagaga	tggtggaggga	ggggtttcac	44460
catgttgccc	aggctggtct	cgaactcctg	acctcaagtg	atctgcccct	cttggcctcc	44520
caaagtgtg	ggattacagg	tgtgagccat	caagcctggc	cttataagca	ctttataatt	44580
tgcaaaagccc	ttctgcaatt	cagttcaata	gcccctccct	ggcccagagg	tggtgggaga	44640
aggcagatgt	gcacacagat	cttatctcac	cttcagggaag	gtctgactcc	atctgtcat	44700
acaagataac	cgctgtgcaa	gttccaaagc	aaggccaaca	tagagacaca	tgcccagggtg	44760
cactgatgtg	aaacattcac	ccgtcattca	actcccagag	gggcctcaga	ggcagcagtc	44820
taaaatgtgg	caggttgata	acaagctggg	accagggtcag	gggtgtgtctg	caggcacaga	44880
gtcccccgcc	aggagggaga	agacaacatt	tggtccttgg	ctctgtggcc	ttgaacaagc	44940
gtcttaacct	ttctgagcct	cagctgcaaa	agatcgattc	tatttgattc	tcacaggagg	45000
ctctgagcca	tcaagagtgg	gtcaggctgg	gcctggcacg	gtggctcatg	cttghtaatcc	45060
cagcactttg	ggaggccgag	gcgggcagat	cacctgaggt	caggagttca	tgaccagcct	45120
ggccaacatg	gtgaaactcc	atctctacta	aaaatacaaa	attagctgat	cggtggggcc	45180
agcgccagct	acttgggagg	ctgaggcata	agaattgctt	gaactcgga	gggtggagggt	45240
gcagtgtgac	aagatcgccg	ggctgcactc	cagcctggca	gatagagcaa	gactccatct	45300
caaaaaaaaa	aaaaaaaaama	aaagassccg	ggcscagrt	ggctmaacgc	catgtaaatc	45360
cmarcamttt	tsggargccr	aaggcgggcg	ratcacaarc	gtccargara	tcaagaccat	45420
ccwkgctaaa	cacagrtraa	acccctctc	tactaaaaat	acaaaaaagt	tasmcaggcg	45480
cgrtgrcrrg	cgctgttagt	mccagmtact	cgggaggytg	aggcaggaga	atggcgwgac	45540
cccgggaggt	ggaayttgca	gtaagccgag	cttgaccay	tgactccag	cctgggcgac	45600
tctgtctcaa	aaaaaaaaaa	aaaaaaaaaag	agtgggtcag	gctgggcatg	aattcgccct	45660
tatcaactac	cacctgaccc	cggacaaggc	agtaggtttt	cctgaacct	aaaatagggg	45720
gagtgtatga	accacctga	tagctattct	ttctttaaga	ctgagctcca	gtgtcaccct	45780
ttccccagcc	cctcgagtc	catctccgga	ctcaccgctc	catgctctgc	acttgccacc	45840
ctgagcctca	ttccgaaaat	acctgcccgt	gctgccctca	aagctcagca	tgtcttgggc	45900
ccccagtgct	tctccaggca	ggttctctgc	acagatgtca	ggccagactg	tccctctttg	45960
ctcagggaaa	aagaagatga	gctctcaagg	tgccagcctg	tagtccctgc	actggggcag	46020
gacaaaaggta	agtagaatca	agaatcgcca	ccaggactac	actttcccca	ggaaaaactt	46080
gaaacgagtt	cacgtagcat	tttgatccc	accmkwacg	cagcmctaga	gaaagtgcca	46140
agagaattcc	tatacccaag	tttcttctct	ttctcttacc	agaagctctt	tggcatttca	46200
caaagcaagt	tgcaaccaga	gtctggcagc	ttccattgta	tcgaacaatt	aaggaataca	46260
atgatctgtg	atcacggcaa	gcttctgggt	aatttatatt	tctaaagatt	gtcaaaaaa	46320
atatctcctt	cgctaaaaact	gttcaaatgt	ctccacaaaa	catcaaaaagt	gtccccacc	46380
ctgcccccca	ctttctctgc	ccgtctctat	ggcaacgtgg	agctgtgcta	ttctgatcac	46440
tgctaccaag	ccaagcaggt	gtccggaaag	ttttggggag	gattttgagt	tgggtaattt	46500
ttggctcttc	ttgacatttc	ctaagtgcg	tgatgcctaa	aattttgttc	tattgtttcc	46560
tgctaaagtg	aacaagaagt	tccctctccc	accagctctg	gctttttttg	tgtggttttt	46620
tttttttttt	tttttttttt	tgagacagag	tcttgctctg	tcaccaggct	gggtgtgatt	46680
ggcgtgatct	tggctcactg	caacctccac	ctcctggatt	caaattgattc	tcttgccctca	46740
gcctcctgag	tagctgagac	taaagggtgca	tgccaccatt	cccagttaat	ctttgtattt	46800
ttagtaaaaga	tgggggtttca	ccatgttggc	cagaatggtc	tcgatctctt	gacctcatga	46860
tccgcctgcc	tcagcctccc	aaagtgcctg	gattacaggg	gtgagccacc	gtgctggccc	46920
wakmtytkrr	wtttgagawm	gatcacagga	gggactcagg	gctgaaagaa	gtgagggagg	46980
aggccagggc	tgggtggctat	tgccgtgtaat	ccagcaggtt	tgggtggctg	aggcagttgg	47040
attgcttgag	cccaggagtt	caagaccagc	ctgggcaaca	tgtaagacct	catctctaca	47100

aaaaaatacc	aaaaaaaaaa	aaaaattagc	tggaatggt	ggagtgtgcc	tgtagtccca	47160
gctacagggt	ggctgggatg	ctgaagtggg	aggattgctt	gttcccagga	ggctgaggtt	47220
gtggtgaacc	gagatcatgc	cactgcactc	tagcctgggt	gacagaacaa	gactctgtct	47280
caaaaaaaaa	gaaagaaaaga	aagaaaaaaa	aaaagaagtg	aggagatggt	gcaaattgccc	47340
ccccacccca	aaccacacct	cggggggtgtt	tgtctaagaa	aacatctttt	gtgacctgtg	47400
tgttatcttc	tttacagcca	cctgaaacgc	agaagggagc	ttgctgggtt	tcagacatgg	47460
gtaagtgtgg	ggtggcattg	cagcagagat	tggaggccgt	cggaccaaag	aggtgaccga	47520
gagtggccat	gggcacagga	ctcaacctct	cagagccctc	ggttcctggt	ctatagcctg	47580
aggacgatcc	tacctcccag	gttgtcaggt	ggatttaattg	ggccaccagg	tgtaatcagt	47640
attcaggaag	ggatggtaat	ggtctgtggt	gtggttatgg	aggaagctga	tgtccacca	47700
ttccacgtcc	acgcagggtta	gctcccaggt	cttcccata	accttttggg	gcaaaggatt	47760
tactgagttg	acgcccaggg	aggtccaatg	agttgtccca	ggtctaacga	cattgcctaa	47820
gcgtgtcata	gcccctcccc	atgctcagtt	ccctgattta	aagtcagtgc	ctcttggaag	47880
caatcaccgt	gtccttcggg	aggtgagtag	atacataagt	ggatacgtaa	gctgtggtcc	47940
atccagacaa	tggactatta	ctcagcaata	aagagaaatg	agttatcaag	ccatggaaag	48000
ccacggagga	aactgagccg	catatcacgg	agtgaaggga	gccaagctga	aaagtctacg	48060
cactgcaccg	ttccaactct	gtgacattcc	ggacagggca	caaccatgga	gattgggaaa	48120
agatcagttg	ttgccaggag	gcagcgggag	ggaggatga	agcagtgagg	tgtcaagagc	48180
cttaggacag	tgacgtgct	ctgtatgatg	ctgtcaggtg	ggtccacgtc	attctacatt	48240
tttccaaacc	acagaatgc	acaatgccca	gggtggaccc	cgatgtaaat	gctgcgtctc	48300
aggagatagc	aatgtgtcaa	tgcaggttat	ccattggaac	aggtgtgggg	aggctttgca	48360
tggggagggtg	tgggatctac	gggaactgtc	tgcactttcc	actcagcttt	gctgggaatc	48420
ccaaactgcc	cttagaaata	aggtctatta	aaaaggggta	gggggcggct	gggtgtgggg	48480
gctcacacct	gtactcctgg	cacttttggg	gggcagagag	agatgggagg	atcacttgag	48540
ctcaggagtt	caagaccagc	ttgggcaaca	tggcaaaacc	ccttctctac	agaaaataca	48600
aaaagtagct	agatgtggtg	gtgtgtgcct	gtagtcccag	ctactttgga	ggctgaggta	48660
ggaggatcac	ctgagcctag	gaagatcaca	ccactacatt	ccaacggagt	gagaccctat	48720
ctcaaaaaaa	aacctggggg	gagtaggggg	cagaataaag	ccagcacctc	ctccaggag	48780
ccgtccctga	ccaccatcac	ctgctgcaat	ttctccccct	gccagggaatc	cgcaggctgt	48840
catcacttct	cctctggtta	gcccctcccc	agaataacag	tggctggggg	ttccagcttc	48900
cggacctaac	aagcccctcc	agggcaggta	cggggctgtg	tgccttagac	ccttcacct	48960
cacaccaggg	caccagtgga	gacctgtgag	ggagcgggta	gcagggtgtg	aacgattgcc	49020
ccttcctgcc	agtgactgac	atttgtaaga	gagactcagc	atgaaatgac	agctgcacgg	49080
tgtgggcaca	ttgatgtact	tagcaaatga	ggcccctgct	gctgccgtgt	cctgtgtcca	49140
gtcctggtga	cacagccctg	ggacctgaga	cctgtgcccc	ggcccatgct	tggctgctgt	49200
catggtctcc	ctgcatccag	ggcaggctgg	gcccatttcg	aaggtagagg	ctgggggagg	49260
tgggggatct	cagctggcac	tgctcagtga	tgttagggga	tgactgggac	acaggcagge	49320
ctgggaatcc	cgtctctccc	cacacgggca	tttctctct	tctgcctcaa	agttgctttt	49380
gcactcctgg	gttttttttt	ttttaattcc	ccaaatgaaa	cttcccagtg	cacttggtga	49440
ctcgtctgtg	ggctgtgaag	tggcgttcgc	tctctgcctt	cagagatgag	cacatcacca	49500
ctcagaccca	tgggagggct	cagaactacc	cggcgacaat	gcagtgtgtg	tgtgtggcag	49560
gtgggtgtgt	gcacgggggt	gtgtgtggag	gtgcttdchg	ccvttgbcct	htgatgtdgb	49620
accamgkcb	tggtvacack	accgcccgtg	gcccavcacb	tvbcccchca	hgvacgccc	49680
hcchghcaca	acbhchgcyc	acthgbccctg	tcaygagtc	tdgkgdtact	abavavcdgg	49740
hdgggdgbtv	dggttbhtag	dggtdavac	tgggcaggvg	gdaggagtgr	tgggcbgagg	49800
gtgbgrtdtg	dghadtgadg	tgggavrggr	craaggabgv	gggtgggdgb	tgagagbcbh	49860
tabgbtctas	vdscvtgvag	stgbdgggwa	tgttwkgbtg	gdavbtttch	thhccbthad	49920
hccbtsggag	agtgaaggaw	ggctgccccg	tgtgtcacat	tgytgtagg	aagatctgtc	49980
ggggtatagc	agcaaaagagk	agcttccctac	cttagatgtg	gtcaaggcct	gggtgggatgg	50040
cctcaggaaa	gaggcyagtg	gatkgggkkc	acatggcctg	kagtgaagtc	cagkaccttg	50100
ctaaattgca	aaggcaccca	tgcggttcct	ctgctgcacc	cctatccagg	actccccata	50160
gaatgcagac	ttctggtcca	gctggcctgg	gcaggacaag	ctctccagg	ggcgctatgt	50220
gcatagcctg	agctaagcac	ctccagcttg	cagcatggct	tctctagctt	gctttattta	50280
tttattttaga	aacagggtct	cactatgtca	tccagggtgg	tcttgaactc	ctgggctcaa	50340
gcaatcctcc	tgcccaagcc	tcccaggtac	ctgggactac	aggcataatg	caccactggc	50400
tccaacctta	atgtgcatgc	aaatcccaag	ggcatcttat	taaaatgcaa	attctgactg	50460
aggaggtcca	tggttggcgc	gggattctgc	attcgttaaca	ggcgtccagg	tgactgagga	50520
atgctggatg	gtgatgttgc	tggctctggtg	gaccatcac	actatgaacc	acactgcttt	50580
atactcatgg	gtctcaaatg	ttcctatgtc	tcacaaacc	cccagggaacc	tgttaaaatg	50640
cagattcctg	ggcctggctc	ccagggtatgc	tgacaaggct	agtcctaggg	tttcgctgtg	50700
ctagaagtcc	aatgtgtggc	cgacatgccc	aaacatgttc	tgttcttttc	tattcttata	50760
tcttttactt	tttctttcct	tatctctttt	actttttctt	ttcttttctc	ttctcttctc	50820
ttctcttctt	ttgagacagg	gtctcactct	gatgcccagg	ctggagtga	gtgggtgcaat	50880

cttggtcac	tgcagcctca	aactccccag	ttcaagcaat	cctcccattt	cagcttcctg	50940
agtagctggg	actatgggca	catgccacca	cgtctggctg	atTTTTaaat	TTTTTgtgg	51000
agatgggttt	ttgccatggt	gcctaggtctg	gtcttgaact	tctgggcccc	agcaatcccc	51060
ctggcttggc	ctcccaaagt	gctgggatga	caggtgtgcg	ctaccatgcc	caaccagccg	51120
cacatgttgt	TTTTTgttg	ttgtTTTTtg	tgtgtgatgg	agtttcgctc	ttgttgcccc	51180
ggctagagtg	caatgggtgtg	atcttggctc	accgcaacct	cagcttcccc	agtagctggg	51240
attacgggca	tgcgccatca	agcccggcta	atTTTgtatt	tttagtagag	acgggggttc	51300
accatgttgg	tcaggctggg	ctcaaactcc	cgacctcagg	tgatccaccc	cccacctcca	51360
ggcctcccaa	agtgtctggg	tcacaggcgt	gagccaccat	gcctggcccc	tgttgttctt	51420
atctcattaa	cccagtgggc	taaaaactca	ttgccacact	cagtagctta	aaccacagaa	51480
atggattctg	ccacagttat	gaaggccgga	agtctgaaat	cagtgtcact	gggcaaaaat	51540
caaggagaat	ctgttccctg	ctcttccaga	ttccaggggac	tgcctgcatt	ccttgacttg	51600
tggccacata	attcctatct	tcaatgccag	cgtcttggaa	tctctctctg	ctctatgtcc	51660
acatcaactt	ctccgttgtt	ggtcaaactc	ctgtctgect	ctctcctgca	aggagataag	51720
ccaggctaatt	ggccccttct	caaaatcctt	aatcacatct	gcaaaaaccc	TTTTctaaat	51780
aaggtaccat	tcacaggctc	caggaagtga	tctctttggg	ggccttgtag	accaatagcc	51840
tgtaaaccgc	cacactctgc	tgtctttcaa	atgacaactc	accaagcctc	tgtcctcatt	51900
ttctttgaat	acttggcatg	tagtccaatg	cctggaacag	gcaggatgtc	actaaatgtt	51960
tatatTTTTt	aatttttatt	tattttatta	ttattcttat	tatttttgag	acagagtttt	52020
actctgtcgc	ccaggctgga	gtgcagtggc	atgatctctg	ctcactgcaa	cctccagttc	52080
ctgggatcaa	gcgattctcc	tgcctcagcc	ctctgtgtag	ctgggattac	aggcagtgtg	52140
catgacgccc	gcctaatttt	tttgtatttt	tagtagagat	gggggtttctc	catgttggcc	52200
aggctggctc	cgaactgctg	acctcaagtg	atccaccac	ctcggcctcc	caaagggtta	52260
ggattacagg	tgtgagccac	cacgcctggc	caaaagtcac	taaatgtttg	ttgagtaaat	52320
ggaagttagt	tttaaatagg	tgtagggaag	gaagtgggcc	aagaacttga	atgcagagtc	52380
tgaaaatcat	gggcagacat	caaaggactg	aattgtgggg	ggtatatttg	gatgtcaggt	52440
taaagagttt	ggacactgtc	ctatgggcaa	gaaagagctt	atatgaagtc	cttgcatagg	52500
tgattcatcc	atccatccat	ccattcatcc	attcaatact	cagcagcaac	atgcagagct	52560
cagctcttgg	gggaatgagg	acagggtgtc	tagaaaagat	agcattgaac	agctggctct	52620
ttctcccacc	agagtttgtt	tttaataagt	tctagtattt	ctagcagtta	ctgctttaag	52680
tgtgtggcta	ctagattttc	tggctcattc	agattcatga	caatgaaate	tttgtggatt	52740
gtgcctggca	cccttacata	ataccactct	tcccgtgaat	gctttccatc	atgcgttctt	52800
ccttatcaat	agtaatttgc	catttttcaa	atgtctgctg	tgatcttcta	cttctcaata	52860
TTTTTgggtg	gtttcttgta	aatagcgctt	aactggactt	tagtttttgc	cccaatctta	52920
cagactttgg	atgggaaatt	cagcccattc	accgtgttac	gaaggcgggt	agccatggct	52980
ttattttatt	tatctcatct	tatgtttact	attattaagc	ttattgttct	tgctattatt	53040
tactttcccc	cttaattttg	cttccttact	ctccctccac	ccctccccc	acttctacct	53100
agtaattcag	gagttctact	ctgcttcttt	cccgtgagtt	gctactttcc	aattcctgag	53160
agtcataact	gaaccaatct	ttccctgata	atgtattaaa	agtaaattgg	aatgaagccc	53220
cctcccacc	accaataagg	ctttccttcc	cagctgaga	gtcataatta	aaccaatctt	53280
tccttgctaa	tgtattaaaa	gtaaatggta	atgaagcacc	cctcccaacc	accaataagg	53340
ctttccttcc	ccactcacca	aatcagatcc	ttttacttcc	tccttctccc	ctcaacaaaa	53400
tgtgatctta	aaatattctg	acttctctgt	gataagattc	tatttttttt	tttagttcca	53460
ggctaataca	actttctctt	gaagcatgta	gcttatgttt	taagaatcct	tatgtggcac	53520
tgctagtaca	aaatcacagg	cacatgtgga	ttatccatac	tgtatatttt	gcaagggtca	53580
ttgtttaaca	ccacttcctg	ttctgagcgt	ttgtctatc	ttgaaatctc	tactgtgatt	53640
gaactgtctc	ggtgacgggg	gaactctgaa	tatcttcttc	tgaaggggga	catcactgag	53700
gtcctttctc	tgtcttgcca	cagtggatat	tttctctctt	ttgtccacat	agatgaatcc	53760
tgtagttagc	atggtaagga	tccttgatcc	ttctcataga	gtccctggac	attgtctcaa	53820
agtcccctag	gaaccacttc	aacttttctc	cccttagatg	tgacctgttc	tttctggaac	53880
tctgcaagac	cgtctcttta	tccttggcat	ctgggatttc	cagggacacg	ttctcctggc	53940
actttgtctc	cctctgtttc	ccctccagct	cttctctggg	tacctgtcct	ttgtgcaata	54000
cacctcctgg	aactgtcttt	ccagtctctg	ctttttgtcc	tgatgatttt	catgtgcttt	54060
tcctctacat	catgaagcat	ttactccaca	ttatcttcca	gtttgtctcat	ttgtcctcac	54120
ctocactctt	ctctttctga	atttgctgtg	tgttttttca	gtctcttagc	tcctgtggagt	54180
atgttcagtg	ttgtctgtgt	ctgatagagg	ctccttaagc	catcttgtag	atTTTTgttt	54240
gcacttctct	tcttccctta	gacctccaca	ggaggaactt	ttcaatctgt	cctcttctct	54300
ctgtttaatg	agccccctga	aagggttttg	gaagtgtctc	agcctctctg	tgattgtgtg	54360
ttcacattaa	tattttattat	tttctttaa	gtgcataaat	ctcacaaatg	gaacagtgat	54420
catcttttag	tgattttttt	tctcctttct	acttttagta	attctccaaa	ttttctacag	54480
ttagtgtgtg	ataaggtgga	aagacatctt	caagactttg	ggcaaataac	tatgtctgag	54540
cctcaatttt	cacatcaata	aaaaatgggc	tcagtgccac	ctccctcctt	gggtcactag	54600
gggggcccc	gaaagctgtg	aaagccccca	agccaacctg	gacagagcag	gcgaggctga	54660

cggcaggtgt	tcttccttcc	tctgtgagcc	tcacagggtc	acacgtgaac	attggggatc	54720
gggggtgggc	agtgggggca	gctggagaat	caaagtgggt	gactgacatg	aactacgccg	54780
ctttgacaaa	agtcctccga	agtagtgtgt	tcagaactca	tctccaaagc	catctggaat	54840
atttgctccc	aacatgttgg	taagcattat	ctctgacagt	cactccgagc	cccagtttct	54900
gctgtgataa	ctaggacagg	tagctcaggt	tgggtgtggg	gaccagagac	agagcaggca	54960
gggtctcacg	ttccccaggg	cctctcaagg	atagaccctc	gccctcatct	ccaaaccacg	55020
cctcccagac	aggaaccaa	ctcccagagt	ctccaaactg	cctgagcctt	gcccactccc	55080
tgggctaaca	cacactttta	aggaatccca	cagtaccgtg	gtgaaaagct	tgctacactg	55140
catttgattc	tgggactga	aagcagtact	tgggtgcaga	cactcgtttc	aaacaggccc	55200
catttttcca	tctctgctgc	tgttattagg	ggagccctta	gactctcttg	cagcgcggga	55260
ataggcgctc	aagacgtgtg	ttaatatgtc	aacagcaaat	ataatgaatc	tgcagttggg	55320
gacgctgagg	ccggagtggg	ggatgaaagg	tggccggagc	cttttccacg	ggtccaaacc	55380
acctgttaca	ggagaaggcg	agcggcctcg	ctaagcaact	ggacgttccg	cgggcggggc	55440
ggggggcggg	ccggggcccg	agtccgctcg	gaaactttcg	ctgtgggcga	gccggaccgc	55500
ccttctggcc	cctcgggccc	aaccacgcag	ggggagtgcc	gggcccgcagc	taggcgaggc	55560
gcaccgtgat	tggcggagat	gtggagtgat	tggcggctac	accggccact	cagcaggccg	55620
agctggcgcc	gcatccgggg	ggccgcgtyt	ggagtggagg	gaggccgaaa	ggccccgccc	55680
ctgycccgcc	ccctmgtgca	gaaggccgcg	ctagccggct	cttcagcagc	gagtgcagat	55740
tgctcccccg	cggccgcaga	tctcccgttt	gcgcccgcgt	cagctgctcc	cgaacaactt	55800
ttctgcccgc	ccagaggccc	cagggcgtcg	cagcgcgcgc	tgcggcccac	tcacgggccc	55860
gtgagtactt	cggcgctggg	gcagtggcgc	gctggctgtg	ggcagcgcgc	aggaggcggg	55920
caagagccct	gaggcactgt	cctcttcggg	cctcagtttc	cccttccgag	ctgatgggtg	55980
gctggcccca	aagtcccgac	aagggtcccc	aagttggagg	gccgggggtc	ccgcccgcctc	56040
tgcaacgcgc	aaggcgaccc	ctgttccggg	cccgaacggg	tcacccgggg	ggcgcgcccc	56100
ggtccccgcg	gcgctgtcgc	ctggagcccc	gccgcggggc	ggacagcagg	cccagagggc	56160
ggagcggccg	gcgggcaggc	cccctccccg	cgccccgcgc	catccccccc	gagttgcccc	56220
gtcatgcccc	tccccgcggg	tcccgggacc	cacggccgcc	ctcgggtgccc	gcccggccgt	56280
tggaaacgcg	ctgggcccc	gggaggtggt	gtggggggga	agggggggtc	agtccccag	56340
ggggaccceg	cccggcccag	gggcagctta	ggggctattc	tgaatcccca	cagcccactt	56400
aggagcgctg	tggcagttcc	tctctctctc	ggggcccctc	agtagagagt	tgagggtttt	56460
cagtggcagc	acctggaccc	tgccctcgat	gaactccacc	ctctggatca	ttagcttttt	56520
gtttgatcaa	cgaaaacttt	ctggagaatc	ctaccacagc	cttttggtatg	tgatggcgcc	56580
ctggcctctc	acccacttag	cagatgatgt	tatgaattcc	aaggaaagtgc	catttgtgca	56640
acccccacc	accagatttt	aacctctca	gtagccttag	gcggagaagt	tatagtcccc	56700
gtttgacacc	ccaggaaagt	gaggctcagc	agggtttggg	gccagcccag	gaccacgaag	56760
ctgatggggc	agagcctggg	gtgaggcctc	tgccctatct	ctccagaagc	agccccgtct	56820
ctcctcacct	tggacagtga	cccctggcat	ttggcccagg	gctttgcagt	ttgtaaaggg	56880
ctttctctta	tgccagcatc	catcactcaa	ggagctgtgc	cctgggtacc	ccatgtgctg	56940
gctgcctggt	ctctgcagca	ggagagggag	cccacgggaa	gcccagaggc	cacctttgtc	57000
actgtcgcca	cctgtttact	tctgtgtcca	agggtctgtg	attcccattg	ggtctccgtt	57060
gtatccaacc	agggtatttg	agggaggcct	ctccacattt	cagcctcttt	tcctacctg	57120
ctggtttgct	ctcccttcgc	agacacagga	aaagtgggt	gggagacccc	atctcacctt	57180
ctttcccagg	atggaagagc	atggagggcg	tctctgactt	aggcctcccc	tgcccatccc	57240
ggaccagtgc	tggacaggct	tctggggctg	gtcacagagg	ggacctcagc	tcagtctcaa	57300
ccccagaga	tgtctgcact	gccagacaga	cccgaacac	ccatccttga	cggtggcaat	57360
aagaatcata	ataggtcggg	agcttttatgc	ctacacggct	cccctcccc	cccacttccc	57420
tacttccgga	agtggtagca	ccacagccag	ccagccccag	ccacaaacca	gaccaccccc	57480
tgtgcccctc	attcctcact	cccagttggg	tctctcctgg	ctcctgagcc	tcactcggat	57540
gctgcccctg	gttcaggacc	ctcgcctctc	cctggacgac	ccccaggctc	ctccctgggtc	57600
ccgatccggg	cctggctgca	cgcagccctg	ctggttcttc	agctgccact	tcctctggg	57660
ctatcgggtc	agggtccgct	cccagaccag	gagccggcat	tctttcgggc	cctcagggac	57720
ccgcctcgct	gctcactcag	cctctccctc	ctgtgtcctc	tctccagcag	tcacctccca	57780
gccacctgcg	tgctcctggc	cacaagcctg	gctcactgtc	cctctgctgc	ctcctcttct	57840
gggcacaacc	cctgctggaa	tgcccagcca	cctcccagct	tgcttggtc	ctgcttgctt	57900
gtccagaagg	ctcagtcaag	tctcctgca	ggatttctgg	cctgcctctt	cccacagtgg	57960
agtgaggggc	cccttctgtg	ccgtctttgt	gggtgtctgt	ttaggtgtta	acccttccca	58020
tctagatgaa	gctgctccaa	tgctggccct	ggacaagact	tctctagggc	agggggggcc	58080
agcacagtgc	ttggcacaag	atggacctac	cctcagtcca	cacctgctgc	ccatccaggc	58140
caggctcggg	gcaggtgcca	ggtgtgtggt	gggggcttgg	ccactatggc	cgtcatgaat	58200
gctgcttggg	gcagtcccaa	ttcaaaccct	tctgttctctg	tgaatgtgcc	acattggata	58260
gagctggaat	gttccttggt	ttgtccctta	atactctgag	caaaaatagg	tacctgggat	58320
ccatcaaggg	ctttgtgccc	ttgtcttgag	gagcagccct	gtgccagggg	gctgggtcag	58380
gccaggccag	agcagacatc	ccagggccag	gacctcctgg	gcctgctccc	ttagagcttg	58440

ctcacagatg	ggtttttaaaa	taacatttgc	tttaatttca	aaaacatcac	acattcatta	58500
tagaaaacta	gggaaatatg	tttaaaagaa	gaataaaatg	aaaccgcgca	taagctttat	58560
ccccagagac	aacaagtatc	tttttttaggg	ggcgttttct	tccgtttttt	ggcagataaa	58620
ttttgttttc	atcctaataa	gactccggct	aatatcttct	gctgctttta	atcctgcctt	58680
aacagtgtta	ggcccacctt	ttccttgtct	caaaacgttc	atgtacgagg	tcacgtttac	58740
cagctgtaca	gcgttgccac	atatggaggg	gtgtaggctt	tatagccagc	ccctttcttg	58800
acagtgttga	aagtgccata	tgatggacat	tgtgtgtgag	ccccgagggc	atctccagtg	58860
actcccctgg	actggcatcc	tggaggcaga	ggcactgac	agagagagtg	aacatcatct	58920
tggtctccca	caggggctgt	ttctgaggca	ctggcttggg	agatgggggt	gccccccag	58980
agagaacaga	atgggggtgg	cctgggtgag	ggccagagcc	cttagggcag	aaggccacgt	59040
gtgggtcattc	tgctgcgggt	ctgagtggat	gcatggtgcc	tcgagccctc	tccaggtggc	59100
ggcctctcag	ctgaactcct	tggtgccggg	gtttgtgttt	ggacgggata	aaaatatgcc	59160
tcattgtctca	tgaggaaaga	atgctagcaa	ctttgggttt	gtggatctta	cacagtgcag	59220
gcttctaagc	cattgctgtg	gtcaccagta	gggagttggg	gctgagtggc	ccaccgtgca	59280
ggtggggatc	tgaggggtga	gagtggatgc	agctggagat	gcctggatgc	tgggggtctgg	59340
gggagggact	tgctaaggtc	ccacagcatt	attgcctgga	tggtgctcct	gccctaggcc	59400
aggctgcctc	aggettctgc	ccacatgcat	taagtgccta	acgtattcct	ggcaaggcag	59460
ccggctcttc	gagtggataa	gctgcagccc	tgccctcagg	gctcacagtg	gctgtaacct	59520
gcaggaagac	tcagagaggg	aaggaccaga	cagcaggtcc	ttccaccggg	agatcttttc	59580
tgatcttcat	tgctccctgt	accaaccatg	accaggaatt	gttgtgcttg	ttttgaaata	59640
acaagccctt	tgatccaaac	cagacttggc	caacccccag	ggaacctgaa	aattaatcct	59700
cctgtattca	tccattctta	ctaaccagag	attttacctt	taaacagttt	ttttttaact	59760
gcagtgtgac	atacatggta	cataggccag	ctagaatctg	ttttcctgaa	attcctttta	59820
tgaagtgttt	tccaactgaa	catgcctttg	tttagcacct	gggagtaatg	gcttaggggt	59880
tttcttttcc	tttttctttt	ttcttttttt	tgagacggag	tctcgctttg	tcacccaggc	59940
tggagtgcag	tgggcgcatc	tcggctcact	gcaagctcca	tctcctgggt	tcacaccatt	60000
ctcctgcctc	agcctcccca	gtagttggga	ctactggcgc	ccgccaccac	gcctgggtaa	60060
ttttttttgta	tttttaatat	agacgggggt	tcactgtgtt	agccaggatg	gtcttgatct	60120
cctgaccttg	tgatctgccc	gcctcggcct	cccaaagtgc	tgggattaca	ggcgtgagcc	60180
accgcgcctg	gccggcttag	ttttttttta	atgcccaata	gtttgctttc	tcttctgcca	60240
cacacgtaat	ccccatagca	cccctatgtg	ggaggtgcta	tccccatttt	acatatgggg	60300
aaacagacac	agtgaggtca	tgtggccact	agtaagggtg	accgacgccc	cacaccatgt	60360
tgcttccagc	tgtaacctct	agcagagggg	gggctctgat	ggagaggtga	tcgcctgagt	60420
gctgtgtgtt	tacctgagta	ggtgaggaag	acagggactc	gggacagaca	tagcttgga	60480
gctcccacaa	aggaggtatc	gctggagctc	ttgacttgaa	gggtgcttag	ggtctaggct	60540
ggggggagggg	ggtaagaagg	cattccggga	agagggccct	gcagaaacag	aagtgtggag	60600
gtcagcattt	gtatgctgat	gttgaagggt	agccagtgtt	ttgcagtga	tgggccccgg	60660
gagagaagggt	gcagtggcat	ggcggctgta	tttcaaagtc	gtctttttca	gaaatgagct	60720
tgcaagaagca	ttagaattgg	gcagggtctg	atttgaattt	cagggtctgg	acctggagct	60780
gtttgacctt	gagcaggctc	ctccccctcc	tgcacctggg	ttcctgtctg	tgaagtgggg	60840
tgaggttgaa	ggataaaaaca	tttccccatc	tataactctg	ggatgacaat	aggatctacc	60900
ttccaggtcc	atgcgaggaa	ctcacgacaa	taggacctac	cttccagggc	catacgagaa	60960
actcatgaga	aaagacaagt	acagagaaca	gagccgttgg	tcttgatggc	agagatgccc	61020
tggcgtaggt	cagccctcag	taaagggtgcc	ctctctctct	gtctgagaaa	gtgacacctg	61080
acttcggggc	agtgggaacc	atgggagaga	aggtagacaa	ggccacgtgt	catttgaaga	61140
cctgactttt	caccatctca	ggtggtccgg	tggcctgcag	gaccgtgggt	ctgtttgccc	61200
acagcgtgtg	ggttctacgt	gcgatcctgt	atttctctgc	cacagctgac	taaggggaca	61260
cttaggtctg	cacgtgcagt	taaatggctg	cttttctgga	agggtgccagt	tcccgggagc	61320
tgggaacttg	gaaacaggat	ggagcaggct	cccaagcttg	accatgcatg	gtttgcacct	61380
gggggatgca	ccgggggggtg	cttgaccatg	catggtttgc	acctggggga	tgacgggggg	61440
tgggggtggg	gggggggggtg	tgcttgacca	tgcatgggtt	gcacctgggg	gatgttttac	61500
actaagggtc	cagtccctct	gagggaggaa	cgtgtggatt	gaaatctgca	gagttcttga	61560
gcgacaccag	tctgatcttt	aggactcatt	tgacgcggga	atggagcaga	aattgttgtg	61620
tgtggagcct	ggggccactc	ctgactcttc	cagtcacagc	tgcccccaaa	agtgcacctc	61680
gggcacctac	tcagacctgg	ctgctcagtg	ccaagcgtg	ggtgttcaga	ggtggccagg	61740
ggactccctc	gtgctgcccc	tggtgtctgg	tctcactggg	cctcacagtt	gccccgtccc	61800
cattttcaga	tgaggaggct	gaggtgcaga	gcgggatgtg	ggctgtcag	gaccacacag	61860
ctggtgggca	cagagccagg	agtacagcgc	tgcggcagct	tggggctggg	agcagactc	61920
tctgttacca	gcctctccct	gctctgtgcc	tcagaggatg	gctgtggccc	tgagctgggg	61980
aggggtcattt	gggaatctga	ggaaaagtgt	ccacagcctc	acacagcagc	aggttcaagg	62040
tccagcagtg	ccaggggttt	gcatcccacc	cctaacgcgg	ctcatccagg	gcccctccgg	62100
gtccggggct	cgggatcctg	cagcgctttc	agctctgtgt	ctgtggccgg	tggttgtcct	62160
tcattacagg	gatggtgggt	tttttccatg	ttgctaagca	gcatgtgagg	gcctctgttg	62220



aataaaataa	agcccttgct	ccggcgtagc	acgggctcag	ggatctctgc	tcactctagt	62280
ctcttctgat	gccccaccg	cactgtttgc	cttagtttgc	tttttactct	ctgtgttggt	62340
ttctggggca	tcagtcctct	gacttcgggtg	ctgtggcttg	ggcctggggg	gggggctgtg	62400
gagcggcaga	tctgggtatg	aatcccagct	ccacccattt	ggctccctct	cttctctccc	62460
ctgccctctt	ctccccctcc	cagctccctt	ccccctctcat	atttacttaa	ctttactcag	62520
taccagcgta	ttagttttct	aggggttccg	taagaaacta	ctggaaactt	ggtggcttaa	62580
aacaacagag	gtttgtttct	tgatggttct	ggaggcagaa	gtctgaagtc	aagggtgtggg	62640
cagggtgggt	ccctcctgga	ggctctgagg	gaggctcagt	tcctcgccct	tgtccagctt	62700
ctggcagtg	ccagtggtec	tcctgctcct	tgccactgt	caccgctctc	cgcatggctc	62760
tgttacactt	ctcttccat	aggccatcag	ctcttggagc	cagggtctcc	ctactccagg	62820
ctgatctcat	ttcaagatcc	ttaaatacat	cttcaaagac	ctgtttttcc	aaataagggc	62880
acattcacag	acattgggtg	gcacatgatg	tggggcccaa	ttcagccccc	tgcagccagg	62940
ctccacatgg	gtgggctctg	gggtgttgcta	tcacatcccc	cgtttcttgg	atgagggaag	63000
gccagggttg	tgtggctcat	gcccagtgag	gcagggactc	caggcctcgg	catgtgcagg	63060
tctgagattg	taagtccat	gccatctgta	gagtcacgtg	ggtgagtgct	ctcccatggt	63120
ttcctccctg	gaagcgggtg	tggcccatgg	ggactgtact	gagtgtcagc	gagatcctgt	63180
atggagtgtc	tggcagctcc	cacctgcctc	cctctgcttt	tctgtctcca	gcagacacta	63240
agtgccagag	cgggctctgc	cgggtgctgga	tgtgcctgac	cttgactttt	cttccaggca	63300
ggatggactc	caacactgct	ccgctggggc	cctcctgccc	acagcccccg	ccagcaccgc	63360
agccccaggc	gcgttcccga	ctcaatgcca	cagcctcggt	ggagcaggag	aggagcgaaa	63420
ggccccgagc	acccggaccc	caggctggcc	ctggccctgg	tgtagagac	gcagcgcccc	63480
ccgtgaacc	ccaggccag	cataccagga	gcccggaaag	agcagacggc	accggtaagg	63540
gagcaggctg	ggaagcccag	gctggggatg	ttcaggagata	gctgggtggg	aacgggttcc	63600
agccaccctt	ggagggtccc	cccggcagggt	cctctgcagt	tcagcattgt	gcagctccca	63660
tgtgtgcac	aggcgtccat	ccagtggggc	taccacctc	ctcagagcct	tgcacctgtc	63720
acctttgtgg	caccactctg	aggtggtgct	ggtgccccca	ctcctctgca	gtccttctct	63780
tcccaggggc	tctgcagcac	ttcacagctt	ccatttgcaa	cagcgtccaa	acatgtggag	63840
taaattcacg	ggccctctgt	aaccaactag	ggtggcaggc	cagaggtgac	agccacactc	63900
tcgggagtga	ggccacatgc	gggccaagcc	cttgggtgctg	agtttccctt	ctccctgagg	63960
gagacttctg	agggacgggc	gtccttcacc	tccatcctga	ggcgggatgc	tggggccctg	64020
ggtgttcaca	ggcagagctg	actgaggccc	ttggtcttca	caggccgagc	tgactgaggc	64080
cctgggtgtt	caaagcagag	ctgaggccct	tgggtttcac	aggcagagct	gacaggtctt	64140
ttggttctct	ggtggtgatg	tgagggtggt	gggtgtgagc	caggggagtc	cggccctctg	64200
gcaccttctc	cagctgactc	aggcctcggt	cagccttcac	ttttgctaga	gaggccgctg	64260
ccagggaggc	tcagtcccag	ctcatcactg	ccccctctgc	ccatgcagaa	gccccagacc	64320
catggtgagt	gcctgctgtg	tacaccagcc	ttttccatgt	gcctgcagga	ctcctcatgg	64380
cagtctgag	aggggaaact	gagacaccga	gtctaggtga	cttgcccaag	agaccagcg	64440
ggtgagagac	gaggtgctcg	agtggctccag	gtttccttct	tgtcccagtc	acccactgg	64500
cagggccgtg	gggcctccct	gctgtggtcg	cagcgcgctg	aggctcccat	gtaccactta	64560
tgctgggcgt	gcccttgga	actcactgca	gccctggggc	ctgtttgtct	ttgcatctcc	64620
ttaaaagatc	actgtgctcc	ctctgtttgt	tttggaggcc	tctgggcgga	tgagggcctg	64680
accccgggat	ttggggccag	cctcacggct	ttcaggggaa	agataccagg	gctcggaagc	64740
ttggtttcaa	tctgggtaat	gagaacagcc	cgcaaaggac	agagtccaag	actgtgtgtt	64800
tcagataaga	agagtcagga	agcagctgtg	gtttgtttgg	cttcggtctc	caatgtgggg	64860
gtggtgaaga	gcaagccctg	ggcgccgcct	gacagcccag	tccccaccac	tgggcctgca	64920
gctgggggca	gtgggcatcc	cgtctcccag	tcactggtca	ctgatgtggc	caaagcaggc	64980
ctggccctgc	atgcccagtg	gccgcaggga	gggcaggggc	cagggtccct	gccagtagca	65040
gctgctgcga	gaatctgtta	tttagctccc	ccatccagcc	aacatagggt	ggtgagcatc	65100
agttgaaata	ccaataggta	acaacaaggg	tagctattta	actgacactt	ccccgagcta	65160
ggcatctttt	tagggcatta	gcccacttgc	ctctttaaca	gccctgggag	gcaggctctg	65220
ctgctgccct	gtttttcaga	tgggaaaccg	agggatagag	ggcttaagta	gatgaccacg	65280
cgtcccgtgg	ttggtgaagg	gtggagggga	gatttaaaaa	taccgtggag	cctgtgctca	65340
ctatgggcct	caggctcatct	gcgcccaggg	atccccatgt	cccaggctca	gagaagtgcg	65400
cagagcaggt	tggcctgtcc	ctagatcagt	gcctggccag	gccctggtga	caggagtga	65460
ggctcagtc	tggcctccgg	gagccctgag	caatatggga	gacaggagtg	aacaaggaa	65520
tacattctgg	ggctcatgta	gcgcggggga	caaccacat	tgcagtcccc	taggggcacc	65580
ccaggagggc	ctggctcactc	ttcagggcct	cagggaagact	gcctggagga	ggcatcgctg	65640
gagccccatc	tgagctgctc	cttggcctgt	acacttggga	aacaggagaa	gagcagcctt	65700
ggggttgccc	ttctctgggt	gcctccctga	ggaactgacc	cccttttcag	cccttcattc	65760
agcaaggctg	gggaggggct	gcttcagaaa	cgctactggg	ctggagcccc	acacttcctt	65820
cccatcctgg	ctctgtggcc	ttggcaagtc	acctgccacc	tggggaacca	ctgccaacgg	65880
gtcggggctt	ggaagctcag	gggctcctgg	gccagacag	gtaaaggaaa	cagtactcc	65940
ggctagaaa	gagactgcag	ggagttgtga	ggctcttggg	cgctccctgtg	ccagggcggg	66000

actcctcatg	gcagccctga	gaggggaaac	tgtgtcctgt	gtggagcgtg	gatgcccacg	66060
tgctgagagg	tggtgtctgt	cctgattttt	gacagcagcc	caagtgatgt	gccagtgggc	66120
cagggccggc	acctgcctgt	cgggtggctgc	cccagggctg	atgggcaggg	gccgtttctt	66180
cacaggcagc	tggtgtgagt	cctgtgatca	cctcagtggt	gtctccagcc	ctggggggat	66240
ctgttgttct	gctcaacaag	agaataaagc	tgggttgttc	acacctggtc	ccaggtgacc	66300
cagcaggcac	agagaggtag	agttgacacc	aagcctcact	cagccaccgt	gacacggctg	66360
tgcgagtgca	cgccctggca	gagagcctgt	tctgggcctg	ttctgtttag	ccctggggct	66420
aaagggcggg	cctcagatgca	cagagggaca	ggcctgggtg	aggtggggagg	aaggaaaagca	66480
gactgtgtca	tcgtctcagc	ttcaggctgg	gcatgctgtg	gctatcatgt	gcttggcctg	66540
tgctaagtgt	gtgctaagca	tgtggccctg	gtgggcactc	aggcctcctg	ggtaccagcc	66600
gaggccccac	cccttcccac	tatgcggccc	tgagctctcc	tgctgtctct	gtcattcacg	66660
ggtctaccag	taggacaagg	cctgggggtg	gtggaggagg	gaaggagggtg	agattcggga	66720
gctttccgag	tcgtaccgcg	cactccgtct	ccgagcagca	gcactctcat	ctctacaagt	66780
ctctacagca	gtgctgccac	cgccctgacc	agggaaatcac	cctactgtga	ggtggcccag	66840
ctcactgtga	gactctgggg	cagtcataatg	ccctttctgt	tgaccccagt	gggtggccag	66900
cccacacgac	tgctgaatct	gccaggcctc	ccagccattg	ggggtagggg	gattgctttg	66960
gcagccacag	ggacacagat	gcggacagga	gcaggagccc	tggggaggag	gtgcacccca	67020
ccaggaagca	cccaccaatg	ctgactgagg	ctgcactgcc	agttagagcc	gctgggcgag	67080
ggacaaagaa	gggccttcgg	gtgtggggaa	agcaggcacc	ccagctccta	cactaagggc	67140
accctgggca	gagagggagc	ccagtggggg	gcacccaaga	cccatgagga	attggctgtg	67200
gtgtcaagag	gtcagccagg	ccaagcaggg	ccctgagggg	cagggaaagg	agagggcatt	67260
gtcgtgagtg	gggctcagct	gttagatgga	ttgtttacat	taaaggccag	ccaggaggcg	67320
gagcagagag	aggagttagcc	aggccacaag	aaggctgagg	gacaggtaga	catggagggg	67380
agaaagccag	ggtggcctcc	aggtttctgg	ctggggctgc	caggtggacg	gtggtggcac	67440
agcctgaggt	agggctcctg	gggtggttcc	cgggcggggtc	cgagcttagt	cttagagggg	67500
acaagggggc	ccaggaggga	ctggggctct	gatgcagatg	tgggagtgcg	ctgagccctt	67560
gctgccctgg	ggacaggcac	agcaggaggt	gctactcagg	gcacccaccg	ttgattattt	67620
aggaagcagc	gttcacgcct	gttctttatc	ctgacctggc	ccatctgatt	gctgatgtgc	67680
tcctgctgag	ccccccacac	cacactgagg	actggccaca	ggatctggtg	gcactcagtc	67740
ttctgggaac	ttggcagtg	gcctgtccta	ctttgcgctc	caagcctcgg	acgtcacctc	67800
caggaaccct	cccactgtgg	gtgatgtcta	cagtcacctc	cacagcccca	actctcatgg	67860
gtggacgtgc	tcgttcttgc	ctggcccagg	gcaggccgtg	gtgagctcag	gggtcctgcc	67920
tgtagtattg	gtgccctcgg	ctacgcaggg	cctgttagaa	gggtgccctc	cctgccaggg	67980
cctccagcca	ctgtctgtcc	tgttcccggc	tcagagttca	gccagcatag	aaagagaggg	68040
ctgaggacca	ttcagcctgt	ccattcacga	gaatcattgt	cagtgtcaca	gaggctgatg	68100
ggatgccctgt	ggtgcagggt	gaccccagct	tccccatgtg	ggggatgcgc	cggtgggtgca	68160
aggccaccac	ctgtgcctc	gtctctggca	cagggatgat	gacagcacac	agcacatcct	68220
cttttctttc	tacctttccc	tttggcacag	ccccttggtg	tgggcgctac	gagaggcgca	68280
gagagatcgt	ggaggtcaag	ggcttgccca	ggaccagtga	gggaggagg	gagagggcag	68340
cagcaccctt	ggagacggga	ggattacatc	atattttattt	accacatgcc	taagatcgca	68400
ctcttaagag	catttgacat	acatccaaaa	atttttaaac	actatggaag	tatgtctgga	68460
tgcatcagta	atatgaaagt	ggaagccagc	tgccctgtct	ccagccact	ttgggaaaat	68520
tttgtgcatg	ttttgagcca	gctgtttggg	aagggaggcc	ccagccactg	ccccttgggt	68580
gggtttgatg	ttcattgtgt	gggaagaagc	cttccctcca	tccttttcta	tttctgcaga	68640
atatctgctc	aatcagggag	ttgagcttgg	cagttcagct	gctcagccag	ggaggtgctg	68700
tgtcctggag	tatgctagga	tttcagaagg	agagagggca	gctgcaggcc	ctrtttgcag	68760
tggtctcttc	ctggaatccc	cgtctgtccc	ctgtgtactg	tccagcgtcg	tagtgggaagc	68820
tggtggcgag	acgggtgaga	cccacggaca	tagatggcat	ccacgaaggc	tggcggagcc	68880
tgtgatagac	gatggacgat	gacccagggt	ccagcaagat	atggcagtg	gctgtgccgg	68940
gaagggggcg	atcctggagg	atgccctagg	tagtgccctga	gaaagtgagg	gtcattgact	69000
gattccacgt	ggcatccatg	aatctctcaa	atccataggg	cccgtgcatg	acaaataatt	69060
aaaaagatgt	aggggtgttct	ccatagaacc	tcacagaggg	aaggagacct	gcccatggta	69120
tccagctctg	atcacactgc	tattttgtga	ttgataggca	gactttcaaa	gaatgagtta	69180
gattcaggac	ccttttagtt	gtaagtga	aaatctcaat	ataaattgac	acaagccaaa	69240
aaagtagagg	ggcaagggat	tgatgagtc	atagatctgt	agagcctaga	gtagtttget	69300
tcaggcacgg	ctggatccag	gggctcagat	gatgtcatca	ggaagtactc	ccccgcccc	69360
attccactct	gctttcctgt	gctgcctgtg	tctcaggggc	tctgcccaca	gggtgacctt	69420
ccacagttca	agctggcatc	cacgtgccaa	gatgagcaga	aggtgaaagc	ccatttccca	69480
gcagttctag	cacaaactcc	gctgggtgtg	gtccatccct	gaaccagggtg	ctgtagtccag	69540
ggagatgacc	tggcaactct	gattggccag	gtgggggtgc	gggccttctg	tgacgcgcag	69600
gggagggggc	agtgccaccc	agaccatgag	gactgagagt	ggcgggggtc	ccccaaaagg	69660
acatcaaggt	gcagtcacac	gaaaaagcaa	ggaacggagg	tcgagcacac	agaaaacacg	69720
tgtgtttgat	ggttcttggg	ggtccacact	gatgcagccg	gcttctgggg	gtgatctttc	69780



tggcactgag	cagtgagcat	gctgggattt	gcctttgagc	ccacgaaggc	tcctacttca	69840
tggactgagc	taactggctc	gcaggacgag	cccaccactg	ccatatggaa	gctggaataa	69900
tgaagagggg	gtgtgtccat	ctcaaagaga	ttctgggctg	ggcgagtggt	ctcagacctg	69960
taatcccagc	actttgggag	gctgaggcag	cagatcacct	gaggtcaggg	gttcgagacc	70020
agcctggcca	acatgggtgaa	accctgtctc	tactaaaaat	acaaaaaac	ttagctgggc	70080
atggtggcgg	ccgcctgtat	tcccagctac	tcaggaggct	gaggcagaag	aatcgcttga	70140
acccgagagg	cagaggttgt	ggcgagccga	gattttgtca	ttgcattcca	gcctgggcga	70200
tgagagtga	actctgtctc	aaaaataaat	aataaaaaag	agagagagat	tctgtatatc	70260
ggggagatgt	cttgaaatgt	caggctgtga	ataacttctg	tgaaaaatta	attatggact	70320
ggaagaatct	tttttagacca	ccatatagac	ttggaccttc	catgttttga	tttttttaaa	70380
aaagggaaga	ataatatgac	ttgtgaactt	aggtcaagta	aggagacttg	aattcactag	70440
aggtgctggc	gttgtgtgtg	gaagtacagc	aacagccctg	gggtctcctg	gggaagtggg	70500
ggaggggaaga	gaaagcctcc	tcttgtgaac	agcaactttg	gaccactcac	tacaaagcat	70560
ctcttttcat	cataaaccat	cctatcagat	tgatgttaac	gatcagattg	aagctgcttc	70620
ggagcagtg	tgtggcctgc	accaggtcgc	acagcacctt	actgtggagc	atggatccac	70680
acgtgctgtc	gtgtcattgt	gatcgctcac	gctgctctgt	gggcccattg	ccttggtgcc	70740
tgcaggctct	gtgtctgcag	ttcctctagg	gatagtgaag	ctgctgtgta	gcccgcagcc	70800
agaaaccacg	ctggggggct	ggcaggggtg	cggcagcaag	gaaggagaac	tgtccttgat	70860
ggattcaggg	agcaccaagg	tctgggggct	ctggggaggg	tgggtgtcca	aaagggctgc	70920
cctgcgggac	ctgatgccat	ctctgagcag	cgtccttgag	gaccccgcca	aggaagctga	70980
gcccgaact	ctgtgcaaga	gttgcgtcca	gggagagtta	catccaggga	gagttacgtc	71040
caggagagag	ggcgtccagg	aagaggggca	ttcagggaga	gggacattca	gggaggagtc	71100
ttccaggggac	ggggacatcc	agggagaggg	gcgtccagcg	agaggagcct	ctagggaggg	71160
gtacatccag	ggaggtggcc	tgtcagggag	gggtggtgtc	agggaaagca	gcatacaggg	71220
agaggggtgt	ccagggatgg	gggcatccag	ggaggggggc	ttccaggggag	aggggccttt	71280
gtgttgccga	gttgtccatc	cacagggctg	gagtgctgtg	gcctgaccac	gagagcttgt	71340
gaagaatcca	tctgattctt	tccttctcca	aacacatgcc	tcaccacac	agccttacct	71400
gtgagggcct	cacctgccac	ctgcgacttt	tgagttgtcc	cagcctccct	ctgcctcttc	71460
caaaactggg	gtgacccttc	ctctctgcct	ttgcacctgg	ccacatccca	tgggtctcca	71520
ctggagtcct	gtctcctgta	cacctgggtc	atctgaaggc	agtggccagg	cagcacttgg	71580
tgctgcagag	ccggttcaga	gcctggcacg	gtatggttct	gggaaagccc	tgggtgagtt	71640
ggaccagaaa	ggctggctct	cagtgtgggt	ttactgggaa	ccatgcagcc	tgtcccgttg	71700
tcagccagcc	ttgggtgaaa	tgggtaagac	tgcatgatgc	ttttgtaaat	tcaggtaact	71760
tcttaggaag	taaaatgcag	cacaaaactgt	agttgatgtt	ttgacccttg	gtctaataat	71820
tcaactggag	aacctgtgct	aggaaaatga	cttcccaaaa	gaaaagaaac	ggttcatggc	71880
accaccgtag	aaaacaagag	gttattggaa	gcaacctaca	gacctgatgg	agaggagggg	71940
agggtcagta	acctgactct	gtctccttga	tgaatctagg	agccaccaaa	atggtgagct	72000
gactgcagcg	catcggtgga	agccagagaa	aatccactg	ctgtggactg	aaagtttgtg	72060
tctctcccag	attcatttgc	tgaggctctc	acccccagtc	ccatggtgtt	aggaggtggg	72120
gcctttggag	gtgatgaatc	atgagcgatg	gctttacggg	ggaattagtg	ccctataaaa	72180
agaaacctca	gggagctccc	ttgccccttc	cacctgtgta	ggacacagcc	agaagacctg	72240
aaacaaaaag	caggccctca	gtagacacgg	agtctgcaac	actatgatct	tggacttccc	72300
agtctccaga	atcgaaagaa	atacatttct	gatgtttgta	agccaccagc	ttgggtctatg	72360
gtattaatat	ttttgttata	acagctcgaa	cagactaagg	cattcactct	taagaaggaa	72420
aaggtaatat	caagatgtat	atacactgat	tataatatcc	aaaaaatgtg	gtttttgttg	72480
gtacaatcat	ggaaaacatg	aacttgattt	gttgggggtc	tgggcttcgg	gtacaggtgc	72540
tttgatttat	ttaggctcatg	ggctgtcaaa	cttgagctct	tggatctttc	tagagcccca	72600
gctagagcag	gcctaggcca	aggggtgtga	tgggtgggact	tggctctgtg	ctgcctcctc	72660
tcccatgcct	cccaccccca	gcgctttgag	ttgctgttga	accacctcac	ccgcatagag	72720
tttgctcatc	ttgctctggc	gctgcttgtg	accggaaggc	aaacagtggc	tttctgggca	72780
tcttccctgt	ctgtgtctgt	gtctctctgt	actcctggcc	tggatttgaa	agtgacaagc	72840
agcagcagat	ctgaagaccc	tcatgccttg	tcccctccat	cctgacaagt	gacaaagtct	72900
ggctttgtga	catgtgtgtt	tgtttcttct	gtgttaaagg	gcctacaaaag	ggagacatgg	72960
aaatcccctt	tgaagaagtc	ctggagaggg	ccaaggccgg	ggaccccaag	gcacagactg	73020
aggtgaggag	tgcggtgcgc	gcagggactt	cgggacgcgg	cccccgccac	aacaggcctg	73080
gccacgagct	ccacagccca	cagagaagtg	tcggtgcctg	agatcggggg	caggagccag	73140
cgtggtgcac	cctacccccc	ttgagcccca	tgttggttagg	gtgcccattg	tcactgtgcc	73200
agttttcttc	ctggcactcc	tctgggggagc	agcgctcatc	ccccttttgt	ccaactcaca	73260
cctcatcttg	ggcatcacct	cctccaggat	gacctcctgg	cttctctcag	ctgcctgctc	73320
agtgccaccc	ctcaacatac	actgtgtatg	ctgcccactc	ttgtctccct	gactggcctt	73380
tcacctggct	gttagctgtg	tgcacggggc	cctcagagcg	gtgaccattc	acttgggcat	73440
cagccaaggg	ctgggctttg	tgccagtgtc	ggggacatga	tgtggccctc	tcttcatggg	73500
tgacaggtta	gtggaagaag	cagacccaaa	aaacccaagt	agacaagaca	cagaaataca	73560

gtgattttga	attctggtga	ggggagaagc	cagcagaacg	ctgagacggg	aggtggcagg	73620
gggtcctgtg	tcctctgtgg	aggcaagttc	tcaccacctc	actctgtccc	cttgcacagg	73680
gctcaagcaa	gtgaccacag	ttatcctgag	cagtttcctg	ccccctcttc	tccttaaaga	73740
ggagaaaagc	ttccacgcga	aaccataaat	taagaatttc	tggctgggag	cggtggctca	73800
cgctgtaat	cccagcactt	tgggaggctg	aggcgggtgg	atcacctgag	gtcaggagtt	73860
cgtgaccagc	ctggccaaca	tgatgaaacc	gtgtctccac	tacaaataga	aaaattagcc	73920
agacatggtg	gtgcatgcct	gtaatcccag	ctacttggga	ggctgagaca	ggaaaatcac	73980
ttgaaccag	gaagtggagg	ttgcagttag	ccgagatcgc	accaccacgc	tcaccaactga	74040
gcaacagagc	aagactctgt	ctcaaaaaaa	aaaaaaaaaa	aatttctttc	ctgacctcac	74100
agccatattg	tacttttaaag	ttcctcccac	atccttttgc	ccaggcattt	ggaggcgggg	74160
ggagcatagt	aagccctttt	atgggtcttc	tgtgccctgg	gcctcacttt	ttccatctgt	74220
agaatgagaa	gactggacca	tttcagcagg	gattcttttt	gcaaagggcc	agatagttaa	74280
tattctggac	tctgcgcaat	ctctgcctgt	ttgctcagct	ttgctgtgga	gcacgtaaaa	74340
gcagcatgga	caacatgtaa	atgaatgggt	atggttgtat	ttcaataaaa	ctttatattgc	74400
aaaaacaggc	agtgggccag	tgctaaccct	tggtttagctg	gcgtctctcc	agccctggct	74460
ttctatggtc	ccctgactgt	tttgagaggt	gtaaaaggac	cagtcatggt	tctgatttcc	74520
atgcattgat	ggtgagcctt	ggcaggcagg	agcaactcaa	ggaagagaaac	ctgtaccagt	74580
accagtggga	ccccgtgtct	ccctcgccgt	gtggatgggg	tggccacacc	ttcctcacccg	74640
tgttttgagg	agcgagtggc	cggaggtcca	gtagggccta	gcctagtgga	catgcctggt	74700
gtgaccccat	ttctgcccct	tccttccctg	cctgggtgac	aaaggggaagt	gggtgaaagg	74760
aggtgggctg	gcagggagca	tggggtggga	gagggctcga	gaatctggag	gctgactggt	74820
gtctggcttg	caggtgggga	agcactacct	gcagttggcc	ggcgacacgg	atgaagaact	74880
caacagctgc	accgctgtgg	actggctggt	cctcgccgcg	aagcagggcc	gtcgcgaggc	74940
tgtgaagctg	cttcgccggg	gcttggcggg	cagaagaggt	gggtctgtgt	gaggcttaga	75000
acagcctctg	gaggggttag	cagcttgtaa	tgtgtcttgc	taactgaaca	actaaaatct	75060
taccaaacct	aacgctgggt	atgctgttgg	gaaatttcag	tttctgtttt	gctgggtggc	75120
ttctcatttt	agacactgtt	tctggactta	acatgggata	tttaacagac	caagccattt	75180
tcattctctt	tggcttgtgt	tggatatctc	aagtggtaac	tatacatcct	gcttccctgc	75240
tgggttctga	tcctaaactga	gacatcgatc	ctgggttcag	ctgagaggca	gtttccctga	75300
ggcaaagctg	gagactgtaa	tgtggcctgc	agtcagagtg	gcccattgcc	ctgagctgat	75360
gtccgtcgag	tctgggcaga	ccagctgagg	ggctgtgggc	ccacacagac	ctggacaagc	75420
atgttcactt	tgggaggagg	caggctgacc	cttcatagat	aatctctttc	aaacagagag	75480
gcaggggagg	aaagggacgc	agctcaggcc	aggggtgggt	agttaggacg	ttgtcctgcg	75540
caaggggaagt	ggctgtccct	ggtgccgtgg	ggcagtgtgc	ttcctgaagg	ttccacgcct	75600
cagggaaaga	tgaaagtggg	tgtcacaaag	gtgttttttc	taatgatacc	ttttttttca	75660
gattgtaaga	gtattttatg	cttatcatag	aaaacttggg	ctatgtagaa	aacataaaga	75720
tacaaattac	tcataacctt	gaagcccaga	agcaactccc	catatttttg	tgtatttccct	75780
tctgtgtttg	ttgttgttgt	tttgagatgg	agtctcactc	tgtcgcccag	gctagagtgc	75840
aggggtgcca	tctcaagtca	ctgtaacctc	cacctccctg	gttcaagcaa	ttctcctgcc	75900
tcagcctttt	gagtagctga	gattacaggc	gtgcattacc	acacctagct	aattttttgta	75960
tttttagcag	agacagggtt	tcatacagg	ggccaggctg	gtcacaaact	cctgacctca	76020
ggggatccac	cctccttgge	ctcccaaagt	gatgagagta	caggcgtgag	ccaccatgcc	76080
cagcttgtat	catattttta	gagttacatt	tattatacag	agtcttctct	ttgaaaatta	76140
aactgatgat	tttgaaaaac	taacagtggc	attgttagcc	agaatttctc	accaaccagg	76200
cctgtctgatt	ccagagcagt	tggaaatgacc	tggagggggc	tcaggcggcc	cacacggctc	76260
attgttgggt	gccagggata	gccagaggc	gagcgtgcaa	gggaggaggc	gggaggaggc	76320
cgggttggccc	cgtgttcccc	cagctgcaca	caccttctga	tgtgcagttg	tgttttctga	76380
tttgaaaaga	aatacatgct	catgtggaaa	attttggaaa	tgttcaaaag	gagaaaaaca	76440
tcagaccccc	cgtgccagtc	ctcctgccct	ctgcttgggt	gtgccagtgt	cccaggccgt	76500
tgggggtaaa	gggaggaagg	cagctgctga	ccagcggtaa	aacctgctct	ccctctcccc	76560
gctgtccaag	ccttccttag	aaagggtggt	gctgtgtgtg	agacagagga	aagctctgta	76620
gacacagggg	tggccctgcc	agtgcaccca	ggctgggtgac	tgcagttagt	ccaccctggg	76680
ttcaagacag	ctctgcctct	ttctgactgt	gtgaccttga	gtgagccaga	acacaggcct	76740
gtgcctccgg	gtctgcacct	ctgagagagg	ggaggaacag	gaagaggctg	ccttcttccc	76800
gccagctagt	agggggcact	tgggggcgtc	tgggtgggga	ccagtctggc	ctcccagctg	76860
gagagtgggc	gtggcgcgat	gtcctcttga	ctcagatgtc	catgcatacct	tccttggtta	76920
ccaagtctcg	acaccttcta	tgagtctcgc	tgcgaagcct	tcagggcaga	gttggcaggg	76980
tcagagtggc	accgaaagcc	taggcagggc	acacaaggcc	tttgaccaca	tcctatccct	77040
caggcatcac	gtccgagaac	gaacgggagg	tgaggcagct	ctcctccgag	accgacctgg	77100
agagggccgt	gcgcaaggca	gccctggtca	tgtactggaa	gctcaacccc	aagaagaaga	77160
agcaggtggc	cgtggcggag	ctgctggaga	atgtcgccca	ggtcaacagag	cacggtgcga	77220
ggattcaccc	tgggcaccag	ccttcctctg	gcgccagcct	tcacacagga	gccaggacct	77280
tcccataggg	gctgggacct	tccttcaggg	gctgggtctt	cccacaggag	ccgggacctt	77340

ccctgtgagg	acagggccct	tccttgtggg	gaccagggga	ccagaacctt	cctgtagaga	77400
ccgtgcccta	gtggtgaggt	gtgtgggtgg	cattttgaca	gcatctgccc	tggtctcaagt	77460
gtcactcat	tgaataaacc	agaggggtatt	ctgcccagtg	ctctgtgacc	acgtctacca	77520
atgggacgga	ctgtgtccat	caccaagtgg	gagcacgcta	cgtgggtgctg	agtccacccc	77580
agctactgga	ggtacagagg	tgtggccccct	gctctgcctg	ccctgggggc	cctatgatcc	77640
ccagaacgta	ggatgccccct	ggaactggcg	tgccctagga	acagtgcgcc	agtttctggt	77700
gggctgcagg	gcacgaggag	atagtcaact	tgtctgactg	ttaatccacc	ctgtcccctg	77760
cagatggagg	ggcgagcca	ggccccgtgc	ccaagtccct	gcagaagcag	aggcgcatgc	77820
tggagcgctt	ggtcagcagc	gagtgtgagt	gcagccccctg	ccccgtctca	cccatgcctc	77880
ccagcctgca	cctgcagggc	gacctctctc	tcctgtgcga	ctccatcctg	gcctgcccta	77940
tctcaccctg	gcctcccagc	ctgcgcctgc	agggcgacct	ctccttcctg	tgcgacccca	78000
tcctggccct	gctaggatct	caggcggtcc	gtttggggct	cagtgttctg	gacgtgggga	78060
gtagaccctg	cccacctgga	gcgcacgcac	tggagggaag	gcagaccag	gacagaaacc	78120
atgatgtgcc	agtccctctt	ggacaaggaa	atactggggg	tggggactgg	cgggggggtc	78180
ctgagtgggg	aaggatgagg	agggcattag	gggaaggggc	tccgggcaga	gggaacagca	78240
tgagcaaagg	cccaggagac	ccagcagggt	gtggaagggg	ctctgcccc	gcgtaggccc	78300
tttgtaggta	ggcagggaac	agagtgggca	gagcctaggt	tgggggatag	agtctctggg	78360
gcacactgag	ctgggggtgc	ctctgggatg	tttgtggtca	aagactgaga	agagactgca	78420
catcctccac	gtgcagctgg	ccagcctcac	tgtcttccat	ccacgtgggg	tagactctgc	78480
agtctgaggg	actgggagct	cctgtcctgg	agaagataga	caggcaggag	gcttgggggc	78540
tcagtatcaa	tggggggatg	ggccaagacc	caggctctgc	acagactctt	cttgtgacat	78600
gggcagggtct	catttttctt	tcctgggtgtc	agtttccctt	tctgaacagt	gagatgatca	78660
gacaagggga	ctgaaggacc	tcgcccaccc	tagaagcctc	tgtggcatgt	agggcagagt	78720
acagggtggga	gcacagatcc	caccttccca	ctgggcccgt	gaggaaaccg	tccatagggt	78780
gtggctcagag	ccctgcctc	tgcgtgggcg	gacatgggtg	cttgcgctgc	tgttttctctg	78840
ctccattttg	gggagacaaa	gaaacacctc	acatggaagt	gggaagaaat	ctgtgactct	78900
aggaagcccc	aggaccagag	aggctgtgac	agtgtcctgc	caccgagggtg	gcatggtgcc	78960
tgctgtcctg	aagtgaggtg	cctctgggca	ggagcagccc	agcctgggtc	tcctcctctg	79020
ggggcactgc	aggcagagtc	tggaccccaa	cctcacttcc	cagtcccaca	ggggtttgtg	79080
atgagccggg	cacacctgct	gctggggcct	gtcgtgtgtg	ctgggggcga	gttaggagtc	79140
agcgctgcca	gcctgtggtc	ccctccgcca	ggccctcagg	gacagggccc	cagcaccccc	79200
attgtttccc	ctctatcaga	acgttcccat	caggcatcat	ctgtttctct	gccagctttt	79260
ccaacagaa	tcccagaaag	gggctgtgtg	catccccctc	tctcgctctc	cgctctttgc	79320
tctcaggcct	ctgccatgtt	attccaccaa	agcggtcctg	ctaggccatc	agtgaccccc	79380
cttgctcagt	cacttcttgt	ccttgtctga	cttgatctgt	cagcagcgtg	ggcagagatg	79440
actgtctctc	tccttagagc	cctctcccc	accaggcccc	gggcccctgc	tgccacactg	79500
gctgtctctt	cttgggggtc	ctagactgat	gtcctgtctc	tcaggacagg	acatcctgcc	79560
caaggatatt	atccctatga	ggacaggggc	cttccttgtg	gggaccaggg	tcttcccgtg	79620
gggactgtgc	tctggtaggg	agatgtgtgg	gtggcattgg	tgaccactct	cgtgtgtcag	79680
acgccgtcct	gaaccgcga	gccccagcc	cgcccaggct	gcatccagcc	cgtgtctctt	79740
ccacatctcc	tgtacctggc	tgtcccagtg	tcacctcaca	gctcagtcta	cagtgaagta	79800
ctgaggcctg	tgtacctgc	cacttgtgtg	ggccccccca	aggctgcctc	atctctttgc	79860
tgagctaca	cctgggtgct	gccccgactc	ctctcctctt	gcacacacag	ctgatccatt	79920
aggaggtctg	tcagcgccca	ctatcacggc	tgccatcttg	gatgcagcct	gcctcctccc	79980
tagggtttct	gcagcaccct	ggcttgtctc	cctctgccct	gccccagcat	ggctctttct	80040
ttcccatcct	tccccggag	gccctcctg	tcacctctc	accacggcaa	ctggggctct	80100
tcaggggcct	cattccctcc	taggggatca	tgttgatag	aggggtcagt	gggcacgtag	80160
ctctcgcgga	tcacgttgg	tggagggatc	agtgggcacg	tagcaggctc	ttggtggaag	80220
atgttggtg	gaggggtaag	tcggcccag	gcaggacgca	tgttgaatgg	acgggttagc	80280
aggcatgtag	tagggccatg	gcagacactt	gttggtgga	ggtgtcagca	ggcacatagt	80340
aggtgtgtg	cagatcatgt	tggatggagc	ggtttagcag	gtgcacagta	ggccctgggt	80400
ggatcacgtt	gaatggagg	gttggggcg	cagatcatgt	tcgatggagc	ggttggcagg	80460
gtactgccct	acagggcggc	ttgtcacccg	tgtgtgaga	agccccacgc	tggtgaaga	80520
ggagggtgtc	agcatgcact	ggaggtgcat	gttgtaaggc	ttggcagggtg	aactgggtga	80580
aaggtgtggg	tgagtggccc	caggcataag	gagctaggca	gagagggaca	cttgggggtg	80640
gggacagcac	accaggggc	cggggggcag	gagtgaggc	tggcacttgg	caaacctgcc	80700
cccttctctc	tcaccagcc	tggctctcaa	ccctcaggcc	gcccagggaa	gggtttctct	80760
cacctgaacc	cactcagctc	ctttcttagc	ttggccccac	gccaccgtcc	ccagccatt	80820
gctctgtgtg	aggggtggcag	tggggctgca	gtgtggggcg	cccatgtctg	tttctctcat	80880
gcttcagcca	agaactacat	cgcgtggat	gactttgtgg	agatcactaa	gaagtacgcc	80940
aagggcgta	tccccagcag	cctgttcctg	caggacgacg	aagatgatga	cgagctggcg	81000
gggaagagcc	ctgaggacct	gccactgcgt	ctgaagggtg	gtgaccaaga	ccccggtcag	81060
gccggagcct	gcctcccaag	gactcgcgca	cctcaggcag	ggcaccttcc	aggaaagctgc	81120

aggtggggag	gttcgcgcct	aacaaagagt	gtcttacagc	cgtgccgctg	gtacctttgg	81180
gtcatcatct	atcgtcataa	ggatgtgtcc	tccggagaga	ggccttttctt	ttctgcgcgc	81240
tcaggctcag	aaaccagggg	cgggtgttggg	caggagtgtc	aggatggcaa	gcaaggggccc	81300
cctgggtctt	tctgtgcagt	gtagggggca	gtggggcggg	ctggacgcag	actttcatct	81360
agacttcatt	acttagcaga	tttctccatg	tatgggtccag	agtggaggcc	agtgccttga	81420
agatgccttc	cccgaataca	aagtgccgtg	tccgtcaggc	cagggaggac	gtgcagaggc	81480
gcctactgcc	cctggatctg	caagggtcca	gggagcgagg	ccagtgtggg	agcgtggtgg	81540
gtgacacttg	tgcagggtgc	cattgggcac	acctggagga	catgagcagc	tttggcgcca	81600
ggaggaaagc	ggggagcggg	gagcgggaag	cccagcagtg	cgggccctac	tcctggcctg	81660
acagcttggt	ttcttgccca	tgtggcccta	tggcctctca	cagagttgct	cacagttcag	81720
ctcgcattgt	tgaattagat	gtgtgcctgt	ctcactctgc	agagaacacc	aggatttcca	81780
gaagcttggc	ctcctgaccc	aggatcccca	agctgaggcc	agcacagggg	gccccagcag	81840
atgattgtca	cagaggctgc	gggcagtatc	atgcaggcac	cctgggggttc	tgtcttctga	81900
actgactgag	aacctggagg	aactgccatc	attgtattca	gatgggcgcg	tgagtcaggg	81960
ccaggaccag	gagatggttg	ggccaccaac	gttcaggcag	gcagcaggct	gaaaggctac	82020
cgtcctcgag	ccaggagaaa	ggtcagagta	ggcccgcctc	ccgggtggggg	ggaaggcagc	82080
gaaccaggt	gctgcaggag	cagcttcagc	ccaaagagca	gcaggcacag	cagccctgct	82140
gcagggactc	ggagccagac	aggtctgagt	gtgagccccc	cgagtgcaca	gagctgcgag	82200
tccttttaggg	tggcagggtg	aaggctctgc	tcctccact	tgggacaggc	tgtatgtcca	82260
gggtatgaca	ccgaccggtc	tgcagagggt	ctgagacatg	ggccaggatg	gccaagaact	82320
tgaaccaagg	gagcacatgg	tttttactga	tggctctgctc	agagctggcc	ctaggcaagc	82380
atattcacag	attgggtgcc	atcatctcct	tactaatggg	agatgaggaa	gctgggggtgc	82440
tggcatgggt	ttggcaaaaga	cactcccga	atgagagtga	gggtcacagg	tgaacgggtt	82500
aacttgagga	agacccttgg	gccaggcgcc	catggcccag	gtgtcccagt	ttatgccatc	82560
tgggtgaagt	actattataa	taatgcctcc	ttgcatatgc	gtcctgttcg	gaaaattatg	82620
tcacctaagt	attggtggtg	agtctagtgt	tgtgtagcat	ctgaaaatcc	tatttattta	82680
tgttacttaa	tgacagggtc	tcgttctgtt	gcacaggctg	gagtgcagtg	gcacgggtcac	82740
agctcactgc	agcctcaacg	tgccaaactc	aagtgatcct	cccacctcag	cctcccaaat	82800
agctggacta	caggcatgtg	ccaccacacc	cagctgattt	ttttgaaaac	atttttagtc	82860
gatgggggtc	tactatttgt	tatctacgct	ggctcctaac	tcctgggtca	agcgagcctc	82920
ccactttggc	ctcccacact	gctgggattc	aggcgtgaga	cactgtatcc	agcctgaaag	82980
tccttttttag	aaggagagaga	tttaagctgt	tttgacaaga	agtaaacaag	actctgtttc	83040
ccttttagttt	tggatgctgt	cagagcactt	cgattccctt	gcagtttgtc	ttcttagaag	83100
tctcttgtag	gggaggcaat	gaatcgctac	aagcgtctcc	cagggtctgag	agctgtccca	83160
ccttttagta	gccttttcta	gaacaaggag	aggtcttcac	tcaaagtga	aatgacagac	83220
acctctttgt	gagccaccct	tactcccaca	aagaatgttc	cagactccac	acagttctct	83280
tctggagcct	ggagggtgcaa	gctgtcatcg	tagatagaat	cctctgaaaa	caaacttaat	83340
atcttaaaat	cgtaacattt	ttaacattac	ataattggaa	gatccgacac	gggaacattt	83400
ttgccacacag	gtttgagcag	aatctcgtct	cggctccctt	ccccagcctg	ccttcttcac	83460
gggtccgctg	ggccatcggg	gtggtgacgc	tgtctcctgg	tttctcgtgg	cagcagaagg	83520
gccgatcacc	acaggcccag	acagagagct	ctgcagtgtt	ctattcatag	aggcagactc	83580
ctcatagttt	ttaagtttcg	ttctttttcc	atctcaggag	ttgaatttgt	ttggaccttc	83640
tttgagaaa	aggagactga	acttttttaa	cccatgtcag	agggaaggct	tgggtgtaca	83700
ttgcaggag	cagaaattgg	ggcttttaaa	agggagctgt	tccttggtca	tcgagttcag	83760
gtgggggacc	agcccctcca	cactgtccaa	gacagggcta	gacgccatcc	aacgtaatgt	83820
totagaatat	tccttgtctt	ttaaaggccc	tctcaaccag	gtggttgtgt	gtgttctagg	83880
caaaagaatg	tgcatggctt	tgagtaagac	aggatttcag	atttattttt	accaaggcca	83940
cccccttgct	accgtggcgg	tcgtgcgtga	aactggtggg	gagcagtgcc	gggcccaggc	84000
accttttagtt	gtcctgctgt	tcgcaaggcc	cccatacggg	gattaactga	gcagcctgcc	84060
ggctgacgca	catgttgact	cgtgtagctg	ttgattttag	ccagctggcc	tggcgctcata	84120
ctacaggggc	ttgccccaaa	caaaccctgg	agtaggttgg	ttttcataaa	tgccctctgg	84180
ctctctggca	agcgttggaa	atgccctcaa	accctgtagt	gcctgggtctt	ccctggccat	84240
ctcctggcag	tgtgagcgcc	tctctgctca	tgtagaagggt	tgttgacccc	agagagagct	84300
aggggagctg	ttagctgctt	taatcgttta	tttctgtgtt	ataaaacaga	gattaaagtgg	84360
actgtcacaa	atatacatga	agcagcagag	ctgttcccc	acgtgtagac	gtgcatgcac	84420
acactcctaa	acacttcctg	ttcttccatg	agcctgtcct	tctcatctgt	ggaaggctca	84480
gtctgtgtag	acatgcatgc	acacactcat	aacacttccg	tttctcccat	gagcctgccc	84540
ctctcctctc	atctgtggaa	gactcagtct	tctggttgtt	tccagggtgc	ctggtcctcc	84600
agagctgata	gccaggctgt	tggcagggtga	gggccacatt	ctggtgttgt	cacctagtgt	84660
ccattcacct	gggatccctc	cttggccttc	tgggtggcct	ggtggagaga	acctgcccc	84720
ggggatttgt	ggggctctgt	gcttccccga	ggcccggagc	tgatgggggg	ctccagcctg	84780
gatgtgtcat	gtagccctc	agtgggccc	ggacatgcag	ccaggcttcc	ctacccccat	84840
gtggggcgcc	cccctaggcg	tccacttctc	ggtgttggtc	caggccctg	gcacttctga	84900

agatgcacag	aacctgcttt	gtatgccacg	ccatgctgtg	tgagcactgg	caccatggcc	84960
actttgtccc	ccatcccctc	cagtcccctc	gcctggctgc	cctgtgttct	ggcagggctc	85020
agggcctctg	agttctgcac	agaccaggaa	ggcatgaggg	ctggccctgg	gtggcagcgc	85080
tgcttcaccc	catcctgagg	ctgctcccag	catgcctccc	tcagccctct	gctcctcttg	85140
gctgtggtga	aggccaagag	ctctttctga	ccttagcgct	gcagtcagag	caggggagca	85200
ggaccacacg	gtcgggggaa	ggcagccttt	ggccttgact	atggggaggt	aggggtgcgc	85260
tggtgtgtat	gtgtaggtgc	acacgtgtag	gggtgggtgt	gcagtggtga	gggtgcacgt	85320
gtgggggttg	gtgtgcacgt	gtgtgtaggg	gtgggttgcg	tgtgtgtgaa	tgtgtatagg	85380
gggtgggttg	gtgaatgtgt	gtgtaggggt	gggttgctgt	tgtgtgaatg	tgtgtgtagg	85440
gggtgggttg	aatgcaggta	gggtgcgtgt	gtgtgtaggg	gtgggttgcg	tgtgtgtgaa	85500
tgtgtgtgta	gggggtgggt	gtttgcgggt	aggttgctgt	tgtgtgaatg	tgtgtgtagg	85560
gggtgggttg	gtgaatgcgg	gtaggttgcg	tgtgtgtgtg	taggggtggg	ttgcgtgtgt	85620
gtgaatgtgt	gtgtaggggt	gggttggttg	aatgcgggtg	gggtgcgtgt	gtgtgaatgt	85680
gtataggggt	gggttggtgt	aatgcgtgtg	tgtaggggtg	ggctgcatgt	gtgtgtgtag	85740
gggtgggttg	tgtgtgtgtg	tatgggtggg	gtttgtgtga	atgcgtgtgt	gtaggggtgg	85800
gtttgcgtgtg	tgtgtgtgca	cgtgtgtgta	cgggcagaag	gtggcctggc	agctgcttct	85860
caggggtctcc	ggccataggg	agggcagctc	acccggcagc	cccgctgacg	tgaacggtat	85920
ttttgctggg	agagtgggtg	tgggcccctc	gcctgtgtct	gcactgaact	ccctttccct	85980
aatgcttgct	ctgccacccc	tccggggact	gcctgcccgt	tctcctcctc	gtaaggatcg	86040
ccatttccct	tcattggaggc	tcagggaggt	gacatccttg	ctgtagtga	gagctgggtc	86100
acaaaaccag	ctcccagaca	ggcatctcag	ggctccgtca	tctcttcattg	tgggtgaccc	86160
tgaggggagg	gaagtgggga	gcccgtgggt	ccctccagtg	ctggaggtct	tgcagggaga	86220
gaagcacaca	tgcatctagt	cacgctggta	gaaggtgggg	agccaggcac	ggggcagagg	86280
ggggctccag	gcccagaaga	gggagggtct	acagggaccg	cgagcatggg	gagggccacc	86340
tggagaaggg	gggaggagg	accactagga	tggggctggg	gatgggaaaa	cgcaagggtg	86400
cgggttcctt	ttgccagag	gcaggggtgg	cagaggagg	cgtgagatgg	gagcagtggtg	86460
ggtcctgtcc	cagcctcggt	cccacgtacc	atctttcccc	caggtggtca	agtacccctt	86520
gcacgccatc	atggagatca	aggagtacct	gattgacatg	gcctccaggg	caggcatgca	86580
ctggctgtcc	accatcatcc	ccacgcacca	catcaacgcg	ctcatcttct	tcttcatcgt	86640
cagcaacctc	accatcgact	tcttcgcctt	cttcatcccc	ctggctcatct	tctacctgtc	86700
cttcatctcc	atggtgatct	gcacctcaa	gggtgtccag	gacagcaagg	cctgggagaa	86760
cttcgcgacc	ctcaccgacc	tgtctgtcgc	cttcgagccc	aacctggatg	tggagcaggc	86820
cgaggctaac	ttcggctgga	accacctgga	gccctatgcc	catttctctgc	tctctgtctt	86880
cttctgtcatc	ttctccttcc	ccatcgccag	caaggactgc	atccccctgt	cggagctggc	86940
tgtcatcacc	ggcttcttta	ccgtgaccag	ctacctgagc	ctgagcacc	atgcagagcc	87000
ctacacgcgc	agggccctgg	ccaccgaggt	caccgcgggc	ctgctatcgc	tgtgcctctc	87060
catgcccttg	aattggccct	acctgaaggt	ccttggccag	accttcatca	ccgtgcctgt	87120
cggccacctg	gtcgtcctca	acgtcagcgt	cccgtgcctg	ctctatgtct	acctgtctta	87180
tctcttcttc	cgcatggcac	agctgaggaa	tttcaagggc	acctactgct	accttgtgcc	87240
ctacctgggtg	tgcttcatgt	gggtgtgagct	ctccgtgggc	atcctgctgg	agtcacccgg	87300
cctggggctg	ctccgcgcct	ccatcggtca	ctctctcttc	ctctttgccc	tccccctct	87360
gggtggcggg	ctggccctgg	tgggcgtgct	gcagttcgcc	cgggtggttca	cgtctctgga	87420
gctcaccaag	atcgcagtca	ccgtggcggt	ctgtagtgtg	cccctgctgt	tgcgctgggtg	87480
gaccaaggcc	agcttctctg	tgggtgggat	gggtgaagtcc	ctgacgcgga	gctccatggt	87540
caagctcatc	ctgggtgtgg	tcacggccat	cgtgctgttc	tgtgtgttct	atgtgtaccg	87600
ctcagagggc	atgaaggtct	acaactccac	actgacctgg	cagcagtatg	gtgcgctgtg	87660
cgggccacgc	gcctggaagg	agaccaacat	ggcgcgcacc	cagatcctct	gcagccacct	87720
ggagggccac	aggggtcacgt	ggaccggccg	cttcaagtac	gtccgcgtga	ctgacatcga	87780
caacagcgcc	gagtcctgcca	tcaacatgct	cccgttcttc	atcggcgact	ggatgcgctg	87840
cctctacggc	gaggcctacc	ctgcctgcag	ccctggcaac	acctccacgg	ccgaggagga	87900
gctctgtcgc	cttaagctgc	tggccaagca	ccctgccac	atcaagaagt	tcgaccgcta	87960
caagtttgag	attaccgtgg	gcatgccatt	cagcagcggc	gctgacggct	cgcgcagccg	88020
cgaggaggac	gacgtcacca	aggacatcgt	gctgcggggc	agcagcgagt	tcaagagcgt	88080
gctgctcagc	ctgcgccagg	gcagcctcat	cgagttcagc	accatcctgg	agggccgcct	88140
gggcagcaag	tggcctgtct	tcgagctcaa	ggccatcagc	tgcctcaact	gcattggccca	88200
gctctcaccc	accagggcgc	acgtgaagat	cgagcacgac	tggcgcagca	ccgtgcatgg	88260
cgcgctgaag	ttcgccttcg	acttcttttt	cttcccatte	ctgtcggcgg	cctgaggatg	88320
gtccgccacg	aggagcttcc	agtgcattgt	gccatgaggg	ctttccccag	tgtggcccca	88380
gcccgcagcc	catgcaccag	tgcgcctgtg	gcccacgtgt	gcagactgtg	gctgcagaga	88440
ccttgcgacc	atgtgtagat	tgcgtggacc	ccgacaaagg	gaaggctgct	gtgtagctct	88500
gtccactctg	aataccaagt	gtgttgggaa	ttgtcatgcca	tctccaccct	gagcctgacc	88560
tttctgagtg	acatgggtgt	gccaggctag	actaggaggt	tccggtgtct	ggaaaaagcac	88620
tttacagatg	agattccctc	tcctcccca	ccttcaagca	ccctgttccc	tctttctttc	88680

ttttgtgttg	gatttggtta	aaaacccaat	aagcatctgt	gtaacctcca	cagtagcatt	88740
tcttatttgt	ttggctactg	ctacacctta	gcagctcttc	ccctttcctg	ggggatgtgc	88800
acggcagctt	gagcctgtca	cgtgggtcaag	gccccggccc	atcagaggct	gggggaggcg	88860
gcacattggc	agtgtgtcac	actgagctgg	gcaccacagg	ctgcctcatg	accctcctgt	88920
ccagcaggta	gtgggtgaat	gtgtgaagggt	cttgccctgaa	tccatcagga	cttgggaaac	88980
agagaaccct	gtgggggccc	ctgtggggga	ggctccctgcc	agtgtttaga	agagcctgac	89040
tgtgttcagt	gccttggagc	agaaaagccag	ggctcctgagt	ggctgaaata	aaagcctctg	89100
gtggaacctg	cagcgctttc	cttcctttct	ttaccgaaaa	gaagtctttc	ttgtacgtgc	89160
gtgagaatca	gcagagcctg	cactcctggt	gaatgaaatg	caagtgcaat	ttgagttata	89220
aaagagcaag	gttgatgttt	cacagttgat	ggcttcctgc	cacagcgaga	ccctggccttc	89280
atctccagct	ggaggggccc	ctggggcatc	tgccgtaact	gtggggtggc	ctggggcatgg	89340
gctgcctgtg	cagagagacc	tgtgtctgaag	gtgaccatgg	agtgtcagcc	cagccatctt	89400
cagatcttac	tgagcggaaa	gtgcacggtc	ataattatct	ttgaattcca	gttaccatg	89460
aagtggagcc	tacagggtga	ttgatggcgt	gggggctgct	gtccatgcgg	gagtgtgttg	89520
tgaaccacc	tcctgtgttc	cctaacctgc	agtgatgacc	ccatgggatt	ataatcagaa	89580
cttagtcatt	tgggggcacc	cgagcagctg	caggcccttc	agcaaacctc	acccctcttg	89640
ggcagcctgt	ctgtcccagc	cccttgggtc	tttgggtgtct	tccctgaggt	tgaggacgtg	89700
gcctgtacct	gctcctgtcc	cccgtagget	gggctgctct	ctgctgggca	ccaggcctca	89760
cctctttgtc	gtgggtggga	agcgtcgagt	ggctcacacga	tctggcttgg	ccacctgggtg	89820
ttgccattgca	ggatgtgggt	gctccatttt	ccttgacaga	cactgggtgg	tggcagctac	89880
accgcagact	gtcctctcat	cctggtttgt	cctgcctgga	ggggctgcgt	gaaaccacac	89940
gagaggctca	ggtggtgtca	tcactccgag	ccacgggtgg	tggaagctgc	acccccacac	90000
tgtcctctgc	gtgaaaccac	acgagaggct	caggagggtgt	catcactccg	agccacatgc	90060
tcgcccctgg	gtttctttcc	caggcaatga	gatgagggtg	gggttcagcc	tcatcttctc	90120
tccccattct	gtggatttgt	gaagccatgg	aaggccctcg	ccctgtgact	ctgccccag	90180
gatccccact	gactgcagag	gagggaaagt	gcctgatgct	ttccaagtga	acaaagatga	90240
caacacagca	tctccctcac	aacccttggga	tgaggaagat	gctccaacat	ccccatcta	90300
cagaagacgg	caccgaggtt	cagagtggag	gccatagcac	attagcacgt	tatcacatgg	90360
cacatagcag	agcaggaagg	acagagctct	gcctgtcccc	ttccccctggg	ccaccacact	90420
gccactcagc	atccacaatt	agtttctaac	caaccggcag	aggcacaggt	tgaggagaga	90480
gtgggtgctgt	cttttgggca	gagtcagaaa	tgggctgggt	cccgggttcc	actcattctg	90540
ccacaaaccc	ctgtgccacc	cggcaccatt	taacacctgt	ccccaggcct	cagtgtccca	90600
atctgtaaaa	cggaaagcct	gggctaagtt	agtgggtttc	aaaacttctt	agcaacaccg	90660
tttttgtttg	tttgtttgtt	tgaaataggg	tctcactttg	tcaccagggc	tggagtgtag	90720
tgtatctctg	gctcactgca	gcctccacat	ttgttctggg	ttttacagag	aggctccccg	90780
ggccccgcgg	accaccccac	ccaggaaaaga	acctgcccgt	tgcaggaaaca	gccattatatt	90840
aacaccccg	ccgggccacc	tgtcttggtc	tgcccccttca	ccgtatggag	ctgtaggaca	90900
cccagggagg	gaccgggggc	agggtctcac	tttgcttcta	cgaagtagta	gcatttgaga	90960
gaatgagtca	ggaaagaccg	aattgggtgg	tgccattcta	agtgccaaaga	gaggggtttgg	91020
cgccagagtt	tccaagccct	ctggaagccc	agctccctag	gggcattctt	tcaggggggc	91080
ttcactgtcc	attcttgggt	agcgaagcca	tcagaaagac	ctctctgcct	cctttgggaca	91140
tgtgtttaa	gaccagtcac	tcaaagctca	atcattcaag	tgctctcttc	cttttttttg	91200
atcctacatc	atgcaagtac	actcccaagt	gaggtgacaa	aaacgcacat	ttctgcagat	91260
gcccattgaac	caggacctgt	ctctcaagtc	tgccacctga	ggacagaatc	ctgtaaccac	91320
cccagctccc	aatcagcagg	atggggtgtc	agggctatta	aacaaacagc	cacgtggccc	91380
aacacgtctc	atccggcagc	tcggggaaaag	cacactttga	cagccaggac	cctatccgat	91440
aatgggtgct	tcctcttcat	gacaaagaaa	atgaacactc	attcactcaa	aatattcagc	91500
acctgctgtg	tgttctactc	ttcctggcac	aggggatgca	gaatgaacag	agagcccctg	91560
cccactggg	aggggtgttt	gtggggagat	ggaccaggta	ccagtcagtg	aatatgacac	91620
aatggcaggt	agagaaaagt	gctacagtca	tctaccgtga	gcgctgtgat	gctctgcccc	91680
gtttcaccac	attaatggag	caccacttat	atgctggaca	cataccatgc	attttctcat	91740
cctagcggct	gttgcaaaat	agacacgtcc	attgtgaaga	ctgcggggcg	tagaatcgca	91800
gccccaaaag	gtgtccaggt	cctaattcccc	aaatcctgtt	tgtgtgttcc	cttgcattggc	91860
aggagggatg	ttgcagatgg	gattcagtta	aagatcttga	taccggggag	atgattctgg	91920
actttcctat	ccagaagggc	ccaaagtaat	ttcaagtgtc	cttgtaagag	ggaggctgga	91980
gggtcaggg	gtgagattgg	aagatgccac	cctgcaagct	tcaagatggg	ggaagggggc	92040
atgagccaag	gaatgtgggt	gtctctcacg	ctggaaaagg	tgaggagatg	gttctcgcct	92100
gcagcctcca	gagagacaca	gctgacagag	tcagactggg	ccactgacag	ggctctagcg	92160
tcccagatc	ccatgcccc	acccctctgc	atggctcctg	agccctctc	tgagggtgtct	92220
cctggaaaac	ctttgggctc	ctgctccctg	cctgttatcc	ctgaatgttg	ctgccttttt	92280
cagcttgtct	gtccctctct	gaggctcatg	ctgtcatctg	cgtggggccc	ccgcgtaatt	92340
ctaacagcac	ccaggtaaa	ataaagggtc	tttgttgttt	ttctaaaaag	gacttcgctg	92400
ttgcttgagt	cactcataac	ttgatcaatt	atttggagct	ctaaaagctt	cccagttgct	92460



aggaaaccac	accttgagg	ctggcaaacc	attgttaaag	ttgttcctaa	agtgtgaac	92520
ttctacagt	actttggaaa	gtagcttggg	gaacaaaaca	aagcaaaaca	aacagaaaag	92580
actcgggttc	ccttttcttt	ccgtccagaa	gtgatcaaat	cagctaaact	cactgtttca	92640
agctttcctc	taactagatg	tgtttttttc	tgccgttagc	cagaaaggcc	ccttccttcc	92700
tatttttagtc	acagaataac	ctgtctcttt	aggacagtgg	ggtcctgtgc	tgaatccac	92760
cccaaagat	gggaagaact	cgggtgctgc	gttttgggaa	gccccggctg	agatgagtgt	92820
ataactgggg	ctgagagccg	agagcctggc	ccagcaagcc	aggcagttag	gtgacccggt	92880
atcccgtctc	ccatttctgc	tggagctgga	agagcccaa	ggacaccagc	cccatcagag	92940
ggagctgggc	ccagagctgg	gtggggcagc	cgactactcc	ctgcagaaca	cctaccgcct	93000
gcctgacact	ggtggctgct	ttgtggacat	gcttttgaaa	acctcgtgag	ggtgatgtta	93060
ttgtccccac	tttatccagg	ggtacctggg	cacggagcag	ggcggttaact	caccttggat	93120
gtctgtggca	gcctccaaga	tggttcccagc	aatccccacc	accttcctgc	tgctccttcc	93180
atgtagcagg	ataggtctgt	gcgaccagta	gaatatggca	gatgtgacga	gatgtcactt	93240
ctgaggtttg	cttacaaaag	gctgtggctt	tcagtttggc	tgctctctct	cggatccatc	93300
actctgggtg	aggaagccat	gccgcgagca	gccccgtggg	gaagcctgca	cctcaaggac	93360
ctggagcctc	aagccaactg	ccacatggtg	cacttggaaa	cagggatggc	tgccacggcc	93420
cacactcgcc	tgcggtctcg	gggagacacc	cagccagaac	ctcctggtga	atccactcct	93480
ggattcccta	ccccacaga	gtataagatg	acgaatgtgg	ctttaggctg	ttaaattcgg	93540
gataaccgat	acagtgccaa	cactggtaag	tgacgaggct	gcaatgaatc	ccaggatatcc	93600
tgtggctgca	tctccacctg	catgggccat	cctgtacctg	gcaggcccca	tccttagcct	93660
ctttaaaagt	ccaggaacct	tggaaatgtt	ttctgacatc	tcctaggctg	ctggatttac	93720
caggaaaagg	gacggacceca	caccttttcc	ctggttgaat	ccattgcatt	tcttccaggt	93780
gtttcaatcc	cttctgactc	gatttgcctt	aatgaagctt	gaggcaagtg	caattttctg	93840
cccattgggg	tgtaacactg	ttcaaagtca	tcctggagct	aagctaagtg	gaaaaaacca	93900
tatggcattg	tcgccttctc	agcctgacct	ggcattgcact	ctcaccctca	tctgtcatgc	93960
ctcctgcttt	tccacctggg	gggctgagaa	gtccggccat	cgaaaccttg	gttcctgcca	94020
gccacgggag	tttggaaact	ttatcagatt	cctgaagcct	cgtttctcct	tgggaaacagt	94080
gcagggtgaa	gcaccttctc	ctcggaaacc	gggggaagat	gagaggaaat	taaatagatg	94140
tatggccccg	cagcaggact	ggcgctctcc	attgtgtctg	aaattggcag	gttcttgggtc	94200
tcacttactt	caagaatgaa	accacggacc	ctcgcggtga	ctgttacagt	tcttaaaggc	94260
ggcgtgtctg	gagtttgctc	cttctgatat	tcagatgtgt	tcgcggtttt	cctccttctg	94320
gtgggttctc	cctctcgctg	gttcaggagt	gaagctgcag	accttcacgg	cgagtgtcac	94380
agctcataaa	cgcagtacag	accaaagag	tgagcagcaa	ttagatctat	cacaaagaac	94440
aaaagaacaa	agcctccaca	ccacagaaga	caaccgagg	gtgtcaacat	tactggctcc	94500
agcagcctgc	ttttattccc	ttatctggcc	ccaccacat	cttgcctgatt	ggtccatttt	94560
gcagagagct	gattggctctg	ttttacagag	agctgattgg	tcctgttttg	agggtgctga	94620
ttggtgcgtt	tacaatccct	gagctagaca	caaaagttct	ccaagtcccc	actagattag	94680
ctagacacag	agcactgatt	ggtgccttta	caaaccttga	gccagacaca	gagtgtgat	94740
tgggtgattt	acagtccctt	agctagacac	aaaggttctc	caaatcccca	ctagactcag	94800
gagcccagct	ggcttcacct	agtggatccc	ccaaccgggc	tgacgggtga	gctgcccgc	94860
agtcccgcgc	cctgcgccct	cactcctcag	cccttggggc	gtcgatggga	cccggcgtgc	94920
cgcggagcag	ggggcggcgc	ttgtcgggga	ggctggggcc	cgacggagcc	cacggccagg	94980
gggaggtctg	ggcatggtgg	gctgcaggtc	cccagccctg	ccctacgggg	aggcagctga	95040
cgcccggcga	gaattcgagc	gcagtgcctg	cactgtggg	ggacccggcg	aacctccac	95100
agctgctggc	cggggtgcta	agccctcac	cgcccggtgc	gggcggcgcc	gaccggcttt	95160
tccgagagcg	aggccagctg	agccccgcc	caccgggaac	tctcgctggc	ccgcaagcgc	95220
agcgcgcagc	ccggttccc	cccgccctc	tcctgcaca	cctccccaca	agccgagggga	95280
tccggctccg	gcctcggcca	gccagaggg	atccggctcc	ggcctcggcc	agcccagaga	95340
gggggctccc	acggtgcagc	ggcgggctga	agggccctg	aagcgcggcc	agagggggcg	95400
ccgagagcga	gcggggctgc	cagtacgctg	tcacctctca	ccatcactgc	ccttgcttgc	95460
tctacggctg	ctcagaccca	aggggcaagt	ttctccaggt	atttccaaac	cagggagggc	95520
tttgtgttta	gtttaagtca	aggaggtgt	cccctttctg	aggctgtttg	gatttctttc	95580
agcaaaaact	agcagaagtt	attacgcagg	aactttttgt	agcatataaa	gaatgaatcc	95640
cgatagggtac	tgtgatggtt	accgttaggt	gtcaacttga	ttggattgag	agatgcctag	95700
aaagctagt	aagcattggt	tctgggtgtg	tctgtggggg	tgttgccaga	ggagactgaa	95760
atttgagtca	gtggactggg	agaggaagac	ctctcctcca	tgtgggtggg	caccatccaa	95820
tccgctgcca	gcgcgcctcc	aactaagcag	gcagaagaag	gtgggagaag	ctggcttgc	95880
gagtcttcca	ccttcactct	cctcacatgc	tggatgcttc	cttccactcc	tcctgccctt	95940
ggacatcaga	ctacaggttc	ttcggccttt	ggactctggg	acttacacca	gtggtttgcc	96000
gaaatctgtg	ctttctgcca	cagattgaag	gctgcactct	tggcttccct	acttttgagg	96060
cttttggact	cgggctgagc	cactactggc	ttccttcttc	cctagcttgc	agacagccta	96120
tcaggaaact	ttgctttgtg	atcatgtgag	tcaattctcc	ctgataaacc	ccctttcata	96180
gacacataga	tcctataact	tctgtcactc	cggagaacc	taatatagtt	accaatagaa	96240

accttacaac	tttccctaga	ttctgcaggc	tgggtggagt	tcaccaccct	ttgctttgag	96300
gtatcagtgg	aggaagaaca	gaggcactgg	ggtcaggaca	gaatggggcc	agaccccagc	96360
tccagaacct	atgaccgcat	aggtttgaga	gacctgcgtt	ccagcctggc	ctctgccttt	96420
actgtgtggc	cctgggcagg	ttccctaacc	tctgaagctc	aagttcctta	cctctagaac	96480
aggagcaata	ataggacctg	cctcatgggt	ttatgtagaa	tacgatagag	tgcaaagtgt	96540
gcgacacaag	gcccagcaca	cagtaggtgt	caatcagtgg	tcacacttgt	cactatccta	96600
taggatgggc	cttgggcaca	cctcctaact	ttccagcct	cagttggctc	ctctgtgaga	96660
tcaggattat	aaagatctgc	ttttcagggt	ggctatgatt	tgttgagaaa	tgaagtatct	96720
atcacaccat	catttacaca	atcattcatt	catggagcca	ttcattcctt	caatcattta	96780
ttcaatcatt	catgaattta	tggatttagt	ccatcatcca	ttcattctcc	agttctcaag	96840
gctcctgtgc	tgggcatggg	caagacacgc	tcccttccaa	tgggcagata	ggtaagcggg	96900
ggcctgagga	agtgcaggga	ctgtcatcag	caaaccctgc	tccagagtgg	agacagagca	96960
gagcatgttc	caccagga	ccccttgggt	tggaggcatc	tccatctcct	gccagcccag	97020
ctcaggttct	gccagtccct	gaacccttct	cacactctcc	accccaccca	tcaggagtca	97080
tatggcaggg	ctgtcgaggc	gtgtgaacca	gagcaactcc	atcttgaata	ggagatgggt	97140
aaaatgaggg	tgaaacctac	tgggctgcat	tcccagacag	ttaaggcatc	taagttacag	97200
ggtgagatag	gaggttgaca	caaaatacaa	gccatacaga	ccttgctgat	aaaacagttt	97260
gcagtaaaga	agccggccaa	aatccaccaa	aaccaagatg	gccatgagag	tgacctctgg	97320
tcgtctttgc	tggcacactc	ccaccaccgc	catgacagtt	tacaaatgcc	atggcaatgt	97380
caggaagtta	ccctatatgg	tctagaaagg	ggaggcatga	ataatccgcc	ccttgtttag	97440
catatcatca	gaaataacca	taaaaatggg	caaccagcag	ccctcgggct	gctctgtcca	97500
tggagtagcc	attcttgtat	tcctttactt	tcctaataaa	cttgctttca	cttttctcca	97560
tggacttgcc	ctgaattctt	tcttccacga	gatccaagag	ccctctcttg	gggtctggat	97620
tgggacccct	ttccggcaac	atctttgctt	cctttctctt	taaattaaat	taaatgctca	97680
tggtttttaa	agccccctac	cctttgctct	cacccccagt	tgccatgcct	cagaggaacg	97740
gcctccaccc	ctttcagctg	tttcttctgc	taattacctt	catgttttgg	aataacatgt	97800
tcaaatgcta	tttctgattt	tccagtttga	gataatatgt	gtagacacca	tgaagaaaaa	97860
atcgtctctc	atatggcccc	tctggcctcc	ttcaacgaga	ctttaatgga	caagccacct	97920
tcccagtatc	accatctcac	tgggtcctgt	taaatcagtg	tccatcattt	ctgtgctgtg	97980
taaataggat	tactgctgg	gccacggaag	gcactatgat	tatgtttctt	tctttttttt	98040
tttttttgga	gactgagtct	cactctgtca	cccaggctgg	agtgcagtag	catgatctca	98100
gctcactgca	acctccgcct	cccgggttca	agcgattctc	ctacctggc	cttccaagta	98160
gctgggatta	caggcacaca	ccaccacaga	gacagggttt	catcacgtta	gccagtctgg	98220
tcacaaactc	ctgacctctg	gtgatccacc	cgcttggcc	tcccaaagtg	ctgggattac	98280
aggcgtgagc	cactgcggcc	ggcttatgat	tactttttgt	ttatgctgtg	cctaataatt	98340
atctagtttt	ttgtttgtct	agttttctcc	acattgacca	ctaattcatt	tgtgaaaaat	98400
agaaaatttt	tctcaatgtg	ttaaaactat	cagataagct	ctcaatttct	gcttccccag	98460
ccccgtagat	tgtttgttgg	gaacttccca	tcttctgtg	tcaatctgga	ctgttcactc	98520
tctaggccca	ccaccagct	gtcacctgg	ggactccctc	actgtcaccc	gggtgttctt	98580
tttgtgtctc	tcctccgtgg	tatccctgtt	tctgggatcc	cagatggatt	aactgggaaa	98640
caggctaggg	tgctataaca	aagagacccc	ccaatacaga	agtttatgca	aaccagaatt	98700
gtattttctc	ctcaggtcac	catctgagta	ggtaggctag	gctagtgtgc	tggctccagg	98760
caggtttctt	ctctctgtgc	gctctctctc	ttttgaccca	cattttctat	cttgagatct	98820
aaactagttg	ctccaggtcc	tgaaccacc	tttacaaaat	tataactgag	gaaattatga	98880
cagtgaaaaa	aatcagacct	aaccgactcc	atcttctctc	taaccttta	gctgtccttg	98940
ttcatttctg	gacataggcc	aaactaactt	tggaaaggaa	ttcagttcat	ggtttgactg	99000
aaacaaaatt	gataacagcc	ctttcccaaa	aaagcccccc	ttcttgccca	gggtccagtc	99060
tgcccttgca	ggactaacia	attagctaca	agattagaaa	tcacagttta	gaggtcatgc	99120
agcctctggc	tctaagagtc	tgaacctcgg	catattgtct	ctggggataa	catcattatt	99180
gtaaaacctc	agatcagtgc	ttgagatatt	ttgcaggccc	tgtgctcgat	ggattagcca	99240
acaccaccca	gaccagtaat	ctggctcaac	cagttctacc	attgcaccta	ggaagagaag	99300
acattaagaa	aacctcactt	caaccactta	tgattccatc	tccaacctga	ccaatcagca	99360
ctctccactt	cccaagcccc	taccacccaa	attgtcttca	aaaactgtga	tcccggccgg	99420
gcgcagtaac	tcacgcctgt	aatcccagca	ccttggggagg	ccaagatgag	cagatcactt	99480
gaggtcatga	gtttgagacc	agcctggcca	atgcagtga	accccatctc	tactaaaaat	99540
acaaaaatta	gcgggtcatg	gttgtgggtg	cctgtaatcc	cagctactcg	ggaggctgaa	99600
gcaggaagaa	cgcccgaacc	caggaggtgg	aggtctcagt	gagccaagat	cgtgccactg	99660
cactccagcc	tgggcgacag	agtgcagctc	tgcttccaaa	ttaatttaatt	aataaagtta	99720
taattgaaat	taacactctg	atccccgaat	gcttggggag	actgatttga	gtaataataa	99780
aactccagcc	tccctcacag	ccagctctgc	ataaattacc	ttctccattg	cagttccctt	99840
gtcttgataa	atcggctctg	tccaggcagt	gggcaagggtg	aaccactgg	gtgggttacac	99900
tttcagcact	gtgtctacag	tctggccagc	ctttaggatg	ggagggcagg	tgaagacag	99960
gcttctcccc	tcttacagta	gtgcctggag	cagatcactt	ccattgtcct	cgctgttggc	100020



```

cccacctggc tctgggggac aatcctgtgt ccagataaca actccaatgc gacgtacgaa 100080
gggaaggtca gatgtcaggg acaaccagga gtccctgcct catgtgtttc cttctttcct 100140
ggtttcgtgt tagtggcgca caccctccag caacttcctg agaaattgcc tttatgtgaa 100200
cgggagccag tctgaaaact tccaacata ggtccatacc tttgggtcat ctccctcac 100260
ggtgacctgg gcttgctcct gtgacttggt ttggcccatg agacgacagg aaatatgaca 100320
caagcagaga cttgagaggg aggtgtgcct tggggccttat cttactgaca ctgggggctc 100380
cagtgtcaga gacattggaa ccagagtga cccatcttga ataggggctg ggtaaaatga 100440
ggctgagacc tgctgggcta tattcccagg aggttaggca ttcttagtca acaggagatt 100500
cagatgtgg gaacaagtga acgatgttta ccaaacagac cccggactta acagatccag 100560
gagatgtcct gatgtccga cacttaaga acaaagcat tcttagttca aaaataagtt 100620
tggtggctgg gcgtgggtgg tcacacctgt aatcccagca ctttgggagg ctgaggtggg 100680
cagatcacct gaggtcaggg gttcaagacc agcctagcca acatggtgaa atgcatctct 100740
attaaaaata caaaaaata gcaaggtatg gtggctggca cctgtaatcc cagctacttg 100800
ggaggctgag gcaggagaag tgctgaacc tgggaggcgg aggttgcagt gagtggagat 100860
cgcaccattg cactccagca ctccagcctg ggcgacagag caagactccg tctaaaaaaa 100920
aaaaaaaaaa aaaaaggttt tgctttaaag attcttgtag aagacagtag ttgcacaaag 100980
atgaacaatc cttagtacc agccctagta gcagagcaca cctccccag gattttgtgc 101040
ctttgtctta tatatgaaca agcactgtac ctaaggcaca tgtgttcctc atcttgctct 101100
tggaacacc gtacgtgcc tatggagtag caattccttc ttgcctttac tgtcttaata 101160
aacttgcttt cactttactc tgtggactcg tccgaattc tttcttgctg aagaaccaa 101220
aaccctctct tgagtctgga ttgagaccgg gatctggtta caactggggc gatcacagg 101280
ctggcctggg agagccgct gggtgagaga gatgcctgct gatggcatct gtgttgcct 101340
gagccaacca gcaaacctgt gagtgaggcc gttctaaaac attcatcctc agctctgcct 101400
cccagcccac acacggaatt gtaagaaata gtcaatgttt ttactctttt tttttaaga 101460
cactaaattc tggggtgttt cattacacac caaaagctaa ttggtacaaa acctgcatg 101520
ggtaaaaagc cttcatttcc ctctcacgtg taatcaatag tttgaagggg catagccagc 101580
attcgaggtc caagaatttc ttcttagagt ttgaaagcag cgctcccttc ccttattgct 101640
gctgggaagc ctgaagacat attctgattc tcctaageta tegtttacag tgttctcagt 101700
ctccctgagt tctgacctc aaagggatgg cctgggaagt gggtaggctt tccaccattg 101760
cgccgggcac tgtagtttct tttcatctgc aaagtttgat tcttcaggtc agaacattt 101820
tgaatatatt atttctcca ttttcttctg tgaactcctc atatctgtgt ctgaggcct 101880
ctttgaggag gttagctttg tttgtttgtt tattatttta tttatttatt tattttgaga 101940
tggaagtctc ctctgtcacc caggctggag tgcagtggca tgatctctgc tctactaag 102000
ctctgccttc cgggttcaag ctattctcct gcctcagcct cccgagtagc tgggattaca 102060
ggcacgtgcc accacgccc gctaattttt gtatttttag tagagacggg tttcaccatg 102120
ttggccagct tgggtctcaa ctctgacct caagtgatca gcctgccttg gcctcccaa 102180
gtgctgggat taacaggtgt gagccaccac gccagccga ggttatctct tttctcacc 102240
tattttcttt gggattctct ttgatatttt ttgttctact tcctgagaaa tttcctcaac 102300
cgtactcttc aatctttgca gagatcttta tttttgcaat catgcttcta atttccatg 102360
tttctttaga tctccacgt gtttcttgg ctatgttttc catattctct tatctctatg 102420
cagatatcca ttatccaggt tttgaaaacg gtattccacc tggcactgta gctaaaggtt 102480
gcagcttctt tctctctc tttgtttgtt tgcttgtttt tgtcttggtc tttccacag 102540
cagggtgtc cttgagtgtc tggcattctg ggctgtctgc ttctatctca gcagctgcct 102600
ggaatctctg tgtgcctgtg gcagagtggg gatgcgtgtc aaactgccag cttccagtt 102660
ggatgctttg gtggagcagt accttttttt tttttttttt tttgagatgg agtctcactg 102720
tcgccaggc tggagtgcag tgggtgtaac ttggctcact gcaactcca cctcccatgt 102780
tcaagccatt ctctccctc tcagcctccc gagtagctat gattctaggt gcatgccacc 102840
atgcctggat aatttttgtg ttttttagcaa cgacagggtt tcgcctgtt ggccaggctg 102900
gtctcaact cctgaccact ggtaatccgc ccgcttgggt ctcccaaagt gctgggatta 102960
caggggtaag ccaccgtgtc tggccgatgg agcagtatct cgagggacct ccaagtgtcc 103020
aaacctaggt ctttctctc cagctggcca gtttccaggt gagggggcct ttaaccttcc 103080
ccggggtgtg ggtgggttg gtgtgacctg ttctcagttg gctgcctgcc gccaggctct 103140
cctggggctc cggctcccg gcctctctgc acaatccctg gggaatgaac ctccgcctt 103200
ctgcagggtc gggagaggga tgcttgctga ggaagacatt cagaaaacct caattttctc 103260
cccacctca gaggtccctg gtgcctccag gccagagcc tttctgggg tctatgatgc 103320
aaaccagttg ccttgtggtt gccccaccg cgggcttggg ctctgctctc tcagtctcta 103380
agctgtttcc actccccat gtgccttctt gcttcccatc ttcaaggcca cggctcagct 103440
ccggttctct ttgttttgat cccttctttg actctcgagc ctgtgggagc gagggtgttt 103500
gatctgcagt gttgagcagg gttctctggg ctctgcagg ggaccagtg ttgagcccac 103560
atacactcg ctcagtaagt agtccttaag gactgtgcag ggcaccagg acacggtggt 103620
gagtgaatga tggctccctg tctcacatct gtgtccgtgc cagtgccagg gggcctggg 103680
tgtggggaaa ggaggaatcg aggcgctcag ctcaggaggc ttttcaggag caaagggtgc 103740
acagttggtt tcaggcaggg aaagggtgtg gcagcggctg ggaaaacaca caccagaatg 103800

```

tcaccttccg	aggcctgagg	ccccaccagg	tagccagaag	gtccaggata	cagtttagta	103860
attaagacct	tggggctctg	cggacacgct	gcctgggggtc	agaccctggc	cccaacactc	103920
acagtttgtg	gccatgaggg	actcaccac	ctcttcacgc	ttcagtttcc	ttatttataa	103980
aatgcgcgga	aaaatcacag	aatcctcttg	atcaggtggc	tgtgtggatg	gatgagatga	104040
tgtgtacaca	gccctccgta	tagagcctgg	tgtgtcctct	gtgaatacta	ggaatgacat	104100
ggagggcagg	tcagggagga	agccagggtca	cccaggcttc	ccccaccccc	cgccaagcca	104160
atccctggac	ctagcccagt	gggtggaggt	caggtcgggc	aggagggtag	gtcaccagg	104220
ggcgccccc	ccaagccaag	ccccggacct	agcccagtgg	gtgtcaggaa	cgtcaggacc	104280
cgctctccgg	agatgagctc	cggagagatc	cagggaggga	aagcattgag	catcatctct	104340
cccagccctc	tcaaggccat	ctctgcctgc	cacagctctg	agcgcagggc	ctggtgtgga	104400
gtgggggccc	atccatgtgt	gcagaccccc	ctggagcagg	ccaagctgtc	cctggccagg	104460
ggccagctcc	ccaccactcc	acagggtcca	gccctcacac	gcctggccct	ctagaagccc	104520
tgctcactac	ctctgccacc	atctggctgc	ccctctgtcc	tctgcagccc	cataaaccac	104580
caccagaaac	tccccaggaa	agagccctac	ccttgccctg	ctcaagaaag	gcaacgtggt	104640
gccaccaggg	ctacaggccc	cgttttgctg	cttccctgcg	tgctgtggac	ctcccaaggg	104700
cccttgccctg	tgagcaggga	aaatccctac	ctaaaggggt	ggctttgtca	ccaggacgaa	104760
gtgcccaggg	atatgggggtc	cctggcgctg	ccatgacaaa	tgactgcaaa	ctgagaggct	104820
taaaagagca	tatttattat	cttcagctct	ggaggtcaga	ggtctgacac	aggcctcact	104880
gggctgaaac	caagggtgtg	gcagggtctg	ttccttcggg	aagggtccag	gaggctctgt	104940
ttccttgccct	tttccagctt	ctagaagctg	cctgtgttcc	taggctgggtg	gccccctcct	105000
ccatcttcac	atccagcacc	gctggctcag	tcttcatgtc	atgccttgct	gagccttttt	105060
ctggtgctac	agctgtctcc	aatacaacca	ggaacgggtcc	tacactttca	cggacttggg	105120
tgattagatg	ggtcccat	ggataatcca	ggctaaattc	catcttcagg	tccatgacct	105180
taatcacatc	tgcaagatcc	cagagctggc	aattgggtcaa	tggtggctga	agtggggtt	105240
ggggaggctg	aggctgcagg	atccatcacc	accctggggc	tccgcacatg	cctgccactt	105300
ccacccctgg	ggtttgaatc	ctgacccctc	caottattaa	ttctactaac	ttgggtatca	105360
gttaaattac	ctcatctctc	taggcctcct	gttctccatg	tgtacaatgg	gtataacaat	105420
agcaaccccc	atgctctgca	gaaaggatag	actgcagcca	caatgagaca	tcccttccct	105480
gtagggggccg	ggtgacctcc	agcacagcag	gactgcgggg	ttcagtcgag	tcaccccaca	105540
gtactgagga	ggagcggcat	gccctccac	tatgtacaca	cacagtcaga	gaggtttagtg	105600
agtggccagt	gacgcacatc	caggaagtgg	ccacctcctc	cctgtgctct	gtcctggagc	105660
tgtggaactg	agcgccaatg	aagccctgc	cagcagaccc	gcagaatagc	acctgccttc	105720
ctcctgctga	acctgaagcc	cagaattccc	tctgaaagc	cagaggcagg	gcctggctcc	105780
aggcaggggtg	cagggaaacc	caggcgtgcg	tgggacactt	accacacac	tctcctgttt	105840
agctcagcca	ttgtggcagg	tggggcgggg	cctctctggc	ttcctgaaga	atccaggtag	105900
cctgtggttt	ctctcccccg	caggcttcca	ttctctggga	ccctcaggca	cgtctgtggg	105960
ggagcactgg	atgaggagtt	atgtgtacc	tgtgtgattg	cgagctaatt	ctttaacctc	106020
tctgaatcag	tttctcatc	tgtatcatat	tctcatggag	agtgtgagtg	tgtgtggaga	106080
tcatgatggg	ctatgcacac	ctgctgccag	acaaaacaag	acaactatca	ttacggagtg	106140
tcatgtgcca	agcactgtgt	tttgactat	ccaagttaat	cttgtccttc	ctctcccacc	106200
acaaacctac	aagataggtc	gtcttattag	ctccatttcc	tcagtgatga	attcagagct	106260
agggaaagt	aagagctgca	ttaggagcta	gagggagcaa	acccttgacg	tgaacccagc	106320
ttcccagtg	aaagcccatg	ggcatcccca	cccactgtat	tgctcctga	tgggtccac	106380
ctccatgagg	ttggactcac	taaaaacaaa	cagcattctg	gacctcggtt	ttgatgtaac	106440
atgtgttatt	ttattggaaa	aagctggtat	taacatattt	atagttttat	tcaacaattg	106500
ggtaatttgt	gagacaccaa	agaaaaaag	aatgcacctc	tgagttacag	agtccaaact	106560
gatcagggtc	gacaacttga	ccaccatgta	tcccacacca	ccacccccac	caccaccacc	106620
accaacagct	tcgtcctcag	agaagagcta	aattaaaaac	aaaaccacaaa	aaaccccaac	106680
aacttcacaa	tgactatgtg	aacgcccgtc	cattcgagag	taccaggaaa	tgtaagcaga	106740
gccaggatgc	aagtctgtga	ctattacact	ggctcctcca	cggtttctgg	ttttgtccct	106800
cccctcgaca	ccttttctta	acacacattt	gatcttcaca	atgtgtcttg	gacatcatta	106860
ttttccaggg	atccagagac	atacttttct	tcaaagaaga	tcttttctct	tcttttttct	106920
tctttttggt	ttggtaccca	aagtttaaaa	cagaagtaag	gaactaggaa	ctgtattaag	106980
acctcctttt	gaaggacatg	taagatttgt	actttgaaga	tggtaaatgt	taaatctatg	107040
atgtgacagt	aacctctagc	tgcaaatata	agtttcttct	cttaacattt	gactcacaaa	107100
gggagatgga	tcgtagcaaa	tatccaagta	atgggtaagg	ccctcagagc	tgggttttgg	107160
ctttaacacg	ctatctatac	aattgaccac	attctcgaac	ctctttacaa	gggggaaaaa	107220
agtaatccaa	tcctttgatt	gttaaattta	attagaatag	ataatgacat	ataaactgtg	107280
ccagggtcaac	tggattttat	agtgatatat	aaacaaacat	tcttcattca	cgttgattaa	107340
aaaaaaatca	atgatccatt	tccctgtgta	aatgttatat	ggccagaagt	gagtcacacat	107400
gcactttgtg	cttttacaca	cacaaaagta	tactgtaatc	cactgagaat	aacctcagct	107460
gggtctgttt	cctgggttat	gttatatctt	gtaaaaaaca	aaacaaaaca	aaacacaaaa	107520
aaaagtttgg	atgttgctgg	gtctctgctc	cccactttct	gaatcaaaat	gccaaactac	107580

gtggctctgc	tgcaagtcca	tgagcaaaga	cgactcagag	gggtgggcag	gtttgggtatc	107640
accagaacag	gagcatctac	catggaaaca	ccaccttctc	tgtggccctc	attgtcagag	107700
gggcagagtt	cccaggggat	gtgtcctctg	ggactgtgtg	gtccttaaag	taaaggtatc	107760
ctaaaaaggt	cagaacatgc	aatttccttt	caaaaggcagt	tcagtgcatt	ggctcaagga	107820
gggtgcaagc	ccaggatgaa	gtggagtcct	ggggaggggc	acactcctga	agccaccaag	107880
cagagcgagg	agctccgggg	ggtcttctct	gtcttccatc	ctgctgtctc	gttctcctgg	107940
acccttgctg	tcgccaagtc	tgccatgtcc	tacttcacaa	gacagaggca	ttcctttcca	108000
aaccttccat	ttgaatgtcg	ctctaacatg	agccgcccac	gagatggact	ggagagaacc	108060
ttgtgtgaag	acccggacgg	gttcttgaca	ccactgcacg	gcacctgcca	tgggtgacct	108120
gtgcatccgc	tcagagcctc	agcttcttct	cgtggacaga	ggggatccta	agggttcccc	108180
cttatcccca	gcatccagcc	cagagcctgg	cacgcttcga	gaagttgggtg	tttatggagg	108240
aaatgaatga	acacccacct	cacagtcagg	aggaagattc	caaaaaatcg	tgcatgggag	108300
tcagtgtccg	ctccgggaag	gtgcccagtg	aatgtcgaag	ggtgaggcgg	cagggagggc	108360
tgcaagrggt	aagtcaactg	cctctagggc	tgagcaccac	gcctggtaca	cagcagaggc	108420
tcagcaaatg	gtcaggtgaat	cagatgagga	ccagggcaca	cagaagacaa	acccactccc	108480
gctcctctcg	ggaaaccgca	ccagacctgg	gacctgggat	gtttcaagac	attcagaaga	108540
cctaggagag	gagcttgcac	ctgcaaattc	tcagcatgaa	ttcaccatcc	aaaaaacaac	108600
ggtgaggtca	tcagctctga	gacagggcga	attgccccat	ttataaccaa	aagaacccct	108660
ggctggctcg	tttgagactc	atcatctgtc	cctggagccc	tgatctggga	ccagtgaggc	108720
atgggggaga	agcagctccc	atcagctccg	gtccctgcaa	caggacgcac	tggagtgaag	108780
aattaacccg	gacgcataaa	aagtcctatt	gatgtggtaa	agaccgcaga	ccgagacagg	108840
aaggagcgtg	aatgaaagaa	ccctgaactg	taagactcca	cagtcatgtc	cattttatga	108900
tttgtggcgg	tgaacgcttc	ctttcctttt	tattttttta	aacagacaat	tactgccaaa	108960
cacaattctg	gcctaggaaa	gctggggcag	ggaggggggc	caaacttctc	gtgtccacac	109020
actgccacct	ctgcagctgt	cctcatcagt	gctgtgactt	tcttcccttc	cttgcatatgc	109080
ggtcgtgaag	gtcatgtcgg	ggatgacttg	catgaggctg	ggtggcaggg	gccgggaact	109140
gcacatacct	agtgcacgtc	agagtttacc	ttgtcctgga	agatgtacag	gttgttgggtg	109200
gcggcgatgg	caatgatgtt	ctcagccggg	tgccaggccg	tgtgcaggat	cttcttgggtg	109260
aagtccaagc	tgtccacact	gatgtcatca	cgccggcgct	tgccccccac	gcacacgcgc	109320
cgtggcttga	gcacagcccg	gggcttgctg	ctttccctcg	aggcctccag	ggtcacgtcc	109380
cgcttggtgt	tccgatcgaa	catgcggaag	aagttgttgt	aggccccggg	catgatgacg	109440
ctggtgggag	aaggagaggc	atcaggtgag	gaggagcaca	agcccccttc	cgagaaataa	109500
gccaggtgtg	gggggctcac	gcccataatc	ccaggaactt	gggaggcccc	ggtgggagga	109560
ttgcttcagc	ctaggagttc	aagaccagcc	tggacaacat	agcgagactc	cacctctaca	109620
aaaaaaaaatt	aaaaatgacc	gtagtccag	ctattcagga	ggttgaggca	ggaggatcac	109680
ctgagcctgg	ggaggcagga	ggatcacctg	agcctgggga	ggcagagact	gcagtgagct	109740
gtgattttacc	actgcagtct	agcctgggtg	acagagtaaa	actctgtccc	aaaacaacaa	109800
acaaatgaaa	aagcaatccc	agagcctaca	gagccatcac	tccctggaaa	gggaaaccac	109860
acctgcctct	attcccctgt	atcttggggg	ctcttatacc	ccctcacatg	tcagctgcca	109920
ccaacatgca	gactttgggg	ccaggagcta	agatcccttt	tatcctctgc	cccaatcatc	109980
atgaaaatac	cctcctggcc	aggcgtgggtg	gctcacacct	gtaatcccag	cactttggga	110040
agccaaggcg	ggcagatcac	ctgagggttag	gagtttgaga	ccagcctggc	caacatgatg	110100
aaacctgtgc	tctactaaaa	atacaaaaaa	tagctggaca	tggtggtggg	caactgtaat	110160
cccagctact	caggaggctg	aggcaggaga	gttgcttgaa	tccaggaggc	aaggtgttag	110220
tgagccaaga	tcgcgccact	gcactccagc	ctgggcaata	agagcaaaac	tccgtctcga	110280
aaaaagaaaa	gaaaagaaaa	gaaaagaccc	tcctgtaatt	tctgttagtc	caggagagaa	110340
agctctggcc	ttccaaacag	actgtgcaac	cacagcagga	ggtagacatg	gaagcagctg	110400
ggacagaaaa	ccaccaggcc	ctgcttccct	ccaggggccc	gcctgtcccg	aggactcggg	110460
cgaataaaca	aacatgcatc	gccatgaggg	tcggggcgag	cagtgtgtgac	gtgcaggggc	110520
tcgctgccct	caccgtcccg	ctaaagagaa	ttccacacca	tttctctgct	ctccctgctc	110580
ctaaggagaa	gggttcctcg	ccggtgggag	gaagggttaag	ttcatccaca	tagtaagagg	110640
caggagagaa	agcacagttc	tgtgggcctg	cgcccagagg	gagggttttg	gggtttggcc	110700
tctgcagggc	cctggagcag	ctgtgagggtg	caaggtaact	ggggaggaag	aggatgttac	110760
gaaaagcgac	cataaagaag	ttgtcctgct	gaaggctctt	cagggaggaa	atcctgtttc	110820
cttttggaag	ctgagctggg	cttccctgagg	gtgacactgc	tctgtgacag	aaccagggtg	110880
atccctgggt	ctccaggggt	tatgcacaga	ggacaaaagc	tcacacgtga	gctccggcac	110940
tgcagttagg	ggcttgggct	ctggccagtc	cgctgggtgc	cggatcccag	ctctgcccta	111000
ccctgacatg	cgcactctct	tagttttcta	taagaactgg	gatcaacaag	ggaacgcagc	111060
ccctgggtgag	cgtgaatcag	gggacatagg	ctgaacaccc	cgcacagtgc	tgggcttgag	111120
gcactttgct	tcttggttatt	taccagggtac	tcctcgatcc	taatcgtcca	tgtgacaaaa	111180
gccgcacccg	ctttatatgt	gactcagagc	ctgggacaag	ggaagcagca	tgcgaggggg	111240
gccgggtgaa	cgagtcccac	agaaggggcc	tgcccaggcg	ccacaggctg	actgggggag	111300
gccacaccc	ccccgcgcca	gcacagtggg	gaggcagccc	cctttgttct	tcagggaaca	111360

gttcacagaa	tgaacctggg	tgatttcaca	caatgctggt	tcttctgac	catttagtgg	111420
aaggagagcg	acataattaa	agtcatttgc	aacccacaca	gttcctgac	ctccccctgt	111480
tcgggtgtgg	aattcagctg	acacgtgctc	tgggggagag	ggaggggccc	ctctcatcct	111540
agagcaccag	gccgcaccac	catgagagcc	attcctcaca	ttcaggcagg	ttctcttaaat	111600
tccagaaggt	tcccttaaca	gggaaaaggg	caggggagct	gcttcacctc	tccatgcctc	111660
atctgcatgt	gggaccacaa	cgccggctgc	tttcagcccc	agtgtccgc	tcctctttcc	111720
tttggggaaa	gaaaggctcc	tgccctcgcc	acccgtggcg	cctgtaatcc	cagctacttg	111780
ggaggctgcg	gcaggagaag	tgtttgactc	caggaggcgg	aggttgcagc	gagccgagat	111840
ggcgccactg	cactccctat	ccctgtgagc	ggtcaatcac	agtgtctccc	tcgccccctg	111900
gcctggccaa	cttgggcatg	tgatatccct	gtccatgctg	attggtgcaa	aaagtgggca	111960
agtgaccac	acagagccaa	tcagatcctt	ccatgagagt	tttacacagt	ccctgggagg	112020
ggttggctgg	ctgaggataa	tggaaagggg	aatgatttgg	gggtcatctc	tgaagagggg	112080
gaggatgagg	ccagtgtgta	agaagaagca	gggaggagcg	gagatgggga	agcatggaga	112140
gaagaaaacg	gccggagaga	aaaaaacacg	cctagggata	cagcatgggc	ccctggggga	112200
gccttgccca	ggactcctca	gagcaagtgt	agggtgtgtt	gactcccgca	cccagcagcg	112260
ctcggtggc	acaaatctct	ccccccaggc	aggacagatc	aaggagaact	tcattggagg	112320
gggggctgtg	aagcctgttg	tgggagggcc	tgccgggattc	ctccgggtag	gtaacctggg	112380
gaagggcagg	cctgccaata	ggatagtcca	cgcaggatca	ctgcggcacc	cctgcgcata	112440
cgaactggga	tcttgctgaa	ggcatcacac	atggtctcat	ccccaaagcg	gccacgaagg	112500
ccagtttcct	agaaccactt	tccagccgag	ctgacttagg	ggcttcctca	agcacacggg	112560
ggcgagggta	gaatgtggac	cagagactga	gagagtccag	caggagagct	gctgcctctc	112620
cacagcacgc	tgcccatctg	cgttctgccc	gtgctaggaa	gccccacggc	agggggccatc	112680
gggcagccac	cacgcggcag	cagcggcgct	ctgcggggcg	gaccaactgt	cagagggggg	112740
caccaggaat	aagagggcag	caactgggag	cctgccagga	ttcgagtgtg	ctttgggtctg	112800
caaggatgtg	ggaacctggg	gggaatcctt	gcttctctcc	tgagcctctg	agggcctgga	112860
aggcaggacc	cagggtctgt	ttatcttggg	acccctgacc	atggggcatg	ttgttctcag	112920
aacagtgtct	aaagtgaact	gggaggtggc	acacctctat	gccttctaga	aacaccacaca	112980
gccactggac	acacctgagg	tccccagtga	agggctcaga	acaggttgag	tcatagtagc	113040
ccccacgggc	acccacacca	ttgcgggagg	caaacaagga	cagaggttcc	agccgggcag	113100
agcagagcca	gctgtggagc	gagagacagt	gagggcgggtg	ggggaccact	aggacagggc	113160
gtggctggcg	tgtaaagtgc	acgcaggaag	tggcggggtg	gaggcaggac	aggagagccc	113220
aggcctagac	accactgtca	gcctggggat	gcttggcggc	ttctccagtc	ctgggagcag	113280
gcatcacctg	gccgcgggtg	ccccctgggtg	gcagcttgaa	ggaaggacgg	gcagtgggtc	113340
gcagccagcg	gggacctacc	ccgcaaaacg	cacataaaag	ctggaatcag	cttgttacag	113400
ctgcaggctc	ctctcgtccg	atgttgatag	acccctctgg	gacccactgc	accagggaac	113460
cccaaatgca	gctcagcagc	atgggaggag	ccctgtctgc	tgggggtgtc	tgggatctat	113520
ctgggggcag	ggcctagaga	gaaggtcctg	tgtcctgctg	acccagctgt	gccagcccag	113580
ccccgggtcg	ggcctccatc	ctggttttct	aagcatcctt	tagtggtccc	ctgtgatcac	113640
catgccagcc	ccttgccctga	gctcgggctc	tgctgagaga	cccctgcggg	ctgggggagc	113700
tccaggatgt	tggcaactct	ctcagaaatc	tccttccctg	gacacaatga	cttggcccc	113760
cacttggatc	cagccctgct	tccagggggc	tccttccctg	tcctgtctct	gccatgtcca	113820
gccctcccc	catccacac	accaaccctg	atggtcccag	ccctatgccc	agagccacag	113880
agagtcatag	tgcggcagct	ctcacatgac	caccacagtg	ccagccaccc	tcagaggctc	113940
gggagagccc	agacctgtca	gttgactga	tgccatccac	agggtggaca	gccccccacc	114000
agggtgatgc	caagtcaggg	ctgctggctc	tcactccacc	ctccttgccc	accacactgg	114060
acaggactgc	ggggaggagg	tgacagtaca	tgggctcctg	acagggtgga	ttctgatcta	114120
gcagccagtg	tagtctttat	ctccacactg	tgtatcatct	ggagacccac	ttctgaatct	114180
gggcggctgg	acaaagaggc	atcctgtcct	tgaggaagca	gctgtaggag	acactgagag	114240
gccacctctc	agcttctgag	atcgaaactc	acagatggag	agtaggcttg	tccatttcag	114300
aatcttacgc	ctggcaggac	cctgagcaca	aagctgatgt	gatttgggag	ggcagaagag	114360
ggattttccc	acctccagaa	tggaggaaga	atcccagaga	agagacacag	aggtaaggac	114420
ccacgggtag	aggtcaggct	aggagccctt	gccacagccc	ccttgtccat	gcccgccttg	114480
ggctgagccc	aggctaggga	gacacaggaa	ctcacttctg	gcactggggc	gccactttcc	114540
aggcagggtg	tggtgagaga	cggctggact	tgtgatttgt	gacaagccct	ggagggtgta	114600
ggagctccaa	ggtgcccctg	agcctcagcg	ggcccagagt	gggtgtcacc	aggaagagag	114660
ggagacagta	gtggtgatgg	gaggaggggt	gagtagaccg	atggtcaaag	ccacaggggt	114720
gcagggtgtg	ctcaggacat	acagggtgtg	atggatgatg	gtgaccgggt	gctgggctat	114780
agccctcgcc	cccgaacaag	tgggagaggg	gagcacatca	ccggggaccc	tgaattaaact	114840
aaacatgttc	ccactactgc	ccatagggca	ggcgccaacg	tggctgtgag	gttcagtgc	114900
agaagatgaa	gaatttcatg	tcctgcccct	tgaatctgag	cgctgagagt	tggacctgct	114960
ctggaaagcg	tgggttcac	ccagacacct	ggacccattg	aggctgagta	gccccatgct	115020
gcgggtcacc	ggaatcccag	cccagacccc	tgcagggcag	aaacctctcc	tacggtgagg	115080
tgagggtgcg	gctgaggtca	gggcttacct	gtcgctcccc	ttccaggcac	attcaaactt	115140

```

gtcgaaaatg cagtcgttct cgtacagggg acagagcttg ctccgaaggt agtcatggac 115200
ctggtgggat aagggatgag gtgagtgga gggcgctccc gaccatcctg gcccttccac 115260
aagaaggggtc tcaaagagca gcgaggggtc gcatgccctg acatggccca gcgcagacct 115320
gctcatctca gcgaggggtc gaatgctctg acacagcccc tgacacagcc caatacagcc 115380
tcgggagggc catgaccagg cacacggctg acccgaccg tgacctccac cgtgacacag 115440
ctgctcatct tatcgggggg ccacgacca ggcacacggc tgacctccac cgtgacacag 115500
cccaatacag ccctgctcat cttatcgggg gccacgacc aggcacacgg ctgacctctg 115560
agctgtggcc agagacggga gtagcaccag ggagcagagt ccactgtgac aaacagaacg 115620
ctcacagcac aggggcccagg accacctggg gtccagatcc tggctctgcc ctcccagctg 115680
tgtgatcttg gacaagtgat ttcattcttc tgagcctcag tttcttcaaa cttaaagtga 115740
taagagggcg aacctcacag tggttctggc attaagtga gggcaggcct tttgagggtg 115800
atgatctccg agaacacagg gtggcgggca tcaagaaagg ggaagaggga acccacagag 115860
gtttctcatc catccacagc acgaggcact gaggtcaca gggtcacaca gcctctaaga 115920
ggctgaccag gaccttccc caggattccc gtacccaca ggagagagg tgacaccca 115980
ggacctgcat ccacctgact gcagccgggt ctacaagccc tgtaccgga gggccgcatg 116040
agtggcagcc cctgctgag gctggagctg ccaggacaac agggcacggg ctctgccctc 116100
tgggtggcga agggaaggta actgggtgcc atggagcctg gtttcaactc ccaggagttg 116160
aaattaacaa ctccaacgaa cacagaaaat gtgaaggggt gtgtgaacgt caatttctgt 116220
tgtcagcttg gctgggcca ggtaccaga tacttgggtg ttctgtgaag acattttgtg 116280
ggggagggtta acatttaagc tgatatactg agtaaagcag gctgccctcc atcatgtggg 116340
gggccttgct caatcagtcg aaggccctga tagaacaag acagacctcc ctgaggaccg 116400
ggggattccg ctaacagatg cgtgtgggct cgcatagtca ctctcccctg ggtcaccagc 116460
ctgcccgcct gctctgcaga tttagaacat gccacgtgag ctaattcctt caaatctccc 116520
ttctttctca gtctctatcc ccatcctggt ggttctggtt ctctgagcca tctgactaat 116580
atggtggcaa ggactacaca ggaaaacaga gtggcactag ggaagcagg attgggagga 116640
agggcctgct attcactgca cacaggatgg ttagacaagg ctacctgact ccgcctggg 116700
gccctgctca tccctcccca gcccccgtgt cctcctgggt acccttgctt tcccctggg 116760
cccctgggct gcagccccac caagctgagg gtcactgtgt tcctgtctgt ctgggacctt 116820
cgaggggtgag gccgaggttc ttccttctct ctgggtccag ggtctagcac tgtgttgggc 116880
acaggggtact ggctcagtat gtgtaacaac taaaatcaag ggggatgaat ggcagcaggt 116940
tttagtggtc gtgtcccacc cccggtctct catttttgtg tgcctcctt actcagctcc 117000
cagcagcctt ggtgatgcac gcgtccaaat gcgcagtctg ttctctctgc cgtgcactaa 117060
gcattctctg ccctctagt gtaggggtgag gaagagctct ggagaaagac tgtcaatcta 117120
aggctcgctg cttgctggct ctgtcacaga tttgccattt aactcaattg tctccaata 117180
aaatgggatg gggagaatac cggccccacc tccaggaca gctgggaggc ttagtagagg 117240
caaagcatat tatggactta cctcagtggt gctcattcaa caaccgtccc cagccccctt 117300
acccttgctt tcttcaacca cagaggtgtg taaaccatta atcttcccag ccactatggt 117360
ggctgccagg gacctattct agacaatgag gtgtaagaag tcttctgaga agcattctgg 117420
ggaagatttt acaatcacag tgaacacgc aacagacccc aggggtgaga tctagtgcac 117480
ttcctatttc ctgcctggaa ttaggcaaaa gtgcttggag gtgtggcagc cactttgcca 117540
ccatgaggta ccacatgtga aggtggaaaa ccaacgcccc aatgatggtg gactggatca 117600
cagaaggaa cactgtggcg ctgcccgggt catggagccc cccaccttc ctggactgcc 117660
ctctccagac tccctgttgt gggagaaaaa tagccccgat ttgttaagca ccgcacacca 117720
gccgaacgca gtctgtctac acacaatttc tagcacatca caagccacca aaaaatgttg 117780
gttgtgtgct tgctttatg tagttattgc tattatttta gcatcaatag gtcagctggg 117840
ccagatgcca agtgcacagc ttacggcctc acgctccaga acagtcattc cctccttctg 117900
tggggctcct catgagaatt tcagaaagct gtgtccccct cccctgaaa atgctcatag 117960
aacacattcc acgtagtttc aggggttcat gggcctttgc tgacctcagg gatggaggta 118020
agtgaccgga caaggggccc gagggggttg gaaatgttca tttccctgag ctgcctccag 118080
agggagccag agagttgctc ctgcaggctt gagccgggct tatcctgtcc ctctcctagt 118140
ctgggggtct tgccattccc acagggacag agggaggctg agtccctgct ggggtgtgca 118200
gtgtgaggag ggggcctgag ggaggagctg gggcagtcgc aagaactcaa gtaaacacac 118260
gtggctgaca aacaggcggt ccccatagcg gtccttgttg gtgtgtggct tccaggagcg 118320
tgagctgttc ctctggggcc caggtcagat cagagcagcc caccctctga gctctgcacc 118380
agtcccagc gaggcctgcy ccaccaggga cgttttctta ctaggctctt gcacggagga 118440
aaggaaagcg tagggctctg agcctgggct ctgaatctgt caccgcccag ccagagagca 118500
cctccctcat ctccctacct ctcagtgcct gagttccctt tccaccaa ataggatgatg 118560
ctccttgtca ccggacagta aagaatggag gtgacagatg tcaagcacgt ggcaccccat 118620
gtgtgaggag tgacacgggt aggaaccggc tgggggttct ggtgggggtg tttcccaccc 118680
atgtttgcac ggccagatct taccatcct tcaaggccca gcacaaatgc cacctcctcc 118740
aagaagcctc cctgatctcc ccacctaact ggaaccagct ttgaagccat cccacatttc 118800
tttcaagtcc acattttatt ttaacatcac atgagttttg ttgtctacce cctaacatat 118860
ctgaatggat gataatagca agataataaa taatactgtc caagaagggc ccaggcttca 118920

```

cctagactcc	aggettatat	gcctgtgctg	aggatctgga	aaggaaacat	gtgctcagtt	118980
cacctctgcg	tgcactgctt	acggatgcac	cctgggaggg	caacgccttaa	ccctctttaa	119040
tggtacagct	ccgatgcagg	ctcccaggga	gtggggaggg	aagccatcgt	ctacatgctc	119100
cactggggcc	cagcctgacg	ctcatctctg	ttcccacatc	tctttcctcc	ctggaattga	119160
ggccctggg	ccctggactg	caggccttgc	tcagggacat	ccaaagctcc	ctgtgaggca	119220
agactgagca	ctcctgccct	ctgccaagct	acgtgtgggg	atgagttgct	ggatttcttc	119280
agcctccgtg	tcttcacctt	cataccgggc	atatgaaagc	cacgcctggc	taggaaggcc	119340
ccctccatgg	ggatctcagc	atagggaaaa	aagaccgggg	attgggggtc	tcctgctgtg	119400
gtgcccacct	ggtaggtctc	tatgggtctt	gcctccatgt	tcagggtcca	gaccttgact	119460
gtaaggtagt	cccgggtgag	catgtagcgg	ccgctgtggc	tgaacttcac	gtcggacacg	119520
gaggagatga	tttccgagaa	gaatgagcgg	ttactggggg	cctcaggctc	ttcaaagact	119580
gtggagacag	agaagcaatg	gccgtcactg	cgctgctccc	gccccatggg	ttggcacgac	119640
ggatgactct	gtttttgcacc	tgggccccatg	ctctgtttat	tcagtcatte	attcattctc	119700
caaaccatga	actaaacact	taccaggga	caagcctggt	aagattctgt	gctgtgcaga	119760
aatgacctat	agtatcccca	ttcatagcca	agaaaatgga	ggagcagctg	gctaaaacc	119820
atgcctgggg	agtcagtgtc	ggaagaaggt	ggtagagtgc	ggatttgaag	ccaaagctat	119880
acttgatgtg	ctgccctcta	ctgcccccta	ctggtgatgc	tgaatgccag	attgcaaagg	119940
tgtcctgaca	ttctcaaatg	tgtctgacaa	tgtcctctac	cagactgggc	actgcttgtg	120000
gctctggcac	taactggccc	tgggaccttg	ggccagtagt	tatctctgtt	catggtgtcc	120060
tgggcaggca	tggctgagcc	ctacttatag	gtgggttttg	tttcattgcc	atggggtttg	120120
taacaaaatc	aaatctgact	gccacagagt	tggtacagtc	tcctgtatgc	catccactga	120180
ccatctcctt	ttttcttgga	gcacctgtct	tgcacaggaa	ggttgcttatc	tggtccctaa	120240
aggcaacggg	ttgctgcccc	cctggacaat	tatagactgg	gacagagtgg	gcaatgagga	120300
ctccccagac	agtgtcccc	ccccactgcc	cccataacct	ggccttcttg	agctgcagaa	120360
gttcccaaag	tgggacaagg	tctctaagct	catttctgct	ggtatctgtc	tactggtag	120420
cagtgaacct	ggggctgaag	tagcgtgggg	actaggaccc	ctggtggggc	aggcactaac	120480
tccctaggac	ctgggccaca	gagagaccca	gggaacgatg	ggaagagaac	aggggtggtg	120540
agttgacagc	cattcaccag	ccaatctgga	aatacctaaa	cctatgacaa	cctgtccagc	120600
tgtccccatg	gaaaccggct	gagtggcagc	cttgccctgct	ggcctgctct	ggtctctacc	120660
ccagaaacag	ggaagcagag	ctgatcacag	caccctgagg	ctcccagagag	gccccctcct	120720
gctggccccct	ctcagccaca	agggtcgtg	tectgcctcc	caggtctgtc	ccagccccctt	120780
atccccctcat	gggaaatggc	agcaccocat	tctccctcct	gtccaagggtg	gacactgtac	120840
ctggccactg	cctctccaga	aatacaactc	ctgtccagct	cccctctgca	ggggccactg	120900
gatgccttga	tggactcatt	cattcattca	ttcatttatt	cactcagtca	accaatgcaa	120960
acagcaccta	ctctgtgcca	ggccctggga	tgatgcagtg	accagcataa	agccactgtt	121020
cctgtgcagc	caacattctc	cttgccagata	cagacaataa	aactaagtgg	cgcctccac	121080
cgccagggag	cagcaagtgc	tggggaggaa	gagccagcag	gcagataggt	gctgggggct	121140
ggtagtttag	gtgaacaggg	cctccgtggg	aggtgctgtt	tgaccaaggt	ctgagtgaag	121200
ttggggagag	attggtggcg	atgcctggag	aggggtgtgc	tgggcagaa	ggacggcaca	121260
cgcaagggcc	ctgaggcagg	gacacgcca	gggcccgtgca	ggcagagaaa	ggagttagca	121320
gggggaacag	ggacgcaagg	ggccacccac	gcaggatctc	atggggccag	gagaggggtg	121380
aggaagtac	cattagggaa	acgggagcca	ctgagggttc	agagacaggg	aggatgaaat	121440
ctgagtcaag	gaggtaggga	ggggcaggca	ggaggctgga	gtccctccc	gacggaggaa	121500
ggaagttcca	gcaccgggtg	ggccagggct	gcagagccca	ggtgtcacca	tcctgatccc	121560
aggccactgc	atgcaggggag	gtgaggggag	gtgagaggag	ggggagggaa	gctgcttaca	121620
gggcaggaaa	aggctccac	gtttatgttc	atgcctctgg	tatcccccca	aatcagagca	121680
ggcagcagga	ggaaggtccc	ccccacctct	cttgagagca	aggcctccaa	acacctgtct	121740
ctgaagcaga	cccctgaagc	tcaggagatc	tatatccctg	tccttagcct	ctccacagcc	121800
tctggtgagc	agtggcagcc	ttcaacccca	cacctctgcc	ctcaaagcca	tggcactgca	121860
ccgggtatcc	tgagggcagg	tggtcgctcc	ttccagtcct	ggcgtcaaga	tcaggaagga	121920
gggagggagc	ctagtttatc	cactaataag	tgggtgcata	ttttggaatt	agaatgctat	121980
caggctggga	ggtgtttaac	gaaactcaaa	actgacagta	ggcgccctccc	tttccaggag	122040
cccaacccac	ccctccacac	gccccagtc	cccaggcctg	cctgcgacct	caatctccct	122100
ccatcgttcca	caggggcgcc	cttctcagtg	gcccagcctt	tcctctttcc	acaagggcac	122160
attgaaggga	ggaccagaaa	gaaaatcagc	accatgggaa	ggaaggggtga	ggccgctcgc	122220
agagggagct	gggagagaac	aggctgccag	ggtctcaatc	cccgagcccc	tcgtgtggcc	122280
ttgaacgctt	tcacctccct	gagccctggc	cttgctcctc	cctacaacag	gagccaaggg	122340
cgcttttcag	gaaggggcag	gaggaggggg	ttgcagccag	gcctggcacc	accctgggta	122400
caggcagggc	cgcaggcagc	aaagatgctg	tacagagtga	gcccagtgca	cgatgagtg	122460
tgcagcccta	ctgacttact	tccctccctc	cctmccctct	taacgaactc	cttttttctc	122520
ctccctcctt	tctctccttt	tttttctttt	ttctctcctt	ctctctcctt	cttctctcct	122580
tccctctctc	tctctctctc	ctccctcctc	tcttttctct	cttctctccc	cctctctcct	122640
ctcctctttt	ctcttcttct	tcccttctct	atttctcttc	ctcttctccc	ttcttctcct	122700



```

ctccctcttc acacactccc ttccctctctc ccccccctttt tttttttttt ttctatectc 122760
ttccctttttc cccctccctcc catctttctct ctccectttc cttcttccctt cctccctctc 122820
ttccctccccc cccccccctc ccttcttccct tctctctctt ttccctccctc ttctctctctc 122880
ttttctcccc cctccctctc ctccctttctc tttcttctct tcttctcttc tttcttttct 122940
ctctctcttt cttttccctt tccctttctc ctcctcttcc cctcttctct tctttctctt 123000
ctccctctctc cccctttccct cttctttctc ctccttccct cctccctctc tctttctctt 123060
tctctctctc ctcgctctcc tctcttcttt tetctctctt cccttcttct ctctctcttc 123120
ccctccccc taccacta tccccccctc ttcttctctc cctctctatt ctctctctt 123180
tcttctttct tccgctctct ctccctctct ttctctctc 123219

```

<210> 544

<211> 160755

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 19206..21206

<223> 5'regulatory region

<220>

<221> exon

<222> 21207..21387

<223> exon 1A

<220>

<221> exon

<222> 21864..22188

<223> exon 1

<220>

<221> exon

<222> 34799..34930

<223> exon 2

<220>

<221> exon

<222> 37172..37409

<223> exon 3

<220>

<221> exon

<222> 50385..50523

<223> exon 4

<220>

<221> exon

<222> 57261..57395

<223> exon 5

<220>

<221> exon

<222> 59355..59458

<223> exon 6

<220>

<221> exon

<222> 60623..60747

<223> exon 7

<220>

<221> exon

<222> 61570..61682

<223> exon 8

<220>  
<221> exon  
<222> 63244..63372  
<223> exon 9

<220>  
<221> exon  
<222> 63817..63916  
<223> exon 10

<220>  
<221> exon  
<222> 64902..65002  
<223> exon 11

<220>  
<221> exon  
<222> 65487..65654  
<223> exon 12

<220>  
<221> exon  
<222> 67211..67282  
<223> exon 13

<220>  
<221> exon  
<222> 67671..67928  
<223> exon 14

<220>  
<221> misc\_feature  
<222> 67929..160755  
<223> 3'regulatory region

<220>  
<221> allele  
<222> 31547  
<223> 99-32148-315 : polymorphic base G or C

<220>  
<221> allele  
<222> 50558  
<223> 19-51-347 : polymorphic base A or G

<220>  
<221> allele  
<222> 63270  
<223> 19-56-140 : polymorphic base A or G

<220>  
<221> allele  
<222> 65025  
<223> 19-44-251 : polymorphic base C or T

<220>  
<221> allele  
<222> 67348  
<223> 19-46-322 : polymorphic base C or T

<220>



<221> allele  
<222> 67963  
<223> 19-47-315 : polymorphic base C or T

<220>  
<221> primer\_bind  
<222> 31412..31432  
<223> 99-32148.rp

<220>  
<221> primer\_bind  
<222> 31844..31862  
<223> 99-32148.pu complement

<220>  
<221> primer\_bind  
<222> 50215..50233  
<223> 19-51.pu

<220>  
<221> primer\_bind  
<222> 50613..50631  
<223> 19-51.rp complement

<220>  
<221> primer\_bind  
<222> 63131..63150  
<223> 19-56.pu

<220>  
<221> primer\_bind  
<222> 63543..63561  
<223> 19-56.rp complement

<220>  
<221> primer\_bind  
<222> 64775..64793  
<223> 19-44.pu

<220>  
<221> primer\_bind  
<222> 65176..65194  
<223> 19-44.rp complement

<220>  
<221> primer\_bind  
<222> 67027..67045  
<223> 19-46.pu

<220>  
<221> primer\_bind  
<222> 67435..67452  
<223> 19-46.rp complement

<220>  
<221> primer\_bind  
<222> 67649..67667  
<223> 19-47.pu

<220>  
<221> primer\_bind  
<222> 68051..68070  
<223> 19-47.rp complement

<220>  
<221> primer\_bind  
<222> 31528..31546  
<223> 99-32148-315.mis

<220>  
<221> primer\_bind  
<222> 31548..31566  
<223> 99-32148-315.mis complement

<220>  
<221> primer\_bind  
<222> 50539..50557  
<223> 19-51-347.mis

<220>  
<221> primer\_bind  
<222> 50559..50577  
<223> 19-51-347.mis complement

<220>  
<221> primer\_bind  
<222> 63251..63269  
<223> 19-56-140.mis

<220>  
<221> primer\_bind  
<222> 63271..63289  
<223> 19-56-140.mis complement

<220>  
<221> primer\_bind  
<222> 65006..65024  
<223> 19-44-251.mis

<220>  
<221> primer\_bind  
<222> 65026..65044  
<223> 19-44-251.mis complement

<220>  
<221> primer\_bind  
<222> 67329..67347  
<223> 19-46-322.mis

<220>  
<221> primer\_bind  
<222> 67349..67367  
<223> 19-46-322.mis complement

<220>  
<221> primer\_bind  
<222> 67944..67962  
<223> 19-47-315.mis

<220>  
<221> primer\_bind  
<222> 67964..67982  
<223> 19-47-315.mis complement

<220>  
<221> misc\_binding

<222> 31535..31559  
 <223> 99-32148-315.probe  
  
 <220>  
 <221> misc\_binding  
 <222> 50546..50570  
 <223> 19-51-347.probe  
  
 <220>  
 <221> misc\_binding  
 <222> 63258..63282  
 <223> 19-56-140.probe  
  
 <220>  
 <221> misc\_binding  
 <222> 65013..65037  
 <223> 19-44-251.probe  
  
 <220>  
 <221> misc\_binding  
 <222> 67336..67360  
 <223> 19-46-322.probe  
  
 <220>  
 <221> misc\_binding  
 <222> 67951..67975  
 <223> 19-47-315.probe  
  
 <220>  
 <221> misc\_feature  
 <222> 11925,11927,11929..11930,11933,11947,11975,11989,12068,12278  
 12350,12475..12574,12622  
 <223> n=a, g, c or t  
  
 <400> 544  
 gaattctttc ttctgaggag gcaagaattg aggttgctgc agggccgtac agattcactg 60  
 ctgctaacat aatcaaacat gcctgaccct tgccttcccg tcatggcccg aactagtttt 120  
 tcagatttac ttgggaatct ccttgccaa gaggcagggg ggctccattt agtagtttg. 180  
 taggcttaga attttatttt tggtttacac tccaaacacc aggtttgcct gatgtttgta. 240  
 cagtgatgta caatgtccct tctgagtgg tgctactctg gagttcattt ctgcttcgtc 300  
 caggacacca taaatgtgaa cacacattga gactctacag tcctttaagg gtagcaattt 360  
 caattatttt atcagattat ataatcttct gtttcacgtg tgtagatctg agatcacact 420  
 gcctgcaggg gctctgcttt ttcttctttc ctgtgggaaa gatgctaaag catgaaaaga 480  
 tgcaaacaca taaaaacaac aaaaaaagta tgctaaggga gccagggaa gtgaagggtcc 540  
 acaccacaac accacgcact cagagaaagg gacatcaaaag ctgatcctgc aggatggata 600  
 ttcttttctc agacaatggg gtgggcagtg gggtagcgtt gtggagggtg ggaagggtgc. 660  
 cctagggtgga gagaatggca tgtgcaaaga cgagtagggc agggaaacagc aggcaacact. 720  
 cccacaggta ggagttcagg tggatggcca gcaatggcta aggaggttg tgggaatgga 780  
 gaatcctggg tgttcatata gaggcaaagt gatagtcctt tcccacacag tgatagccct 840  
 ttccaccatc atcagggtcag tgcctgggtgca aagagatgga agtgtccagg gcagggatta 900  
 caaactctca aacatcacag aggctgggtca gaaacataac gcaggtagga agtaaggagc 960  
 ctgaggccca ccagaagagc ttgtgccctc tccaaaactc aagagtggcc agacagccgg 1020  
 gcacagtac tcacgcctgt aatctcagca ctttgggagg tggagggtgg cagatctttt 1080  
 gaggtcagga gttcgagacc agcctgatca acatgacaaa atcttggtgc tactaaaatt 1140  
 acaaaattag ccagggtgtg tagcacaccc ctgtaatccc aactactttg gagcccgagg 1200  
 caggagatgc acttgaactg ggggggcaga ggttgagta agccaagatt gcactattgc 1260  
 actccagcct gggagaccct gtcaaacaca cacacacaca cacacacaca cacacacaca 1320  
 cacacacaca cacacacaca tacacacaag agtggtcaga cagagctcct gatgctttat 1380  
 gagaagccag aattgcaggg gttttatgtg aaatttcctg gattgcaaag cactgggtgt 1440  
 accaaataaa caccactggg ggctgtagct ggcccacaag gcactggctg gtggtgactc 1500  
 ctgctaataa aggttaactcc ttccatgatc cgccttgaaac attgggctct gcaatgccac 1560  
 agctgcccta gtgacccttg gcaggcacct tcttgagtga ttccaaatag ttatgacctg 1620  
 tccttggtga gagaggaggg gcagggtctc tgagggtagt gaagcagtac aaatgtttgc 1680

atttctcagg	gatgcaatcg	atgtaaacca	gataaatgaa	accacagaaa	gtcagtagct	1740
gaggcagggg	tgaaatgtgt	ccccgtggcc	tcttaagcaa	ttagctttga	tgccccctggc	1800
agctgttgaa	ttccaaaggc	aattccaggg	gctttgattt	gaagccagtc	tcttaagacc	1860
cacttaagag	cagggggtac	ccagagaaga	gcaaaccacg	ggtgggtggt	ggttaggggg	1920
gtggggagag	ggagtgggtg	ttcctgtcct	caatgtctgc	agagttgctt	tgtttaaagg	1980
tgagtaccca	cttcttttgt	gtagatctag	gagctaaacc	cagggccagc	tggtggaagc	2040
tacagggagg	cagatcttga	cctaaagaac	tccctaacaa	tgagagatgt	ctgaagggtgg	2100
aatcagttgc	gtttggaagt	agcaaacact	tcgtcatggg	aggccttcaa	gcacatggga	2160
aatggccact	cttagggcta	caatggtaaa	gagaagtgtt	gttttgata	aactctgaag	2220
tcctttctat	cctagagatt	ttgtgattta	tcttattagc	aatatttcat	ggtgttcaac	2280
tgaccggttt	atttggggtc	ttgacttttt	attttaagaa	aatgtgcaga	aacttcagaa	2340
ctctctttct	actccgga	tgagactctc	tgacgtaaa	atataacaag	tggcaggtaa	2400
tccagaacca	tgatacttta	gaggcacagg	taataggag	tgactggcag	tggtctcatc	2460
tgtgtctgcc	tggaagagt	taaagtatta	tataagccag	acttctgaaa	aacgggaagg	2520
ggaatggaca	gatgggatac	gggagactgg	aattaaatag	aagtc aaatg	gctgagtcac	2580
tgaactaatt	tcaaagtctg	aaggtaacag	gaaaacagaa	aatcagacaa	ttggaaagta	2640
atgaaggttt	tgtaaagacc	ccagggtggc	aaaacaacag	gagaagtcag	gaaaacgtaa	2700
ttacaacact	gatgtgagcc	ctctgagcca	gaccatcctg	tctctggccc	ttccctctca	2760
cccgagtcct	gcctggtcag	tagcagctcc	ccactgcagg	acacagttag	aggggtgggg	2820
ggctcaccat	tcactcaaag	cactctcggt	taatgccgcc	agtgatagt	tctgtaagtc	2880
caccatggcc	agtcactccc	tcttggttaag	aatctgtctc	cccgtgacaa	agaaagtcag	2940
aacagatgtg	aatgctagga	attgtttcac	ccattacaca	gagggaaaaa	ctgtggcccc	3000
aagagtggat	cgtgtgtaaa	gtgcaatggg	gaggattgag	gtatatgaga	ctcaattcat	3060
ttctacctcc	tgaattaaca	gaaaaggccc	atactggcaa	agtttagagct	ttagcttgtg	3120
cttctgcttt	aaaaagcatc	atctctgggg	atgaatgtag	acagtctctc	aaactcaata	3180
actggctttt	gaggaacaga	gatttctcat	gttccacatt	ctaaaaagcc	acctttttgt	3240
tgacaggggtg	aggtttgagg	acgtacttaa	gaaccatcaa	aatctgtgct	ctctctgtt	3300
cacagactga	tgaagagagc	cagcggcctt	tgaagctgct	cgtgtttgtc	tgatttttaag	3360
aggcagagaa	aggcccaaag	atggtttccc	agcaggatgg	gacaagtcag	caagtttcc	3420
gagccagggc	aatcgtatct	ctaacgaact	agagagagaa	tgttcattta	gtctttaaat	3480
ttattttctt	atattttttt	ttagaatcag	aaaatgtccc	cagatgggtcc	ttgtgtgatg	3540
gacttttagaa	agtcattaca	aacacttttg	ttttctggcc	aatctttctc	ctctgacctg	3600
ggagaagagc	ctcaactctt	ctcacactct	ccctcctgg	gtggctccag	ggcctcctga	3660
ccagtcctctg	cttcaccctg	gcccaccgct	ctacacacgg	cagtgggaca	gaccttttaa	3720
aatacaaaact	tgatcacact	accgagctat	gaagtcttca	gtggctttcc	cactgtcttg	3780
agagtaaaag	ccatcctcct	tacagtggcc	aaaagggtggc	ttaaaatcag	gtcactgaca	3840
cttcttcatt	cactctcatc	tgcccttgct	cacaacttgg	gtggcactgc	ccttctttct	3900
cggctcaggg	cgccttctc	caacccttac	cagtcctttt	gaacctggtg	ctgccacttc	3960
ctaactcact	cctccctggc	tctctgcagg	gctgagctca	actcaagaga	acttgaagag	4020
gacatttctg	agcacctggc	cacagatcct	tcccagacaa	tcggagtcta	actcaccact	4080
ctggggactt	gtcaatatct	atccacatct	tacttatttc	cttgtttatt	tgtttctaga	4140
cttttctcct	ggcttgactt	taagcaggaa	tctcatctgt	attattttacc	actatagccc	4200
tggctcatag	aattgttcct	gatacatagg	gatgactcaa	gaaatgcttt	tgagagggaa	4260
ggagaagagg	gagagaagg	gggaagaaag	aagataggaa	ggagggagg	aggggaaggag	4320
agaaaaagaa	agattggagg	gagagaggaa	atctctctct	ctctctctct	ctctcttttt	4380
tttttttttaa	catattctag	ttggttttta	gccagagaag	ggtgatactt	aaaacaagag	4440
acttaaccat	ggactttatg	gcctaagaac	aacaatgttt	gggacaaggt	aagaatagct	4500
ggggactcct	caagtctcac	cttgcaagca	gccagctgtg	ttgcctaggg	gtgggacaga	4560
cagatgctag	ggaaggcaaa	gggagccacc	agttggggca	gaagggaaatc	agtggaggac	4620
ctgggaaatc	ttagccctta	taggtttgca	ggacctcttc	ctgcttggga	gactccagca	4680
tctgcctttc	aatgaatagc	atcaggacta	gcattgcccc	caaggaaacct	ggaatcaatg	4740
agagggttg	tgagtgtaa	atgtttgggc	cagagaaagt	gagcaccttg	gagacggagc	4800
tccgaagttc	tgcaaatgca	atatcttcat	ttaaagactg	gtctgtaagt	ggcactccgc	4860
acacagttgt	gcaatttata	gatgatggca	tggggttctg	gaggctggct	ccagggagat	4920
gaggttgcat	ggaccttagg	cataaagactc	cacaagactc	ctatggatgg	aaataaaagc	4980
agctacagcc	accagcagag	aaatctcttc	ttgtttgttt	gtttgtttgt	tttgttttgt	5040
tttgagacag	agtttcattt	ttgttgccca	ggctgggggtg	caaaggcatg	gtcttggtctc	5100
actgcaacct	cttctcctg	ggttcaagcg	attctcctgt	ctcagcctcc	caagtagctg	5160
ggattacagg	cacccgccac	catgcctggc	taattttttt	gtatttttag	tagagatggg	5220
gtttcaccat	gttgccagg	ctggtctcga	actcctgacc	tcagatgatc	cactcaccat	5280
ggtctcccaa	agtgtcggga	tagagaaatc	tcttctaagc	aagagagttg	tgcacacagc	5340
actggacaat	ttgccgggtg	gggcatgagc	tggctaaggc	attgggaagg	ggctggtgag	5400
gatggtggtc	agaggcgct	ggcaaacctc	agattctata	acattcagac	caggtccatt	5460

tccctgctgat	gaccaagtgg	actctcagaa	gccatcagga	gggtgctcgg	ctcatcaggg	5520
gaaagtcfaat	tccttggggc	tttcacttat	aactttgttt	gcagatagca	agccttttcc	5580
gcccggcttc	tcctcctgag	cctttctgcc	tgtaacaatc	acattattta	atttagatga	5640
gtgaagttac	cctagatcaa	ttatacttat	ttttcctgtg	taatttccaa	agcttaatat	5700
ctccattcgg	gcccagcctg	ggggacaggt	tgtctagcag	agtcctaaac	gatttcagcc	5760
tttaattcaa	ttgtactttt	accatagccc	agcagcgagc	ataattcttt	tatccctaag	5820
atgtctcatt	agcaataatc	taatagcaca	tattaaaata	taggtcactg	aggctgggctg	5880
ccaagtggaa	ggcttgtcat	aactttgaag	gttgagacagc	tgccctgggtg	ggacttgggtc	5940
ccccataaac	acaccaccct	gactctaggg	ttatttctaa	aatgatcaat	aaaacacaaac	6000
aaaaacagct	tactttctgc	agttcaaggt	taagaaccga	cgctggctag	gaaatagagc	6060
tgtggggtag	ggtaagggag	aggggaatgt	tcttgccaac	atgacgtagt	aggaaagatc	6120
tccgacctca	ggaacttggg	ctggaacctc	atcccagttg	tgccgtgaac	atgcagactg	6180
acctgcagta	cagctgttat	ggcccttgac	ccttggtgtgc	acacctgtaa	aaggggaaga	6240
tactgggctt	aaagccaatg	tttcctgaat	tctggcactc	cctgatcaac	ttgtcctagt	6300
atgcatttga	tgttttcctt	taaatcaact	cattcttctt	aattaaacac	atttgtttta	6360
aaaaggaagc	tcaagtatca	acatggaaaa	acctcaagaa	tatttgcagg	aggattcattg	6420
cggataaagg	ccaactgtat	aaactttaaa	actgcacaaa	agtgatgcgt	aaaaatgggt	6480
tagacaggca	aaataaatct	aggggggttca	aggtccagat	agcagttacc	tttggggagg	6540
aggagatgt	tgacagggag	gggcaaccag	ggggactcct	cagattctgg	tcattttttt	6600
aatggcctgg	atgtagtctt	atgagcggtt	ttactatgta	aaaagtgcag	ttataattac	6660
ttcaattttc	tgtgtgttaa	gcctcataca	aataatata	tgttttatat	ataaaaaatt	6720
atataatgt	tttcataat	agtttatatg	tataaaattt	taggaatata	cgcaacattt	6780
taggtatatg	taaatgtacg	tgtgtaattt	taagtaataa	tatatacata	tcgtgtatac	6840
ataggtacat	atgcagtata	tgtatatatt	gagtatgtgt	gcatgtgtgt	atatagtatg	6900
tatatgtatt	attcttaata	atataatatt	atatttaata	ataaatacat	attgtttatat	6960
aattatgcatt	tatatgtatg	tataccatac	atttaatatg	tgctattagg	tatgtattat	7020
gtatgtattt	agtgaggatt	attcccaaat	gtgtatctaa	gctttcacta	tctggcactt	7080
atgaacacta	gagagcaggt	atctagttag	agcagaaata	ctctatagtg	acagtgtaga	7140
tacatgcttg	ggaataatcc	acattttttt	agtttaacagt	aagaaataat	gaaagaaatt	7200
ttatactgtc	atcatgtaat	aaataaaaaa	ccaaaatcac	atgccataaa	tagataacta	7260
aaaataaagc	aacgaaaaga	aagcactgat	aggagattct	agtttcatgc	ggtttggggc	7320
tgaaagttct	gacccaaagc	ctggcttcct	tctgttgaa	tggggattag	taagtttagag	7380
tcattacaga	cacatgaaca	ccagatttag	actcactcct	tccgtaatca	gggctaaaaa	7440
agcatgaaaa	gcagtggaa	tttctccctc	tgtgattcaa	agtaattcaa	atcagggcct	7500
gcatagcctt	gagccattgc	cccttttctt	tggggctgta	cttctctact	tcaggagaga	7560
tctgcaaggt	ccctccaagc	tccaactatc	ctagcttcta	agggatgcgg	gcattggcgaa	7620
aggctctgtt	acaggtgggc	tggaggtatg	ggagaaaaaa	atgggagaga	cgctatttagc	7680
aaaattggaa	aattttgaaa	caaagcccca	ttcctttctc	cagctccccg	gactgggtct	7740
cacaaagcct	gagccagagg	caggggtggg	caggcacaca	ctccttggag	ggcagccccc	7800
agccttccca	gacacagccg	ttccacctgc	ctcctgggct	acactgagct	ggagcctgac	7860
tccttgaagt	gcgtgtttgt	ggctctgggc	ctgctcttgg	gccacacgga	atatatgtgc	7920
agcaccctct	ggtagctgca	tgtccactcc	tgaggccagc	aggtctgtcc	ctcagctctt	7980
tcctaaggcc	taagtctctc	caccaactgc	ctgacctgac	tctccccagg	acatgcactt	8040
cagcttttagc	ttcatggccc	acatccacac	gtgggcagtg	tagaccagct	gccagtcctc	8100
ttacaagaga	actgcgtgtg	ctggagggct	cagtgaggat	tcctgtggcc	cttgggaacag	8160
gcagggtggc	ctcatgatga	cctctcccca	cctttgttat	caccaaggat	ccttccagc	8220
ctggatcctc	ccctcactgc	tgccccaacc	tggaccccca	agtcttccca	gcctcctcat	8280
caaaacctat	ctttcgtgca	cctccttctt	tcagagtgtg	gccaggggca	tggttcaacta	8340
tctgctctga	gaaatgttcc	aaagagagga	cgtaggtgtg	ggaagaccct	gggaccacgt	8400
gtcggagccg	gttctgatct	cttgcctctg	tactaccctg	tgtaattttg	ggagtggaa	8460
tgaggcaggg	aggtacaaag	tggggcaaag	aagtggaggg	ttcttctgcc	agctacctgg	8520
gaggaagggc	aaacctcatg	acacacagca	ttgaggggag	actggcagtg	gatgctgaag	8580
acctggaaga	tgcgagggac	aaaggcaaa	ggggcagaga	agaaaaatag	aagagaaaca	8640
aatgggcct	tggggcagat	cccagaactg	gtgggagggg	tggatctaag	ggcttgagggt	8700
gggaggtgag	ccttgaagag	ggaaggactc	tagctccttg	aggggaaagg	gccagaggag	8760
atggtggctg	acaaaccaca	atgtctgggt	tcagaaatgc	atcagccatg	gcctcaagtt	8820
tcccagccaa	aaagagttag	cagccctact	gctgaatagg	agctcgagca	gagaggtgga	8880
gtgaggcaaa	tgaggcccaa	actggcaacc	gctgagccat	ggagatagaa	caggggtgaa	8940
gagcgtaagc	cctggagcct	gccaggatct	gggtctaaac	cctaccctct	gtccctctct	9000
agccatgaag	tccaggacag	gacgtctaac	cactttcagc	atggctctta	atctgtaaaa	9060
tgagaataat	gattgtcttg	tatgaaatga	tacttagcat	agtgccaca	cccagtttgc	9120
taagtgaata	gaactgccaa	gtgtatagca	aatgtctatc	gtgtttatag	tacgtgctaa	9180
tcactgctga	tgcactttgc	agtcgctgat	gcatttaagc	cctccaactc	ccccaacaga	9240

tagatactat	cataagccca	atthttattat	cattattatt	attgcccagg	ctggagtgca	9300
gtggcatgat	catgcctcac	tgcagccttg	acctcctagg	ctcaagcgat	cctctcatgt	9360
cagccttcoct	gagtagctgg	tactataggt	gtgcaccacc	acgcccggct	aattttttgta	9420
atthtttgat	tttttttgta	gagtcagggt	cttgccacgt	tgcttaggct	ggtctcaaac	9480
ttctgggccc	aggcaatcca	cctgcctcgg	cctcccaaag	tgctgggatt	acaggcgaga	9540
actaccacac	ccggccctaa	gacccatttt	ataagtgaga	aaactgagcc	acgcatcagc	9600
tcgaggtagc	aaagcttgta	agtgaagtc	aggatttgaa	ctcccaggca	gtacagaagt	9660
tgagtggcac	tactcctgct	gatcacatta	aggagaccag	agatcaaggg	cctcctaaga	9720
aactaggaag	ggaggggtgt	ggtattacca	gaaagagggg	tagcaaataca	ttaccctgca	9780
cctacctcc	tagttccct	gtccttacc	aaagaccacc	cagctttcat	tttgagggt	9840
gagaatacaa	aggaggcaaa	cttctgaaga	acatgtttca	ggtaggtgtt	ctctgtatgt	9900
agtccacaga	gggtgaacta	ctgctgttac	caccatcact	aaacaactta	gtaggttcag	9960
gatectgggc	acgaatgcag	agcaggacca	gcccagacta	ggtgcatccc	ccaggccttg	10020
gcttcattgc	agacaacctt	gagccaaggc	ctcatgattc	ccttgaagag	ggtgcaattc	10080
acacctctgt	cccttcactc	ttccacgcct	ctgttctggg	gtattgatgg	atgctcctgc	10140
tacctcctag	atggtaccct	agacagtga	cgtgaagcag	cttttctccc	ttccatgtct	10200
cagaagggac	ccattcatga	cttcatggaa	tagacagccc	aggcaggaaa	tggtcatgtt	10260
ttttgccaa	cagtcagagc	aaaaggagga	cacaccagtt	tgaggggaga	aaggcattca	10320
aattgggcaa	agctgaattg	cccacaaatt	gccacagcca	ctctcaactt	gggacaaagg	10380
ttatgaaaca	cgctactaat	actggagttg	ttatthtttt	aaagagcaac	aattatthtt	10440
tttactcatg	agacttcatt	tggggcaggg	tttaaaggga	atgacttggt	gatgttccat	10500
gatgtcaagg	gtctcagctg	ggataacttg	ggttgctgaa	gctaaaatgg	ctgggggacg	10560
gctggacatt	tctttctctt	cctgtggtct	cagagcctct	ctctctgcga	tctctccagc	10620
atggcaacct	cagggaagtt	ggacttcaca	catggagact	gaaggttcca	agagagagtc	10680
atgggcagag	ctgcaaggct	tctthttactt	acctcacttg	gaaagtccca	gagcattatt	10740
cctaccacat	tccactgctc	acacagagcc	atccctgaca	tggtgtggga	gggcattcca	10800
caggggcctg	agtattggga	agtgcagatc	actgggaagc	catcgtgggt	gctggtcata	10860
tgatttcttt	gctttgggca	ttaccttact	gaatagattc	tgttgtgatt	tcacgtttac	10920
cattttatta	tagaggctat	tgcaaagggt	atagatgaag	agataagtag	ggtggctttt	10980
gggggaagg	gattggagct	tcatgctctc	cctggtgcac	aacctccag	gaacctcccc	11040
gtgttcaact	atctgaaagc	tcaagttatt	thttthtttaa	caagaatata	catgccacaa	11100
acatgcagat	tcctggctcc	cactgcagac	ccactgaatt	caaatttctg	ggttggggcc	11160
caggaatctg	cactthttaac	aaatctgcca	gaggcgtgag	ctgtaaaagt	ggaaaagagg	11220
caaaaggcca	ctaggaagaa	agagtgaact	tgaggactca	actgccactg	cattgtagag	11280
gctaagaaga	tgtgacctt	catacagtgc	taccgcgtaa	ttatcttcac	aggtgttgct	11340
atccccattt	tatagttggg	aacgctaagg	cttagaagcc	aaaagtcacc	cagccagcaa	11400
gtaatgaagc	taggctthtca	acctagcttt	ttatthtttaa	gtccaaaggc	cacagttgta	11460
atagttatgc	caacctatat	ttgctatttt	atccagctct	tgtaatttga	agtcagataa	11520
atctaaatta	aaattctgga	gaagatccct	gcctcccaca	gacatagaga	aattaaatgt	11580
tttgataacg	acaacaataa	gaagtaacat	gtatgtgata	ccaggcattg	tctaggtgct	11640
ttacatgtat	ttactcattc	aattctctca	gcaattctat	gagctaagtg	cccttatcct	11700
cctcatcatc	ttatccattt	cacagatgaa	gaaactgagg	ccaggtctgg	tggtcatgct	11760
cagtaatcca	agcatttcaa	gaggctgaga	tggttggtatt	gcttgaaccc	aggagtatga	11820
gaccagcctg	ggcaatataa	caagacccca	tctataccaa	aaggaaaggaa	agaaggaaaa	11880
aaggaaagaa	ggaaggaagg	aaggaaaggaa	ggaaggaagg	aggangngnn	ggnaggaggg	11940
gagggangga	aggaaaggag	ggaggaagag	gggangagag	ggaaaggngg	aggggaggga	12000
gggaaggggg	gggagagaga	ggggggaaag	aaaagagggg	aagggagggg	agaggagaaa	12060
gagagganag	agggagaggg	gaaggggaaag	gagaaagaga	agggagagga	aggagggaga	12120
gggaagagga	gaggggaggg	ggaaaagagg	aaagggaggg	gagaagggaa	aggaggagac	12180
gaaggggag	aggaaaaaga	gagacggaga	agcagagaag	gacgagcgcg	cgcaggagag	12240
gggcaagacc	gagaacggag	gcgagcgagg	ggcgaagngc	agagcgggaa	agcgacggag	12300
ggcacagagc	ggacgacaga	taacggggcg	agcgaggcg	gcagcacagn	acgcgagcgc	12360
cgccgcacca	acggagaaag	agcgaagatc	gaagagagat	acgagagaga	gaggcaagag	12420
cacgcgaaga	gaagagagga	gagcgcagcg	gccaaaaggga	cggacagcga	ggcannnnnn	12480
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	12540
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	12600
cgcttatccc	ccccctcccc	cnccggttac	atgtatggca	gacagggaaa	accggtgctt	12660
atgacatacg	cacatagccg	gggggttgaa	gggagggaga	aacagctcaa	gccaaagatt	12720
gcaagagaga	aagcaaagcg	acacgaggag	agaaaggagg	aagaagtacc	ggaggaggga	12780
agggaaccag	agagagaaag	aaaaagaaga	aagaaataaa	ggaaagagag	aaaggagaga	12840
gagagaaaga	aagacaaaag	aaagagaaga	aaggaggaaa	ggaaagaaag	aaggaaaaga	12900
aactgagaca	cagagaagta	ggggaacttg	gccaggattt	cacagatagt	ccacagtggg	12960
gtcaggatta	aaattcaggt	tagtggtccc	taagttcatg	ctthtagcct	ggataaccatt	13020

ctgcctctcc	aggctccaca	aaagcttaat	ttgctgtttc	ccaagaatag	acatcagaag	13080
gccagtgaga	caagtaagaa	agaagtggga	agatagctgt	agaatcact	ttgggtccaaa	13140
tatattcctg	gtgaagccat	tggaaagtgt	tttctgagca	aaaagaaaag	agctcagaca	13200
ctagagggca	atcattttta	gagactctga	gatggatttc	atgcaggagt	ttgcaaattc	13260
tcccaaaact	ctattttaaa	tgctgtgtac	attagagaag	acaaatacat	ggaaacatgt	13320
actgtgttct	tggatgggaa	gactaaacac	tgtgtgatg	tcagttctcc	ctcaaattga	13380
tctgtagatt	taatgcaata	acaattgaaa	ttccagtggg	gtttttcatg	gaacgctgca	13440
agatggttca	gaaatttgta	gggaagagca	tggccaagat	atttccaaag	aaaaggagct	13500
cgagaatctt	gctccaccag	ataggaaagt	gtattataaa	acaatgttaa	ttaagactgt	13560
gtggtaattc	ttgggcacag	ataaatagac	caacagaaca	gaagagagag	tccagaaaaa	13620
aaccacaactg	tacaaggaaa	cttggtttat	gatagagaat	tctctgatga	ttagagcaga	13680
gaaggtgtaa	ctacttaagg	actggggcag	gacaatttgt	tatctgttat	tcaaattgaaa	13740
aataatgaag	tggaatccct	acctcacacc	ctatacaaaa	atcaactcca	ggtggacatc	13800
aatatgaagg	acaaaactgt	caaattttta	aatataactt	tggaaaatat	cagctaggga	13860
cagatttctt	aaaccagaca	taaatataga	aaccaaaaga	aaaaattgct	acattaaatt	13920
acattgaagc	taataacctc	tacttaccaa	agtcacccaa	cagagcaaaa	agattttacaa	13980
tgacgccaag	aaaagatggt	ggcaacattt	caaagattag	taccaggat	atattattaa	14040
gtactgtgaa	ttaataagaa	aaacattaat	aagccaatag	aaaattgctc	aaacaatatg	14100
tatcatcatc	tcatagaaga	aaaagaaaca	caaatgacct	atatgtattt	gtgagaagat	14160
gttgaaacac	attagaagtc	agggaggtgc	aatgaaaac	tacagtgaga	taccatttca	14220
cacccaaaag	tttggcaaaa	gttaaaagcc	taggtaatac	caagggttag	ggaggatgtg	14280
gagaaattag	atgtgaagaa	ctgacacggt	gctagaggga	gtttcaattg	gtacaaacac	14340
tttagagaat	ggtttggcat	tgcttgataa	agctaaataa	atacatactc	tacaaaccag	14400
caattcactc	ctaagaataa	accctaggaa	aactcttgca	catttgtgta	ggtgacatcc	14460
taaagcggtt	atagacagca	ttgttcaaaa	tccaaaaga	aaaaaaaaact	ggaaacaatc	14520
caaatgtcct	tcacagttgg	atgaataaat	aaattgttat	tattcatata	atagaatgaa	14580
tataaacaac	actgaaaaca	agtgaactgc	agccaacccc	atcagcaagg	atgaatctca	14640
gaaacatatt	gggccaaata	agtcacagaa	caatatctgt	agtggtattc	cttttacata	14700
aaatttgaag	agaataaac	taacaatgta	ttgttttaga	atatattcat	agatagtaat	14760
attataaaga	aaaaacaaag	aagtgggtgt	tgccaaactc	aggatagtgt	ttattttaga	14820
gcagggaaca	gggggtgaatg	tgcttagggg	gcgtgggggtg	catgtggggt	tgtcagggtat	14880
gggatattct	atttcttaac	ccggaagggt	aggtgggggtc	ttgtacgttc	atattattat	14940
tattatttga	actgtgaaaa	agataataca	tgttttattt	taagagattc	cgagatgaat	15000
ttcatgcagg	atttgcaaat	ctgccccaaa	ctctatttaa	aatgctgtgt	acattaaaga	15060
agacaaatc	atggaaagat	gtactgtgta	cacttttttc	ttaagtacga	gaaatttcac	15120
actaaatttt	aaaatgctgt	gtgtgtgtgt	tgcgcatat	ttctgggagg	aaattccatg	15180
tctcatcaga	ttatctaagg	aatacctggt	gttctaacag	agtgacaact	ggatgtgaagg	15240
tttctgagat	tctgtccaga	tattctcggg	tggatagagc	ccctgtgcag	gctggcagcc	15300
aggtcaactg	gccaaacctc	cctctgtctt	agagaggaac	ctaaaccagc	tgtgagtcct	15360
ctccctccat	aactcacatg	actatcttaa	ggccaaagga	tgtatctggg	gtctcatgta	15420
ggggagggca	agttccctct	tttctcctgg	gagactgagt	ccctttgccc	tgggcacctc	15480
cttcccttct	tccttccctg	gctcttcgac	atgtgtctctg	cctctttctt	ctttctatgg	15540
tccacctgca	tattgtctaat	ggacttggcc	attattgcac	agcctgagaa	cagcaaagcc	15600
tgagtcagga	cccatggtgc	tgtctcacag	cccagtgtct	ttctgccatg	ccactggtca	15660
ctctattctc	cttctcccc	aacacctctg	tctctgtcag	atctggcttc	ccatggggac	15720
tgacgggctc	agctgggctt	gcattggcaa	gtccaccaa	gaatgcattt	atccattcat	15780
ccctgtcacc	cacggaagga	ctttgggttt	tgtttgcttt	tgagacaagg	tctcactctg	15840
tcacttaggc	tggagtacag	tagcatgacc	acagcccaact	gcagcctcca	cctcctggat	15900
tcaagcaatc	ctcccacctc	accctcctga	gtagctggga	ctacaggtgc	gccccaccat	15960
cctcggtctaa	tattttttta	aaaaattttg	tagagacagg	gtctcactat	gttgcccagg	16020
ctggtttcga	acacctgggt	tcaagcactc	ctcccacctc	agccttccaa	agtgtgaga	16080
ttagacttcg	gatttttatc	tgaaggagat	aaaagccatt	ggggagagac	agtgtataggc	16140
tctgaacttg	tttccaaaag	gtgtttctag	ctgctatgtg	gaacttaaac	ttcatggaat	16200
aaggggagaa	gtcaggaagc	ccattcggag	gctatgacat	taatccaggc	aagaggtgac	16260
atggcttgga	acagggacac	caccatgagg	tggggaggtg	tgatgtgatt	tggaaaccagt	16320
catttgcaag	aggattggat	gatggtcaag	agaaagagga	gtccaggctg	actccaaggt	16380
ttgtggccca	aggaactaga	aggaagaaga	tgccatcacc	ttggtaggga	gactgtgggg	16440
aagcaggtgt	ggtgtgggtc	aggaagggga	ggccaaggat	cttactttgg	acatagtgc	16500
ttccaggtgc	ctttgattac	ccaggtagt	atgtccagtc	tgagtttga	taaaggcaca	16560
tgaagttcag	gggagcagcc	cagggagagg	atgtgaatgt	gaagtcagca	ggcaacagat	16620
gctctttaat	gccagtgcct	gaatatgggtc	agctgggcta	ggaattaaga	gaaaaatcta	16680
aggactgagc	cacaccgcac	agatcggaag	tctcaggtat	cccaagggca	ctttagtggg	16740
tgggtgctctg	aaggaggcgg	atttcagttc	atggaggtct	tatgctattt	gtaaatccag	16800

cacaacttat	gccaatgatg	aatgaattca	gggcaggtca	gctgcagtgt	aatatatgcc	16860
tattgtcccc	tgatcaagac	agaaagacag	aatgaaaagg	aagaaggaag	gaaggaaggg	16920
agggaggagg	ggaaaaaaga	ggaaggaaag	aaatcaggga	gagaaaagaag	gaaaggaagg	16980
aaggaagggtg	ggaaaggaga	gagaaagaaa	gggactaagg	gagaaagaaa	aaaggaagga	17040
aggaaagaaa	agagaaagaa	aaagaaagaa	agaaaaaaga	aaagaaaaga	aagaagggaag	17100
ggaggaggagg	agggaggaag	aggaaggaaa	gaagtgaagg	agggaaagaa	gcaaagggaag	17160
gaakkyaggr	maggwsagmk	aaagmarkgk	arkawakgms	wawkrwmmmm	kgawsaaaga	17220
maagararas	agaawgaaaa	graagaagga	aggaagggaac	ggaggaaaga	aaagaggggat	17280
ggaggaaaca	aatatgtagg	caaacctctc	ctcctttttt	tccttagtct	cctcattggt	17340
gccatggagg	tgtaggttct	gatagcgtec	tcagcggaca	caggcccttg	gattctaaat	17400
gtgtcccagc	ccagctgttg	tgtgtcaggg	ccccagtgct	tgtggggaga	tggccagaga	17460
tggactcaca	gcacagcca	ttgcctttta	ccccatggcc	tgtgtcacca	agtgccatgg	17520
taagtgaag	tgatggctcc	ccagagatca	cattagctct	gataatgctc	cagcctccca	17580
tgcaacaact	gccctcaggc	cacctggctg	ggcaggaaga	agggctccca	gagaagccac	17640
atggcccat	ggcggtagt	ctgggcgaga	gatggagaga	gacgccttcc	cttttagccc	17700
agtcccagcc	tagtgtcctc	actgctgacc	cccggtagtc	tctgaaacca	cagatggagc	17760
tcccagactt	gctgattggc	ccccgtgatg	gcgtgcgcac	taggaggaaa	tgccctccctc	17820
caccttcta	gcaaacactt	ccagctccat	gcccacaccc	cttatcatcc	actgttccctg	17880
ccagtgcaga	cccaacccaa	tggcttcctg	ctgccagtac	ctggggctct	gctgttagcc	17940
tttctctggc	agcaggacag	gctcatccct	cttatcagac	aggctggact	tgstgggaag	18000
ttgacactct	gggggcggcc	ttcatggata	aatactstag	tttcttgcc	cctcaagtga	18060
gacaacccca	aggcgtgctc	tgtgcagtct	cccaggcccc	ccaccagggc	tgagcaccwg	18120
tttccccagc	agcaagtgtc	ccttaatact	ctttctctct	gtttccttcc	ctttgtctgtc	18180
tcacttctcc	tctcccaac	gattgcttcc	aggattatct	cctaaataaa	ttaacttgat	18240
tctaactctt	gtttccagtt	gtttcttgag	gaatccaata	caaaacgaaa	ccaatcaaaag	18300
acaccaaacc	caacaaaaga	aagagaactc	ttctggttct	gtattgtaca	tgtttctgga	18360
gcaccattta	agtaacagaa	tacatcacgc	actgtctttg	acgctggtag	ggagggtctca	18420
caaataactg	tacaggcaaa	taaacagcag	tataaaagag	gagtttgact	ctggtgtagg	18480
aggtggttat	caggggaaggc	ttcacagtga	gggtgactgg	aggttttgga	ggatgggttag	18540
gagttctcca	ggtagaaaaa	agaatgatgg	aaacagcata	ttaaaaaacc	cagaagtgtat	18600
aaaaagcaca	aggtactcag	gggaaccact	agtagtttag	tatctctcat	actactggag	18660
aataaagcat	attttggaag	tgataaagga	tttgtaggaa	aaatgaggag	agaattagaa	18720
tagcaggagg	tgtgggttaa	tagccagagt	cttgtctata	ctcctcaaag	tgtttaggca	18780
ttatcttgga	aaggttgga	gattttttta	aattgtgggt	tatctttttc	tgattgcata	18840
aatatcaaat	gctcattgtg	gaaaagttgg	catatacaga	gaagtataga	gaagaaaata	18900
aaattacctc	aaatccagag	ttaattaaat	cacatttatg	tgttggtgtg	tttcagagga	18960
gtttcaggca	gaggagtga	gtggtcgac	ttgagttcta	ggtagagctc	tggcagctgg	19020
tgacgatcat	gcagctggaa	agatactgaa	cgtggggtga	ccagctagga	ggctgctgca	19080
gtgaggggtg	atgaggggtcc	tctgttggtg	ctttgcaggg	tgtttcagag	gtgggattct	19140
cagcacttga	aaactagtgt	gatgggggtg	ggggtagagg	agagaagggg	accatgacta	19200
ctagagagat	tctgagtgtc	tccaccatga	cttggtggag	ggagcagagg	ctggaggcca	19260
ggagacttgg	gttctcattt	ccactctgtg	acttccaatc	tgtgggacct	tggaacaagt	19320
ccttttagtcc	acagagccac	agtttctcta	ctgtatagct	ggaaagatga	ttctcttctc	19380
gctttcctta	caggattgtc	atgatcgctc	aatagatcaa	aggagataaa	cacctttcat	19440
gtgtggaaac	ctacagttct	gaagctcttg	tcctcaaacc	tctgctcaat	cttttccctc	19500
acctgccttc	tgtcatcttc	cccagaagcc	agggggaacc	catacccttc	taggtttccc	19560
ttcctctccc	ctctgcatcc	tggccagagg	acatttgtca	ygattgtccc	tctggtacag	19620
atgctctaaa	caccgccaca	caccaccatt	ctttcattca	ttaactcatt	cacttcayag	19680
gctggttgat	gctctagtac	gttccagggtg	ccagaacacg	tgctgtaaaa	gacagacaag	19740
gtccctgtgc	tcatggagct	cacataccac	ccaagggggg	acataaartt	aaacaactag	19800
gacaaattcg	gatagcgatg	taacaaatga	ataaataggg	tgataggata	gagtgagcgt	19860
gtattttcga	tttgagtcgt	cgggaaggga	cctctggact	gagacctgaa	caactcaggc	19920
agagaaaaa	gcaagtgtaa	aggtcttggg	gtgggtttga	gcttaggatg	ttttagcaat	19980
ggaaagggtca	gtgtggctgg	gctgatccaa	gccccacca	accacttag	cacggccacc	20040
tctctgaagc	ctccttgga	caacaggatg	cttcccttgc	tgattcagct	ccaccctact	20100
tccacacatc	tgtggtcaca	acacatcctg	accacactgg	gttgtgatag	actctataca	20160
ctggtctggg	agctccttga	aggcaggggc	tatctcctct	ctagccagca	ctgttcacgc	20220
acacagcaga	tgatcagcat	ctgctaaagg	gattaataca	ttaatcaata	gatgagtga	20280
tgaatgagaa	aacgactctc	aggtccaaat	ggctcactcc	tttactgtc	taattgttac	20340
cttctcaaat	tccctgaccc	cgtatgcaaa	ctgcagcccc	actgtcccc	sattccctca	20400
cccatcatat	aacgtgtgta	tttattatgt	ttcccgtttc	ctctgtctcc	gccagcagaa	20460
tggttaaactc	catgaggtca	ggaatctccg	agttatgttg	cgccagtgtg	atccaagagc	20520
ccggaacagt	gcctggcaca	cagcgggcat	atggaagaac	aaatgtgtga	aggtgtgaat	20580



gaatgaataa	ttgaaagaat	aaatagtagt	tctcagcctc	acagaacacg	ggtcacaacc	20640
tcaaatgacc	tgctaccctg	cccataaata	acagagatgc	aggagtaagt	gtggggctgt	20700
gacctgtcaa	catgctaagc	cgctcaaaca	aaactgcccc	acagcccgcg	ggccgcctat	20760
ttgcagcact	ggggccctgag	ccgcacattc	ccatttcggt	gataaagaaa	ctgaccagat	20820
agtttaagt	gcctgctgcg	gaagacagrg	ctgggtgctgc	accggctcgt	gcttccccag	20880
tccttttttg	gcctcctttc	tgacgcgacg	cagaccccag	ttctggagag	tctgtcactc	20940
gctccccgtg	gtgggagatc	agaggcctgg	tgctcctggg	agcggcgagc	ggtgctcgge	21000
gcaggataga	aagggagtg	gcgcccaggt	ccccagatc	cctgggaacc	cgcgccaccc	21060
tccccccct	gcccattccc	ggccgcgctg	tcagtctcca	ttagcgctaa	caggctccag	21120
acggagcggg	ccgggcgctg	ggttaatgca	atcggcgcgt	tacctggggc	gcaggctaca	21180
ttaccagccc	ggcccccgcc	aggcacggcc	agaaccagtc	agcccgcgcc	ctgcccggcc	21240
ccccgcgct	cagctctctc	cccgggcccc	gcccgaacgc	cacacggcgg	agccccagcc	21300
cagcccgcgc	cctagagcct	gccaaaggcg	cgccggctcg	gggcccggcag	ggcgcaaggc	21360
accagggatc	ccctcgccgc	cggacacgtg	agtgcgcct	gagcgcggga	cagggttagg	21420
tctgcctggg	aggcccgggc	cgagacgcgc	cagcagaggg	ctagcgagtt	tgtagtgcag	21480
tgacgttaag	tgtccgagaa	ggctcctgtg	gctgttgaag	tgctcgggac	ctgagcttgg	21540
ggaggggggtc	ggcacgctgc	cctcagcctc	ggtgagttca	atcccagcca	tttggggcag	21600
gagaragtgg	gtgaaacgag	gaaaagtgtc	gcarggtctt	cagccgcccc	casarggctg	21660
tcagaagtct	ccaactcttg	agttccggcg	tgcccccaacc	tctgtttccm	aatttttcca	21720
gcgagcgcgc	gctcttttct	gggaaccctg	cgtccgctca	gcgcgcgctc	atcccagtg	21780
ctaaggcgct	cccgggtggt	cttgggagtt	gcaagtaggg	aggaacggcc	gggtaaccac	21840
ctcttttccc	tttatccaag	cagagcctcg	gctgtcccc	aggaccggt	aagtctctct	21900
cgccagccgc	atccatgctt	ctggcgcgga	tgaaaccgca	ggtgcagccc	gagaacaacg	21960
gggcccagac	gggtccagag	cagccccctc	gggcccgcga	aactgcggag	ctgctgggtg	22020
tgaaggagcg	caacggcgct	cagtgcctgc	tgggcccccg	cgacggcgac	gcgcagcccc	22080
gggagacctg	gggcaagaag	atcgacttcc	tgctgtccgt	agtcggcttc	gcagtgagcc	22140
tggccaacgt	gtggcgcttc	ccctacctct	gctacaagaa	cggcggcggt	gagcgtgggg	22200
tcgggctggg	aatttgaatc	tgggaggtcc	actgtctgca	gcggtggctg	ggacaggagc	22260
tggaatacac	acggaaggga	ggcgaggaga	cagggggcaaa	tctggggcgc	agaaagaact	22320
ggacagggct	aacgggaaaa	aaaaaagatt	ggagtctctc	ggaaggtcat	tttcccaggc	22380
tctttgcaga	gtacctcgag	ctcattccag	cggaaagtgtc	aggattgggc	accttggaag	22440
caaaacagca	gaagagtga	atcgagtcat	gacctaaag	tcattgtagg	ggtagtgatg	22500
gaaaggacag	aattctgggt	gccaggttgg	gtgggggagc	ctgacctttt	gatggtctgc	22560
tggaaggag	gtggagattc	caagagctct	tgaaggggca	ccagaagtgg	gtgggatttg	22620
acaaccaggc	ccacagtgc	cctaaatcta	gcactctgag	cctgggggca	ggaacctttg	22680
ggccagaagc	agtgggaata	cttcggtttt	ctgaaggcac	ctggggaggc	cctgtggtct	22740
tggggataga	aacacacaag	aagaagccag	tatcagaaat	aatgccattc	tcaggagagca	22800
cagcccaggt	ggaatcaggc	cagtaggtgc	caagaactgg	cctggtcctc	aaggcaggag	22860
gcccagatga	ttggggtgaa	acctctacct	cctcaagttc	tagccgcatt	gcaggaggga	22920
gtgggagag	ggcctgaaga	agactccagt	ggaacagcca	cactctctcc	cccttctgct	22980
ggatggtcca	actggccacc	tgcttgaaaa	tgagagccta	gagatcacct	acagccaatc	23040
caggagaat	aacatagaac	cccgggccag	ggaaagcgtc	tggaaagtcag	ggtgctggcc	23100
cccacccct	agctccttcc	tgaggggctt	tgctcctgcg	gtgcccagtc	ctgccacttt	23160
tgctgggatg	agctcagagg	taccctgcaa	agagtgtggg	aaaatagacc	ttttgaggaa	23220
gaaattggag	aagggggacc	cagctctgaa	agcctctctc	tctccactgg	gctgcattgc	23280
ttggcggtag	ctgtgactct	ggacttaagg	gaggtcagag	ggaggaaggg	caagaatttg	23340
gagctgggta	gagggaaagc	tcattgacctg	ttcacaggct	ctaggactta	caactctgct	23400
tctatgtgta	ctctggacac	ttgctttggg	acgggcaata	cttgggtgtt	gcaaaaaagg	23460
agtggggccg	ggcatggtgg	ctcatgccta	taatcctagc	actttggaag	gacaaagtgg	23520
gcagattggc	tgagctcagg	agttcgagac	cagcctgggc	aacatggtga	gacctcgtct	23580
ctactaaaaa	tacaaaaact	tagctggggc	tagtggtgca	cgctgtaat	cccagctacg	23640
caggaggctg	aggcaggaga	atcacttgaa	cccggtatgt	ggaggttgca	gtgagccaag	23700
atcacgccac	tgactccag	cctggaccat	gggtgacaga	gcaagactct	gtctcaaaaa	23760
aaaaaggagt	gggatcacca	tagagcacag	gtggctctga	gcagaggatc	ttgagtaaga	23820
aagcagttag	ctcttccaac	gagaaagtta	acccaagggt	ggagctgaca	gatggagggt	23880
tgcgtccatg	gtctccctga	cacctcctga	gatgggtctg	tcattgtcag	atactctgag	23940
accagatagc	tgggacagca	gtcctgagct	tcaggggcat	ctgaggtctg	gggcctgatc	24000
cgtggggaaa	caacttgtga	ctctgcgggc	tcaatgtttg	tgtctggccc	tgggatgggtc	24060
atgggcagag	agagaaagg	gagaaaagga	gaagctaata	cagaggtgaa	actttccac	24120
ctttggcggc	tgacgctct	caggcggtac	tgggcagggt	taagcatggc	tgtttggggc	24180
caggaatgag	gaaaatgcag	attctctgta	tcttttaaga	ggcagggaga	tgatgaatga	24240
gagaccttaa	gacccgcat	cccgctgtc	ctcagtgacc	gccccagact	gcttgctctc	24300
agacagtgga	aggctctgtc	attaatcagt	aatatttttc	tgggtcctct	tggcgtgagg	24360

cacaatgcta	ggctctgcag	gggtcacggt	caccaagagg	catgaaccac	cacttctgcc	24420
tgccaggagc	tttaatcacc	cgagtcttta	ttgtcatgct	gctagaagtt	cttcccattg	24480
ctctatgtgt	ttgttgaaac	taaaagcacc	cagatggcca	atttgacaag	tcagctagat	24540
ggatattcca	gggctttcat	tgacactgtg	tgctctttag	tcattgccag	caaaaataag	24600
agcacctggt	gtatgcagtg	tactataaac	cagggtctta	ggatgcaaaa	tggaagaaac	24660
ttgtcacgag	ttccagtctt	taggtgaagc	tgaccgaggg	cactttctcc	cggtctgtct	24720
atctcaaaac	acagctcact	ccaagttggt	tggtgggttg	tctctttgtg	gggtctgtct	24780
ccaaacagga	aaaggcacia	tgagggcaga	gactgtgact	ttttaatctc	tgtgtttcta	24840
atgcccaaga	taagtcctag	atcacaggaa	tgtggtagaa	ggtgccaag	aaactgctgt	24900
tgaataagct	aatgaaatgc	tccaagccct	caaagacctc	caaccgtatt	cagaaacaac	24960
aacagaaaca	ctcagtggta	actaataaag	tgaagccaca	tacaacagtg	gggcaggggc	25020
agcctattca	ttagtggctt	tagctgtgga	gtcctggggt	ccagtttcta	gctgtaaggc	25080
tttggaaggt	ctccaagcct	cagtttccct	acttgtcaaa	tggaaataat	gggtgctcagc	25140
tcagaacatt	ggtgtgggga	ccaaacataa	taactcatcg	agagcctggc	atggattgtg	25200
gccttaggaa	aggtggctgc	tgattttggt	aatgtcatta	tgatgatgta	tgaatggat	25260
ggagagacaa	gtgctttaga	caaatgctct	aaaggcctga	ggaagggctg	cttaggaagg	25320
gctgggagga	ggtgggctgt	ggttgaagct	cagctgctct	ggatggggaa	ggtgcagaca	25380
agcgggtgaga	agggaggaga	tctccagctg	tgacacctggg	gcaggaatgt	acatggaatc	25440
atctcagaga	acaggagtgc	aggctggctg	cagggcaagc	caggagagat	aaggggtcag	25500
gggcaagttg	gggccaggct	gcagaggcct	tgaaagccag	gctaaggggt	ggggatatta	25560
taccagtga	tttccctttc	tggttaggat	gttcacagtt	ggtgtcaggg	agcagtgcag	25620
ccctccatct	cagactatga	ggtaactcct	tctctcactt	accctcatc	ccttcagaca	25680
tgctcagcta	gctccctctg	ggctttatct	ctgctggaggc	ctcctggctt	ctctgtcttt	25740
ttgtggatca	attctcatcc	agtaattccc	aaattagccc	cagagatgag	agtgagtggg	25800
caggaagggtg	ggtctttgca	gtgcagaag	cagccgttta	agactggagt	ttgagtctga	25860
gctctgcctc	tactgtgtg	atctcgggca	tagtacagcc	cctctctgag	cctcaagttc	25920
ccagccatag	gtgaacatga	cctgagataa	caccacaaga	tttattcctt	tccaatgccc	25980
tggtcaggg	ttacactgaa	gccaggactc	accagctctg	ttatttaaca	gccctcagtg	26040
tgctcttctg	gtgccagtat	taacactgta	acctctgcaa	ttctgactgt	tcatgtctggc	26100
ccagaatgga	ggatattttg	aaatgatgaa	gggtggcaatg	gtttaggccc	ctggctaattg	26160
ttttctgaat	gaattactgg	aaaagatcag	cctgtctgaa	catcttcccc	atggccagct	26220
gctgggatgc	acgggctgca	ggaggctctg	ggaggggaaa	gccactctca	gaaattccgg	26280
agctttgttc	agaaccttct	caaatagtct	gtctccatga	ggaggcagta	tcaggcagtg	26340
attctagagt	ttccctttgc	acctgtgatc	ctggtctgtg	ctgatccctg	gggaagagca	26400
ggaagattga	ctgggtgctc	atttttgccct	ttcttcagg	gaagtggcca	ctgtgaatta	26460
acctttgcac	atggctgctt	ctgtttgagt	cctgtcctga	ggccagctta	gagctgtgca	26520
ttgtagagaa	atatagtctt	taggttcagg	gtctgagtct	aacttttgct	agaaaggtaa	26580
cgatagacaa	atcactcacc	tttgctgatc	tgagcttcag	tttccttaca	cagaagagga	26640
gaataaccac	agcaccttct	tgagggtgga	gatggcatca	gagacaatat	atgtaaactc	26700
cttgaaatga	tgtcacataa	taggggctcc	ataaatgtag	tcattagtat	tttgttattg	26760
ttcaatgata	ttactgcat	gctagactta	ggagtggggc	aggatcctga	ttttggaagt	26820
agcagaattc	atcctaagat	gaaattgata	aaaggaaata	aggctggaaa	atagtccac	26880
ttgggtctgc	agcccaagca	tgatagactc	aggaatcagg	ggatgggctt	tgctccattt	26940
cctaacagcg	ttcaattatc	tcaaaataga	ttcatcacct	ggtaaatggg	gtttataatt	27000
cctgcatggg	gtcccatgac	cctctgtgat	tctgcgtccc	cagcggactc	tctcctctcc	27060
ccaaggaagc	tcagagtctt	agggaccccc	agccctttgg	gagcccttgt	ggccaaaata	27120
tctgggatcc	ttactactga	gtatgaagca	gtagctgcta	cagaggtcag	gagctctgcaa	27180
actcagtgtc	cttatatctg	gcctggctgc	agggggctat	ctacaccctg	ggcttgccaa	27240
gccagacact	gattgtcagc	tcagatgcac	aatgagccag	ccagctgggtg	tgccactcag	27300
ctgacaagtc	tgtacatccc	ttggcagaaa	tgtggtgctc	atctgggacc	ctgatctgag	27360
gtcactggca	tggtttggct	tgtaactcca	agcttgtcaa	aaggatctga	aaggggctgt	27420
tcctgacaag	attgggattt	aatagggata	aatgttatat	cctgccctgc	agtcccaaac	27480
ctaactgcct	aagtaaggat	taggccacag	cacaagtgga	gaaaggcccc	agggctttca	27540
ttagctgcat	ccttcattgt	agatcactgt	agatgcactt	atttagccaa	aaaaaattta	27600
ctaaatgcct	atcatatgcc	aggaatatgg	agatgagcaa	aagaaaatcc	ttgcctttta	27660
ggggctcatg	atatgtctga	gatctcgtaa	aagtttgtca	tttttgattc	caatattgga	27720
ggtattaatc	ccaaatgggg	gaggtgaggt	cctgctctgt	tattttgtggg	tcatatttcc	27780
ctctgtgatg	tagttctgag	caaccctctg	atgtgtttct	cttaaagaga	ctaagatgga	27840
ggaaatggaa	accagaatct	tcacagagat	tttactaaag	ccacagcttt	attaggaaaa	27900
atcaagtcca	gatcctccaa	agtgacgagc	agatggagaa	ttaccacatg	aggaggggta	27960
gccccggcgc	agtttccctg	aattccaccc	ccatttttct	acttagagca	gctgggttta	28020
atccatcagg	ggagtgggtg	tgttccctca	gtgggcctgt	ttccaggtct	ttcactcagc	28080
aacaacaatc	aacacagaag	acgtctgtga	ccacatgttt	gggggtttct	cccagcacat	28140

caggcaagta	atcaagtctg	cagcagacac	cagctgagtg	cctccgattc	aattcaattc	28200
tggtgctgtc	tacctggaga	tagcatcaga	tcccacaggt	tgaggcattc	ccacaagaat	28260
gcccctcact	ttgtgttcct	ataatgagcc	ccaggttggt	ttactgtgct	ctgagccac	28320
tgctataaaa	tcagggttcc	ccccaccct	tgcttgggtt	tgattaattt	gctagagtg	28380
ctcacagaac	tcagaggaac	actttattac	attttctgct	atggtttaga	tatggtttgt	28440
ttgtctccac	taaaactcct	gttgaagttt	gaaccccagt	gtgggagtg	tgaggaggag	28500
ggcctagtga	gaggtgtttg	ggtcatgaga	gtggatccct	tataaatgga	ttaatgtcct	28560
ttggagaggg	taagtgagtt	ctcacgccac	tctcttggtt	cccctcttgc	catgtgatct	28620
ctgtaccctt	gatccccctt	ccttttctgc	catgagtggg	agcagccaga	ggccccacc	28680
agatacagct	gccccacctt	gaactttcca	gtcaccagaa	tcatgagaca	tataaacctc	28740
ttttctttat	agattcccta	gcctcaggta	ttctgttata	gcaatgctaa	acagaccaag	28800
gcactccctc	accttcacct	tggtgccctc	cagctgaggt	cttaccatag	ctctgtgtac	28860
tactatgaaa	cctatctgtc	tatctatcta	tccatctgtc	tatctattgt	tctattgttc	28920
ctggctcaaa	ataccaatag	cccttggtgt	aacattgggg	cacgttaggc	ctcagaaaac	28980
agaacctctc	tctctttgac	cttctcctgc	cctccttcca	tctgtctcct	tatctctcca	29040
aggtaggatt	tttccctggc	ttttctttct	tggagctggc	agtaacaaaa	ttctctgacc	29100
cacttttctaa	ttgtgagtca	taaaaccccc	atttcagaag	gagtcctgcc	ccaggccctg	29160
ggggaaggaa	tgctgcacag	ggagaccgag	aagaatctga	acagacaggc	cttgtctggc	29220
tttcccactc	agcttattag	tattacatca	tactccattc	aatcatgggtg	gccaaacatg	29280
cctatctaata	gacatctcca	tagaaggccc	aagaggacag	ggttcaggag	cttcaggaga	29340
ggcaaacaca	tggaggttcc	tgagtaggaa	atgtctgagg	ggccatctca	gcttcagaac	29400
tcttctaggg	tcagctaagg	tttggcctgg	cgtatcctgt	cccccgctct	ggccgggtgt	29460
tccattccct	aaatctcttc	actgcatgca	tccccctccc	actaccttca	tgccatcctt	29520
catcgagcac	tacagggcat	tctttctagg	taattggggc	ggctgtggcc	tgggggcatc	29580
ccttgtcctg	catttgctca	tggtcagcac	tcttgtttgc	acacaagagt	agagttagcca	29640
gccccacttg	ggacagggac	ttggggatcc	cagagcactg	ccgcagagtc	ctgtgtgtgg	29700
cctccagctg	gcgttcatgc	tgtgtccac	aaaggggcca	gccaccctcc	accacacaag	29760
acagccttta	cttctgtttt	ccagtggaca	gagctgtctg	acatctgtct	ttgagtataa	29820
tgacaagaca	tgagtcccat	ttacggagca	cccactaagt	gcctggcact	tcacctctgt	29880
catctctgat	tatcacagca	aaccagtgc	acaggtatta	ttatcgcat	tacaaagggg	29940
gagctaaggc	tcagagaagg	cacatttaga	caagtacat	agctatacat	agcagggtctg	30000
agggacagga	ttatcttttag	gtccaggcat	gaaggcctgc	cctacctcca	tgcttcagag	30060
agcacaaact	tgcccccttt	ccatctcatg	ggagccaagt	gtgcctgccc	accagcacca	30120
ctccccatac	gaatacccca	ccaccctcca	ataccgggac	gggtggaattc	cctgcccata	30180
cagcctcagg	cacccttctg	ggtctacatg	aacatcttgc	tgggttccct	cttctgtggt	30240
gtgggctgtg	ctgcgggagg	tgggggtgtc	tgcaaggcgg	gtggacatag	cttggacacc	30300
tatgtgcaag	agccctgaca	tggttagatt	gagctgggag	gaagttagggg	caggggcaaac	30360
gggtcttccc	ctgtacctcc	acattccagc	ctggagctcc	aagagctgag	aattccaacc	30420
ttgaacttta	taatagaact	actacaaagg	tctctttgtc	aaagtaggaa	gacagaacat	30480
gttttattta	acagttgttg	atttgtcacc	tttaaatgtg	tcgaagtgtg	agcagccttg	30540
tctctgact	aaagtttcac	cttctcctga	tgcctactgt	gctgttaggg	cacccttggg	30600
gtgttgggga	agggggacaa	atctagcttc	cctaagtgtg	gaccaagggt	ttcttggggg	30660
ctctggtgca	tgacaccagc	agcgacagcc	tgtagctgag	ctgtgtgtat	caagggaagc	30720
attctgtgga	ttggcacttc	ttgcatatat	caaggtgtgg	ccagaattca	cagttcgagg	30780
aatectgtcc	tcaacaaact	aggtgtcagg	ggagcctctc	tccttcctga	agctcctctt	30840
tgaccacact	acctccacct	cccccgagat	cctcagcagg	tcttggccac	tgaccccttc	30900
actgaaccct	tcctccaggc	tttccagccc	tctacctggg	gtcctcctca	cctgctgggg	30960
gctgctccag	cacatcccac	tctaaacctt	atgaccccg	gcttcccttc	ctgggtactt	31020
ggcatttgca	cagaggcttc	cagagccctt	ctgtaccacg	aagagtttct	ctctaacagt	31080
gggatgggag	gcagtgtggt	tgggccagag	gtgatgggac	taatgctttt	cttactaaat	31140
tcacccaaag	gccactgttc	agagtttctt	tcatggtcga	cagttctttt	tctcatgtgg	31200
ttgtgtgagt	gcgttgacat	gcaaaagtgt	gtgtccattt	tgcatgagta	tgacagggtg	31260
tgcatgtgtg	tggttttttg	tggttttttg	agactccag	gcactgggca	ctgagctcct	31320
catgaggcat	gccctgcctg	tggtttttcca	ggctgcctct	caccagccca	gcacccatgc	31380
agccagggca	ttccaagata	agattctggc	ccttcagttc	tgagactctc	ggaccctgtg	31440
tgaggctggg	tgcatgtggc	actgccacac	atggagatgg	agcaggacca	cacaagtatg	31500
gcagttacaa	gccttgacga	gcagtacttt	ttaggggggt	tgcaacsagc	ctcgggtttc	31560
agagaaccac	tgcatgagctg	tttataaaag	aggcaacttc	agttgacttc	actcatccct	31620
ggagctcctt	cctgactcctt	caacctgaag	agtttacttc	tgcaagagga	gaaggaaact	31680
ctcccagggt	tccttctgca	agagtccttg	ggcaagctag	ctgtcctctt	ttagaataag	31740
gcactggcca	cgggtagctg	gctgtttttt	cattcctact	tagccatttc	accactcttt	31800
ggtcttctta	atctgtttcc	acctgaatga	agctttggct	ggccacatc	aaatgcactc	31860
acagagaaga	gccgcaggca	catgcagacc	catcatcttc	cctccttttc	tcatgttact	31920

gtgcctccca	gccagcagag	gaagaataac	tccaaactgg	gcagtttacc	tatgtgttgg	31980
cagtgtcacc	cagaggttta	gagttgagga	aactggccaa	agtggagatgc	ctgggttaact	32040
ggctgatgct	gcttttcccc	ttccttggcc	atgcagcaga	gtattgagtc	gctgggggca	32100
accacagatg	gcgaggtcgg	agcagcgact	cctagctttt	tccttcccca	cgttcccttg	32160
ggccactgac	ttccatcttc	aggcctatca	aagatttttt	gtttatttgt	ttgttttgtt	32220
ttcttctctc	tttttctctc	tctctaaatt	tttttttttg	agtcagcatc	tcactctgtc	32280
accagggctg	cagggcagtg	gcatgatcat	agctcactga	gcctcaaact	ctgatgccca	32340
ggctgttctt	gagttcctgg	gctcaagtaa	gcctcctgcc	ttggcctccc	taagtgtctg	32400
gactacaggc	atgagccact	gtgcctggcc	ctattaaaca	gtttaataca	gctatctaac	32460
tgcccccttg	cctggctcta	gatcctcaag	gggagtagca	gttggccaca	aggcagagtg	32520
gggctgcgcc	agatccaggt	ttgaagccaa	gcttcatact	tgctagttag	acaagcaact	32580
taacctttct	aagcctcagt	ttcctcatct	gtaaaaggga	ttgtggtaat	tctctctcag	32640
gggtgggttt	aaataaataa	ttatgtaaaa	acttgtgtgc	agcttggcat	ataacaggtg	32700
ctcaacaaac	ggtacttggt	actttcacca	acccactgc	ctacctccat	ctacatcagc	32760
acaccagcac	caccattact	gtcagcaatg	tgcataggga	catgggtcag	gtggcaaacc	32820
agccctttct	atgtgggaga	gggagaaagg	aagagaatga	aaggaagaaa	tgaggaaggg	32880
gagaaatagc	acatggccac	tccagagact	tccagcctgg	agcagtggct	gtagcattgg	32940
gccagcctat	gaccaataga	ccacatggct	tagctggctc	cagatcccc	atttcagaac	33000
aacctaccct	ctgatcctat	tcagactcat	gtccttcac	taggctggaa	tggtccagaa	33060
tctgtggggc	atgttggaaa	cagctctgga	gctcttgagc	caggcagacc	tggaacccaa	33120
tcctagatcc	acaacttatc	agcaggataa	ggctgggtcag	gtcatttaat	ttctccaacc	33180
ctcagtttcc	tcatctgaaa	aatgggtata	gcagttgcta	tgtcagaggg	tttctgggta	33240
gtgtaagtgg	gatcaagccc	aggctctgct	tgatacacag	gagatgttca	tttcccagta	33300
gttttacctt	ttcccccttt	ctgccctgcc	cccccaact	gatccatctt	ctactcacaa	33360
gggactaggt	ctctcagcat	tagggccaac	acttcatgct	tcctacttag	gagaggcacc	33420
ctgagaaaca	agtggagact	gatagtctga	gtagctgagt	gagtttgacc	ctaggtatca	33480
tgtgactttg	ccacagttct	ttgctatctt	gaaaccttag	tttccatata	tgtaaaatgg	33540
aaataataat	gatctttgat	ctttgtgggtg	aggattgaat	gaaagtgtct	ggagctcaga	33600
aggggacgag	caagtgtgag	ctgctgggtat	ccattgttaa	tattgctaata	gttaccattg	33660
ttaaagtatt	tcctgttttc	ttgatgtggg	taggtcagag	agtatttggg	ttccagggtt	33720
acaacacctt	agctaaaggc	cagtggtaac	aggagttagg	atctggcctg	gccacctcca	33780
gctgtgcgtg	gaaaggagct	gggtgtgtgc	tttgggcaca	cttgcaagct	ggggctcata	33840
tgacatgtgt	cccagtgagt	cacctcgcag	agtcagaatc	cactaagcac	atccccgact	33900
gccagggtgt	gtctgagaatt	gtctctgcaa	ctcagacacg	tctaagtcca	ccaggaattc	33960
tcccaggaat	taattgctgc	ctgggtgccc	gggaccccat	caagtttctg	tgatgttctg	34020
gggtgggtgac	ttccctgggc	agagacttga	acctctgccc	ctttgcttca	gccacctgta	34080
acagtgggga	cctagtgggt	cgcaaggccg	gaatgtgaat	ccggcttcca	tcacctacca	34140
gcagcaccaa	aaggagccat	tagactccct	tctctgcccc	tcagtttgcc	ctgggggtac	34200
gtaatgacct	tgactgggtta	ttatgtttgc	aggctgttgt	gaaactctaa	gaagaatcca	34260
gtgagatcat	gcttgggaaa	gcaagccaca	tataccctta	tgtgatagga	tgccagcaaa	34320
attagaaact	ccgtcatgta	aatttaggca	ctgtctcttt	ttctctggtc	tcaattttct	34380
tgctgttaaa	aggaaagggt	tgggttagat	tggcattccc	agagtgatga	ttcataaaag	34440
aaaaagttca	gtgtttaaat	aaatctggta	aaggctacac	ctgtgatccc	cctcctggca	34500
catcacagca	tgcaacttggt	tatcaaaggc	taggagaagc	ctgcaagaag	caaacctatt	34560
ttgctttgct	taacctagat	tttactaatt	tgaccacaga	acctcactat	tatggttatg	34620
attattacta	ccacaaatat	tcttactctt	atgataatta	gwattgattg	ctgcgcgtcg	34680
cctttggaaa	cagccagctg	agcagacgcc	caggatcttt	gcagctcttg	cagacacgga	34740
tccaagactg	ggaggggcag	gggtctgtca	ggtcacactc	tgccccctgtg	tcctccaggt	34800
gccttcttga	tcccgtagac	actgttcctt	atcatcgcg	ggatgcccc	gttctacatg	34860
gagctggctc	tgggacagta	caaccgggag	ggggctgcca	ccgtttggaa	aatctgccc	34920
ttcttcaaag	gtaaagaagg	gggtgggaga	agtcacgggt	gttcataaag	gcttccctgt	34980
tgcccttggg	gaatctgtct	cagtgggtgag	atctaaggta	gacctcctgt	catgtgggat	35040
tcacaggtgt	tgacaaggct	aacagtgtcc	ccatttccaa	gttacgtgga	gagcattcag	35100
tgtgttggga	atgacattag	catagaaatt	ctggaaacct	gggttctaata	ccagcttacc	35160
tgctgagtac	ccagagaatc	tatttctctg	atgggaaatt	tttacgtaag	tatcagaagt	35220
accagcacca	tacaccacta	ctctctcctt	ttgctcccat	ggcaggcggt	agaagttagat	35280
catggatctt	tttgagccca	gccggaaagc	tgattcaaaa	tccttagtac	aatagccaca	35340
actagttgat	tgacgtgaa	atacaacatg	aagcctactt	gcatttggga	ctaagaacac	35400
atctgcagaa	agtaggcaga	gcaactgcta	tttcttggcc	cctatacagc	tgggagaagg	35460
gcatggagga	agagttagtc	tctcccaagc	actgggttga	gaactgggca	cagatggcaa	35520
cgagggccag	tgtgactccc	atgagcctct	tctccgctgg	cacgtgcctc	ctgagtacct	35580
cttgtgtact	cagtccctgtg	ggagatacag	ctgggtgcaag	agtcttataa	gacatgtgca	35640
ttcgttactt	tttttgttgt	taattgtcag	aaattcaact	caaactggct	tcagtataaa	35700

agagaattga	cttctgttac	agtaaagtcc	ggggattggc	ttcaggtata	gatagatcca	35760
gatgcccaca	taatgatgtc	tggaatctat	cgctcttctt	gtgtttcaga	tctgttggtt	35820
tctgttagca	tcagtctcag	gtaaattctt	ctcaagtacc	tgcaaagatg	gcatcagca	35880
accocaggct	taaattttac	caagttttaa	ttttaccaaa	agcaaacaag	taaacaaa	35940
aaaaccctta	tagagtcata	gtttccttaa	aggctccaga	gaagattctc	attgggttaa	36000
cttgagtcac	atgcccacac	actaaccaat	cactgtggct	gtcaggaagc	agtgtcttga	36060
ttggccaggc	atacatcttg	cgatggaggga	agagtgggga	gtagcctcgc	caacacctca	36120
caggctaate	atagcttaag	gctaattcct	tgaaaagcaa	tggtgggcag	gtaaacaata	36180
catctaccct	agaaaaaagc	tatagaacta	cccctaaagg	agcttgtgat	acattgagga	36240
acacgatact	ggcaccggaa	gcaggtggct	gagagtagga	cccagaaagc	acacagggct	36300
gaagttccaa	tcagggagtg	cttgcttggt	tttccccaga	agcagttcgg	agacaaggat	36360
ataagtgtaa	agagtttagt	cggaagtgga	tccttaggga	gcagcaactg	gggataggga	36420
aggggaggga	gccataaagg	gtgtgcacca	agtcaatgcc	actctgggca	gggagctcag	36480
tcccatcagg	ggagaatgtg	aacacctgtc	agtgttatcc	tgcccagggg	gcgaggagag	36540
tggatactca	cgatccagct	cctaaccgtg	ctgcccactg	ggggcaagca	gggtggtgag	36600
gggcagggga	gctccagtg	aaagagagag	ctctcgggca	aagagatggc	aggggcctat	36660
ggactctggc	aatctgctat	agcacgtttc	ctcaatcccc	gggccacgga	ccaataaccg	36720
gcctgttagg	aaccgggcca	cacagcagga	ggtgagcagc	gggtaagtga	agcttcatct	36780
gtattttacag	ctgctcccca	tcgctcgcat	gaccgcctga	gctccgcctc	ctgtcagatc	36840
agccgctgca	ctagattctc	ataggagcgc	aaccctact	gtgaactgcg	catgagagg	36900
atctaggttg	tgtgtctcct	atgagaatct	aactaacgcc	tgatgacctg	aggtggaacg	36960
gtttcatctt	gaaactaccc	ccaccccaaa	atctgtggaa	aaattgtctt	ccatgagaca	37020
ggtcactggt	gctgaaaagg	ttggggaccg	ctgttctgca	ggaaacgaga	gacagaggga	37080
atgggagtg	agtgtgtgag	ccacacccaa	ggagaggtgg	ctgtggggct	gggcctggga	37140
gactcctacc	ttaccccttg	tccctgcccc	ggcgttggt	atgctgtcat	cctgatcgcc	37200
ctgtacgttg	gcttctacta	caacgtcatc	atgcctgggt	cactctacta	cctcttctcc	37260
tccttcaccc	tcaacctgcc	ctggaccgac	tgtggccaca	cctggaacag	ccccactgt	37320
accgacccca	agctcctcaa	tggtccgtg	cttggaacc	acaccaagta	ctccaagtac	37380
aagttcacgc	cggcagccga	gttttatgag	taagtacacag	acccttgtg	ctgggcctgt	37440
tgaggccagt	gcttggtatg	acctgagcca	aacactaagg	aaagtcacag	accaaggaga	37500
cgcagccgt	caggatatta	atgtttactg	agcagccact	ggcctgatgc	tggtgagag	37560
gctgagggca	cgccacggtc	gaggtagttg	gagaagcttg	cgctctgggg	cagggaagtg	37620
gaggcgggca	agataatata	caaataaaca	ggtaagggag	tgagaatgtt	ttagagtgtg	37680
tgmmttcag	ggaatgcaac	actttctggg	gtatgttaact	gctcttaaa	aaactgaaac	37740
aggtatgtgg	gaaaaatcaa	tcattggagg	aaaagaacgg	ttgcgtgggt	agtcaggaaa	37800
ggcctctctg	aggaggtgac	ataggaactg	atgatgtcag	agaagggaag	agctggggct	37860
ccagggcagg	cgatgagctg	caggttgaac	ccgagttgat	ttgacctga	agctgtagtc	37920
tgactcacc	tggtgtgctg	tccttctgga	gttcccatgg	gggaacataa	tcagagcttg	37980
gagaaaatc	aagaagcggg	aagcaggcca	gctgtatgca	gctctgagaa	attatttgga	38040
ccatgtgtgc	acgagaagca	ctggccattg	gtgcaagaca	gaatatcatt	taaaaaaaga	38100
aacttttatg	ttgaaatacc	gttatacatt	aaaagtagta	aaaatagtgc	atatacccat	38160
caccagttt	cccctaattg	tgacaactta	cataaccatg	gtctgagttt	gaaacccgaa	38220
aattaacatt	gatacactgt	tagctaacaa	gctgcagacc	ttacttgaat	ttaccacatt	38280
ttcccaactca	tgttcttttc	aggtatttag	ttgccatgtt	tctttaatct	tctccaatct	38340
ttgtcttcc	ttgattttca	tgacctgac	acttgaaaag	tacggtcagt	tactttgtga	38400
aatattgatt	tgagtttggt	tgtgttttc	tcataattaa	actgtggtta	tgcattttgg	38460
cgtgattacc	ctaggaatga	tgctgtgccc	tcctcagtgc	attccatcag	ggggtgggga	38520
gacatgctgt	caatatcttg	ttacttgtga	tgttaacctt	gcacacttgg	ttaagggtga	38580
gactgccagc	ctcctcctgt	gtagagagag	ttattttcct	tttttaagta	atgtgtcttt	38640
taaggacata	cactgaattt	atgcaaagt	cttgattctc	atcatacttt	tgtccacatt	38700
tcttagcatt	tgttgatgat	tcttgcaagt	aaggactatt	accatgatgt	ttatctagtt	38760
ataatttctc	atttccatca	ttcttctat	tttattttat	tttttggtt	tttgagacag	38820
agtcctgggc	tgttgccac	gctggagtc	agtgccacca	tctcagctca	ctgcaacctc	38880
cacttcccac	atttaagtga	ttctcctgcc	tcagcctcct	gagtagccgg	gattacaagt	38940
gtgcaccacc	atgctggct	aatttttgta	tttttaatag	agatgggggt	tcaccatgtt	39000
ggccaggctg	gtctcaaact	cctggcctca	ggtgatecac	ccattttggc	ctcccaaagt	39060
gctgggatta	caggcgtgag	ccaccacccc	agcttatcat	tccttctaga	ttaattggaa	39120
ttcttcttta	aggaagaatt	gtcccttctc	ccctgtttat	ttattttttc	agttattcat	39180
ttatatcagt	atgggtcct	ggatatttat	tttattccgt	agtcttaatt	cataactatt	39240
attgttggtg	ttattattat	tattttattc	aactttcatt	ttagatttgg	gggtacacaa	39300
gtaggttggt	acatgggtac	attgcatgat	gctgaggttt	ggggtgtgat	tgaacctgcc	39360
accaggttaa	tgagcatagt	acccaatagg	tactttttcg	actcttgtec	ccctccctcc	39420
ctcactcctc	actcttggtg	tccccattgt	ctactgttcc	tttctttatg	tccatgtgta	39480

ctcaatattt	agcttccact	tataagtaag	aacatgcagt	atttggtttt	ctgttccctgg	39540
attaattttac	ttaggataat	ggcctccagc	tacatccatg	tccctgcaaa	ggacatgatt	39600
ttgtccctttt	tgtggctgca	tattattcca	tggtacatat	gtaccacatt	ttctttttct	39660
ttttttgtttt	ttttttgaga	ccgagtcctc	ctctgtcact	caggctggag	tgcagtgggtg	39720
tgatctcggc	tcactgcaac	ctctgtgtcc	caggttcaag	tgattctcct	gcctcagcct	39780
cctgagtagc	tggtgattaca	ggcaccaccc	acaacgcctg	gctaattttt	gaatttttag	39840
tagagacagg	gtttcaccat	gttggttagg	ctggtctcaa	actcctgacc	tcagggtgatc	39900
cacctgcctt	ggcctcccaa	agtgtctggga	ttacaggcat	gagccattgc	acccggccac	39960
cacatttttct	ttatccaatc	catcattgat	gggcacctag	gttgatgaca	tgtctttgct	40020
attttgagta	gggctgcaat	gaacatccac	gcgcagggtg	ctttttggta	gaatgattca	40080
tcttcccttg	ggtagatgcc	cagtagtggg	attgctgggt	cgaatgggtg	ttctattttt	40140
agttcttaga	gaaatctcca	aactgctttc	cacattgggt	taactaattt	acattcccac	40200
caacagtgtg	taagcattcc	cttttctcgg	cagccttgcc	agcatctgtt	atttttttga	40260
ttttttaaat	aatagccatt	ctgttgggtg	tgagcttata	accatcatta	tttaatttgt	40320
ggcttccctg	aatcctctca	gcctctactt	catccattta	tgtccttgag	gagggcgatg	40380
actgacttgt	tttcagccac	ctgatttaaa	atgtttgcat	agcactctgt	tcacaatgta	40440
gcatccattg	tcttcatccc	tcaggcgtgg	gtcaattcca	ttttatcaat	ccctacacaa	40500
acatgctagc	aggtaagcag	aaagtacctg	atacaacttg	tggggcagac	aggatagatt	40560
ccaccagaac	tccaccctca	gggcattcat	ggtctagagc	agagggtccc	aaacttttct	40620
gcttaagatc	atagagtaaa	tattgcagaa	tttgaggcc	acatatgttc	ctggtgcatg	40680
ttctttgttt	tattttacct	ctggaaagta	aaaccattct	tagctcacag	gtcgtacctt	40740
aacagtccat	agctcagatt	tggcctgggg	gccgtgggtg	gctgattcct	ggcctagtgc	40800
aagatttccc	aataaaaactt	cccgccatga	tagaaatggt	ctatatctgt	gcaatccacc	40860
agatgaccca	cttgccacag	gtgggttaccg	agcagttgaa	atgtggctag	tgtgactgat	40920
gagatatatt	tctaatttaa	ttttaattta	tttaccctta	aatagacatg	tgtggccagt	40980
tgctactgta	ttgggcagtg	caaaaaagtg	tggaaaaaaa	aaacatattc	acaaacaaca	41040
aaacttttagg	gtcctctctc	ttcagtccta	tggattcccc	aagcccagaa	cctgggaatg	41100
agtccagatt	atctggagat	tggggttatc	ctgggaccaa	ctctttccct	gccatcttgg	41160
tgcagcaggg	ccagggggat	ttagtttggg	tgaagagagc	ctctggaaag	tctactgcct	41220
cctggggctc	aggggagtc	gtgttctcag	gatccaggaa	ataccctcaa	tggttccactg	41280
cagagaattt	gctaagggtc	ctgtacctgc	atccacctgt	ctccatccat	gattcccatg	41340
gacttctaac	aggcatatgt	aaaaattatg	tgttttagaa	tttttcttgg	agagggtctg	41400
cagttgtcgt	caaattctca	aatacctctg	cagccctccc	agaggatctg	aatcactgct	41460
gtcactgaac	atcagcatct	gctgtaagaa	acctgtcttc	ctcaccatca	cattaatagc	41520
taacctctta	ccatgtgtat	gaggttttct	gctaacttcc	tcctatgtat	tattttgatt	41580
taagcctcac	ccacctaatg	aggtttttgt	aactcttatc	ctcatcacac	tcttggggag	41640
gcttcatttc	acagttgaga	caatacagtc	cacaaccaca	caactattac	tgcacagagc	41700
caagatttgg	accagccag	tgtgcatttg	caaaaccctg	agagtgcgca	tctcccatth	41760
tgcaccgtag	gagcttactt	ctcctcactc	taaccccagc	cctgtctggc	agggaaactt	41820
cacagcatgc	acccttaacc	tctgtgttat	gttggcctct	acccattata	catgtttgtt	41880
attatgcaga	aatattgtca	tggtcacaca	tcacatttac	ccagcttgga	ttgtattcca	41940
gccatagttc	aaagcaccct	ttctatacta	cattttaatc	ctgaccactg	tggtataaga	42000
ttatttttat	gaatgggaaa	acaggcacaa	atcagtaagt	gacttgtctg	aggtcataga	42060
gtttataagt	ggcattaaaa	gtctatttgg	atccaggcag	tctatctcca	aagcccaagc	42120
tcttagccca	gggttcaaaa	ccttgactgc	acatcagaat	cacctggaga	cagtggaatg	42180
ctggattcta	catccagaga	ttctgatttc	attggtccgg	gtacaaccag	ggcatagaaa	42240
tttccatcag	tagtccccc	tgcaattcta	acatccagcc	aacgttgga	gcccttgttt	42300
acacactgcg	ctcttctgtc	ttggagtagg	actcctactg	gaatcaggct	gacatctcta	42360
tagactcatg	tcatggaaaa	tctagggcct	ccttcactct	tctgaggagg	agtatggcct	42420
cagaaaattc	ccgaaccatc	agagagcttg	cagggtgggg	ttttaggcct	ttctgtctta	42480
tgaacatggt	ttggagggga	aggtggtaaa	gatagtggag	cagagtgtctg	ccgacacatg	42540
tgatttgggtg	caccctctcc	ccctcatcct	cccataaagg	aaaaagcatg	atttttcttt	42600
ttgctctcgg	caacccttgt	tttacaattt	aaaattggga	atgatagctt	tgcctctagt	42660
ccagttagca	tttgattcct	ccgctgatgt	cttcattggc	agtatgtcgg	ccccagcaga	42720
ggccccagca	gagacacca	gccagaggga	gaggtgagat	aggttttgag	accctactta	42780
ctttaattac	agccctaagc	ttcctccagg	ctcagctata	aggagagtgg	tgggaaaaga	42840
tggtcatcttc	aggctgaaat	gggtggggga	tgcaggtaga	actgaatgca	gagttgtttt	42900
ttgtttgttt	gtttgtttgt	ttgttttaaa	aaagacgggg	tcttgctctg	tcacccagtg	42960
gcacagtctc	ggctcaatgc	agccttgacc	tcccaggctc	aagtaatcct	cccacctcag	43020
catcccaagt	agctgggact	ataagcatgt	accaccacgc	ctggctagct	ttttatattt	43080
ttttagagaga	tggtgtttca	tcatgtttca	caggctgggtc	ttgaactcct	gggtcagggt	43140
gatccacca	cctccatctc	ccaaagtgat	gggtattacag	gtgtgagcca	cctcaccg	43200
cctacagggc	ttatttttagg	agccttctgc	cctacagatc	ttccctcttt	tttctctctc	43260



cttaaccttc	cctccactaa	ccatgcaaac	cttcattgct	accatcagcc	aagcactgag	43320
gatctcctca	catccaaatc	ccatttaatc	ttcacagttc	atggaggtag	aaattattcc	43380
cattttacag	ataagagagt	gtaggctccg	gttttaggta	agtggcagag	ctgggagtg	43440
aggggcctct	gcaagtagat	aggagtctct	ctcatgctgc	ccttgccctt	tctggcctgg	43500
agcctgcctc	tgtgctttgt	aatgcacagc	actgtcatca	gctgcctctg	gacttttttt	43560
tttaatggcg	tgatgccctt	ttgtctaaat	gtttctgctt	gaaaaacatc	ccctcaactc	43620
agtttgggga	cccagtgagt	gggactccta	gtgccaaccc	tgaggaaata	gaaaattttt	43680
tctctttctg	ccaacctgct	ggccaatttt	gttaccatcc	tgtactcatt	taggctgatg	43740
gactgagcat	atcattcaag	ggaacaaaac	tgctattctc	cccaggctcc	aggcctgaag	43800
ccaagcagcc	coacagctaa	aagaaactct	gcagctctgt	aactttatgt	gtaaaaggcc	43860
acctttgggtg	aacatgtgcc	tggcaataga	aaacttccac	cccatgccgg	tccttggtga	43920
ggaagaaaaa	tctccctcca	gcctagtatt	aatcatctgt	gctaaatatc	aagtgagaaa	43980
ttgagctttt	ttagtgtgta	gacttcggaa	agcctggaca	gtacacttaa	cgatgattca	44040
ttttcattaa	acttctggaa	aactaaaact	gacgtaaagt	tcttgtaacta	aaccccaagg	44100
tttgggcctg	ctggggggaag	gaggctgcat	tctcattgat	tttcttgggt	gtaagcttgg	44160
gagtcagat	cttttactg	atgaaatacc	tagacaacct	ctacaacct	gaaagtggac	44220
tttgaatgca	tgggacatca	gctgggcctg	ttggggggca	tttcaaccat	gagattggac	44280
accagaggca	ttttggcaag	tttcagggca	aggatgattg	gttccatgcc	tttttattcc	44340
cattatttgg	atagtcaagt	caaccaaagt	acaattgaca	caattcaaca	cctgtcccat	44400
aaaggcacag	gaagaagcgg	aattaagcat	cagatagggt	cagtacatgc	ctctggtttt	44460
cttttttctt	tttctttttt	tttttttgag	gcagattctc	actctgtcac	ccaggctgga	44520
gggcaatggc	tcaatcttgg	ctattgcaat	ctccacctcc	caggttcaag	tgattctcct	44580
gcctcagcct	cccaagtagc	tgggactaca	gggtgtgtgc	accacacca	gctaattttt	44640
gtatttttag	cagagaggcg	gtttcaccat	cttgaccaga	ctgatgtgga	actcctgata	44700
tcaagtgatc	caccgcctt	ggcctcccaa	catgctggga	ttgaaggcgt	gagccaccac	44760
accagcctg	gtcctctgtc	tttttaata	tgcgtacgcc	ctgccacct	ttcctcttct	44820
ttttctctct	ctcttaggac	atagcagagg	gggtctaagtc	aggggattgt	tttgagttag	44880
gactaacagg	atgagaagtt	agccaggcag	acaaattgag	ctcggacgtg	tggtctggct	44940
gaaggaacag	aaggtcccaa	ggcccagagc	catggatgca	ccctataact	ggggactgac	45000
aagtagcttg	ctgctgctgg	ggtgaaaggc	aggggtgtggc	aaggccaggg	atgaacttgg	45060
cacgggatgg	actgtggaag	gcctcagatt	ctgagagact	ttcattgtta	tcctccggac	45120
ctcgatgctt	tcgacttttt	cggttgatg	attctttgtt	gggggacagg	ggtgcacact	45180
gtcttgtgta	tctgtgatgt	ttagcagcta	gcagcatccc	tggcctctac	ccctagata	45240
ccagcagcat	ctccctcctc	tccagatgta	acaacaaaaa	atatctctct	agacatgcca	45300
aatgcctctg	gatggcaggg	gcaaagttgc	ctccagttag	aaccactgtt	ttaggtgcta	45360
agaagcctct	gaggcttttg	aggcaggaga	gtggcaagggt	tagaacagca	ctttggatgg	45420
atggttctgc	agtggcacag	acagtggatt	taagggggct	gacaggaggc	agagagactg	45480
ggtttgggag	aggggtgggag	tcattttacaa	tagctctgga	aggacagtgt	attagtcagg	45540
gttctctaga	gggacagact	aatgatatag	atctcatatg	agtttattaa	ggagtatcga	45600
ctcacacgat	aacaaagtga	tgtccacaaa	taggctgtct	gcaagctgag	gagcaaggaa	45660
gccagtccaa	gtcccaaagc	tgaagaactt	ggaatccgat	gttcgagggt	agcaagcatc	45720
cagcatggga	gtaagatgca	ggccagaaga	ctaaaccagt	ctagtctttc	catgttcttc	45780
tgccctgctt	tgttctggct	tcactggcag	ctgactagat	ggtgcccacc	cagactaggc	45840
gtgggcctgc	ctttccgagt	tcactgactt	aaatgttaat	ctcctttggc	aacacactcc	45900
cagacacacc	caggaacagt	actttgcata	cttcaatcca	atcaagttga	cactcaatat	45960
taaccatcac	agacagaatg	tgggtctggc	ctgggatgtg	gacagtgggg	gtgggggtag	46020
agggagcaac	caagagacag	gattagcggg	gaccagacat	ggcaactgat	tgcatgggga	46080
agatgatgca	gggtgagagt	ttaaggccac	aacagctggc	ctgggagctg	cagggatggg	46140
agccattctg	gggagggggc	attggtctgg	gtagaccttg	atgacccacc	caactctgct	46200
cattcattca	cgcatgctca	catccctctt	ccccattgct	ccctccctta	cacctgtgca	46260
cctcctgtca	gctttctggc	cagcagagaa	ggcacctgcc	accttcacag	cggagtctcc	46320
ccagcgcacc	ccctctactg	agttttcttg	gtacccttga	ctctcttgct	gacacctgct	46380
gcctcctgaa	gcctaggact	caaacataat	gatcattata	attaccattt	attgagcatt	46440
tcctgggtat	tattatctga	tattctgtaa	ctcagccctc	atcacagccc	tttcatgtaa	46500
aagagaaaga	ctcagtgatg	ggaaatgctt	acacgcacta	ctgtccctt	gcctgtgatc	46560
cccagggggc	tggagccatc	acctgcttct	ccacagccat	gccaccagcc	cccggcacac	46620
tgccctggctc	agagcagagg	tgacagagaa	gtttgtggaa	tcgatgaaag	gattcgggtc	46680
acacaggatc	tgggtggaag	ggctaggatg	ggaagccagg	tctgtctgac	cccagagctc	46740
agacaatttc	tgtgccacat	ttttctgttt	tccttcatat	tctttcaaat	aacatacatc	46800
tatttttgagt	ggataaatga	tgaagagagt	aatgaaacag	catcgctggt	ggtcttcagc	46860
ctttctttca	cctgcctgga	aacaaatttt	aattcctacc	caagggtaag	ctaagtaagt	46920
ttccagactc	agggatatatg	ttttccttac	aagcctggaa	tcttctgca	tcattcggga	46980
tgattccagc	aagggtgctc	atctgcctct	ggcagacaga	caattgatct	tatccctgac	47040

aggtgtgtac	aatgttgcca	ttaatgtgtg	ttttggaatt	aaagccacct	tccaggggaag	47100
gacgatatat	taagctgttt	gcctttaaca	ctttagtgtg	aatttgtttt	gttttgtttt	47160
gtttttgaga	tggagtctcg	ctctgttgcc	caggctggag	tgcagtgaca	agatctccgc	47220
tcactgcaat	ctccatctcc	caggttcaag	caattctcat	gcttcagtct	cccaagtagc	47280
tgggattaca	ggcatgcact	accacaccca	gctaattttt	gtatttttag	tagagacagg	47340
gtttcgccat	gttgaccagg	ccggtctcga	actcctgacc	tcaggtgatc	cgctgcctt	47400
ggcctcccaa	agtgtggaa	ttataggcat	gagccaccat	gcctggctat	ataagtctat	47460
taagcagctg	ctttctgaat	ggacctctag	ttgagcgcaa	atgcctatag	aatgagacag	47520
ggaagtttcc	gtatgggaaa	atgtgtgggtg	ccctgggcag	tatgaaagat	ctggggcaaaa	47580
gggttagaaa	tttgccacaa	gtgatgggag	gagttgctaa	gagaaagatt	gagagtgtgt	47640
gggaaactga	ccctctttcc	ttactcgttc	tccttggggg	gatcctggga	tctcattttc	47700
tatagttaga	gggattgttg	ggttttagcaa	gaaaggctgg	gagcatttat	ctgtttctaa	47760
tcctatgatc	tctcatgagc	taacaggtct	aactgccagt	tctgggctta	gcactgggga	47820
ccaggaatgg	ttaattcacc	tcctcatcct	gggagaccct	tgtatacagt	tagccctgac	47880
cttgagaaa	caggcaggct	ctccttgcaa	ctgagtcaag	agccacagga	actggaagag	47940
ttgaaagatg	cctatcaagg	atgattgggg	ggcctcccag	gagaggtgac	actggatctg	48000
ggccttgaag	ggtgttgggc	aatgtgcagc	tgactgttgc	ctctgagtgt	gaggcacaga	48060
gaagaaacca	gtgggatctc	gttttggggg	cccttgacgc	tcccttgaaac	ctcccaacat	48120
gtgtcatgct	ttattgtgaa	tttgctgcca	gtgttgccctc	ccatgctacg	atacaagccc	48180
accaaggcag	agtcaggacg	gtgcacgagc	agttcctgtg	tgtgtccgag	gccagatggg	48240
gctggctcac	agccggcctt	cagtgcacaa	tgaacgatta	gggtgcagag	caaataccac	48300
accaagttgt	tcccatttct	gcttgctttg	ccttgcaagg	gtgcagagtg	gtcagggaaa	48360
cccttctctc	ctgggacttg	ctgtactgtt	tcagcagtc	gtcttacttg	acctttcctt	48420
agctcctaac	caactttgat	tagattctca	ttagcaaacg	gtcattttgt	tttcaattct	48480
ctttatcatt	tcttcattgt	agattgtaca	agggacccca	atattctcag	accaccttgg	48540
attgttttgt	tttcttactt	ataaaaaacc	aggcctggcg	cagtggctca	tgccgtgaat	48600
cccagcactt	tgggaggcca	aggcaggtgg	atagcctgag	gtcaggagt	caagaccagc	48660
ctggcgaaaca	tggtgaaaca	ctatctctac	taaaaataca	aaaatttagc	cgagtatgat	48720
ggtgggcttc	tgtaatccca	ggtattcagg	aggctgaggt	atgagaatca	cttgaacttg	48780
ggaggcggag	gttgacgtga	gccgtcatcg	caccattgca	ctccagcctg	ggcaacagta	48840
gtgaaactcc	gtctcaaaaca	aacaaacaaa	caaacaaacg	aaacaaaaca	aaacaaaaga	48900
aaaaaaaccc	aaacacttta	ttgatagcta	acatattaca	aaggagtgc	tatcatcaag	48960
cgacaactca	gcaaatgtta	cccgttgaaac	gcacccagta	acctcaccca	gctcaggaaa	49020
gagcatgatg	aatgtcctga	agtcctcatc	atgtcctctc	ctagtcagta	acccccctcaa	49080
ccccatccca	gggtacacct	ctcctgactt	ctaatecttt	aggctcagtt	tgccgtgtgt	49140
tgaattttat	atgactggag	tcagacggaa	gtgctcttct	ggctttgact	tctttctctc	49200
agcagtgtgt	gctagagcca	tcctcttgga	ggtaattgct	gtataatact	cttactaggc	49260
caggtgtggt	ggctcacacc	tataatctca	gcactttgag	aggctggagc	agttggatca	49320
cttgagccca	ggagttcaag	aacagtctgg	gcaacatggc	aaaaccagct	ctctacacaa	49380
agaatacaaa	aattagccag	gcatgggtgat	gtatacctat	attcccagct	acttgggagg	49440
ctgaggtggg	aggaccacct	gagcctgggg	aggctgagtc	ttcggtgagc	cgtgatgggtg	49500
ccactgcact	ccagcctggg	caacagagtg	agagcctgtc	tcaaaaaaaa	aaaaaaaac	49560
aacaacaaca	aaactccact	ttataaatat	atcctaattt	atccattcca	ctgttgatgg	49620
atgtttgagt	actttgcgat	ttgggggttat	tatgaaataa	tgctgccata	aacattctag	49680
agcatgtctt	ttggtgaaca	tgtgtacaat	attctattga	gtcaatacct	agggcacagg	49740
ataagcctat	cttcagcttt	agtagctatt	ccccaatagg	agaaatgttc	acttttgtct	49800
cagtctctag	accaggtatt	ctcagattca	gcaatatgga	ccttttgggc	aggatcattt	49860
tttgttattg	gagactgtcc	tgtacattgc	agtatgttta	gcagcaccca	tagtctctat	49920
gccagtagca	ccacctctcc	tcaagtcagt	acaatcaaaa	acatctcaga	tatttgccaaa	49980
tatcctccgg	ggtgggggtc	agggacaaaa	cagtcttccc	tctgtctgag	aactgctctt	50040
tatagtgtga	gttctgtgag	gacagaaacc	ttccctattt	attactccaa	ggccaggcga	50100
gcaataggca	cttaagagat	ttttgtcttt	taaaagcagc	catgagcgtg	gaatctcccc	50160
agatgatttg	cctcttctag	gacagagtgg	tcctgggcac	aggccatggc	tgaccagggtc	50220
gggcccattg	ggtgcattgg	agtggctagg	gtccctgagt	taggggagag	tggccagggtc	50280
ctgtctccat	cagcatgcac	ttgcagggac	tggtctgtgg	tcacggcctc	tgctcgtcctc	50340
cctgaogaca	tttaccctgg	tcctctcccc	tctcctctgg	gcaggcgtgg	tgctcgtcac	50400
cttcacgaga	gcagcgggat	tcacgacatc	ggcctgcccc	agtgccagct	cttgcctcgt	50460
ctgactctcg	tcgtcatcgt	cttgtatttt	agcctctgga	aaggggtgaa	gacatcagga	50520
aaggtaatat	ctctgtgttt	ctctttcact	tacttggrtg	atcaaccttg	gggggtgtga	50580
ttattttctag	caataattat	gtagctgggtg	gacaaaaaag	atggagctgg	aagtgcaggg	50640
cctgggttca	agccccctgtt	ctgccactga	cttggacaaa	tccttccctt	tcctttcctt	50700
tccttcccc	aaatctgtgt	ctccaccaca	ataggttgaa	gggggtataag	tggatcagag	50760
ttcctcatat	tttcttgcca	aaacctccct	aatagcagag	accagggact	gggatactgc	50820



caagggcctc	acgacaaaagt	ctagagatac	tatcaacatg	cccttgataa	atcttgaatc	50880
ttgacctaaa	tcttcatgca	aatgttgcac	cctactctgg	aatatgacca	taaaatcaat	50940
aaatccccc	tctgaatttt	tgagaaaaaa	ggatgctcta	gaagatattc	agatgtatgc	51000
tggattttgt	gtttcctcgg	atacagaaat	aagtgcctcc	agggttccag	gtgccttgga	51060
gagaagagca	taggtttaga	tgacccatga	gggccagtc	ggagttggca	ttctgaactt	51120
gggtgacact	gtctcctat	agtcagcctc	tcattgggtg	gaatattcag	gaaatggctc	51180
ctgttgattt	ttagcccaag	gaacatcatg	ggaacaacaa	ccccatttgg	actctacagg	51240
gtctatttag	aagcttgact	attaaagagg	atatggatgg	gaaattttct	ttccagtgtt	51300
gtggtagaact	aatgtctgtc	aacaaaccac	cccaaatgt	agtgaactcaa	aataacaacc	51360
atatttattgt	ctctcacaat	tctatgggtt	gattgggac	agctgggtgg	ttcttctgct	51420
ccatgtgata	ttccctggac	tacatggctt	cactgggctg	gaatattcta	gatgggtgat	51480
acacattgct	agcatttggc	actagctggg	agctaagttg	gagctgcaa	ccagagcatc	51540
ttgggatgtt	tccatatagc	ctttctatgg	tgcttgggct	tctcacagca	tgccggctga	51600
gttccaagaa	catgtcccaa	gcagacaagc	cccagtgatg	tacaagtagc	tcttccagtc	51660
actgcttgca	tatttcttgc	tattgtccca	gtggccaaaa	caagtgttga	ggtaaaaccc	51720
accgtccata	tgggagggga	ttacacacag	gtgtgagttc	attggggggc	acagcgcaac	51780
agtctacctt	aatcaggtgg	gtgtcaattt	gggagaatcc	tcattaggca	actgattttg	51840
gaaagggggg	gtgcaccaga	gttctctctg	atactcttag	agttcttggg	catgccattg	51900
agagcaaaga	aagtagcagg	ggagcagcag	ccagtagaga	tgaaatccat	caagaactgg	51960
agagagaact	tcctatcagc	atgttggggg	cacagtgtct	accctaagaa	agcactcaaa	52020
caaatgcag	accagggcct	ggagaaagtc	tagcgttgag	caaaaccagg	ataggaccac	52080
taacattctg	atgcctggca	cctagtaggt	cttcagtaaa	tatttattgg	gtaattgaag	52140
gatgggtggg	tatataagtt	tggggaactt	cattaagtat	tcttttgaat	ttagttcaaa	52200
atatcaacat	aggagacctt	ctgtgtacca	ggcttgatgc	taatactagt	gatgcaagaa	52260
taagacaggt	tccttcttca	attgcttttag	tctatgtgta	ttacaggcag	ggtatggatc	52320
aaccaatgtc	actagcttct	tgggtctcta	tccagagaac	atatgtgtgt	gtcctcattt	52380
aataaaaacc	tgtggtcaca	aactatgtgc	actattatat	atcttgctat	tttttaattc	52440
taactttacc	tgaagtcaa	tttcacatcc	agtagtcgaa	ttacatttca	atagaataac	52500
aaactgtggg	tttcaaaact	gtaattaaat	cagcttaatg	ggctatcaca	tacacttttc	52560
aaaaatgaaa	aagtctagat	aataagagtt	cattgcacaa	gtaaagtaag	agctgtttct	52620
tgggattttt	gtttcagtta	cagcaatctc	taagtttatg	tgtagtttgt	cttgatattg	52680
aaggcatttc	ttagcctgag	ttgtgggtcaa	aaagtgtgag	atgctgcatt	agtggagaaa	52740
ggaagctctt	tcaactgaaa	gtgtctccaa	agaccataga	gaaggtggca	ttcgagctgg	52800
gtctacaaa	tcaggtgcag	gtagaggtgg	gggtggaagga	agggtattct	agcagaagga	52860
actacatgag	caaaactgta	gagatgtgga	agccccaggc	cagccttgct	tagcactctc	52920
tgtgcctttc	ctgggtacca	ggagcagagt	tctcctggcc	tctgcaggca	cagacagaga	52980
ccctgagggg	agacagggct	caaccctgtg	aattgcagaa	gatatatgag	ctttatactg	53040
cttctggcct	tggcatagga	ccaccacaaa	cttctaacat	tgaccccaa	gattgggttc	53100
cccaatgccca	tcaccaaaga	gggtagagcc	tgccccgtct	agtttagctt	ctgagtagag	53160
tggagtatat	gttgtctgca	ggcaggctga	tgcaaaagag	actgggagga	gtaaggctga	53220
gcatgctcag	ttctttccaa	aatacacctt	cagagaaggt	aatgaggggc	gaaccagagt	53280
gttacactag	gaaagcccc	atgtagaac	acaatgagag	aggaatatga	gtccctctg	53340
catgtgtcat	ccgaaaccac	agccacatt	ttgcataagt	ccctcagtgt	tctgaccact	53400
aagcaggcat	gccacaggca	gtccatggag	aggagatttt	tagaatgggg	agcttcactt	53460
aggacattac	tgtgctctgt	ctttaattgt	ttttataaac	tggcttatga	gaaaccaaga	53520
gtgttgctta	tttctttcta	gactgaacct	ggaacaggac	attgagcctt	tcttagcagg	53580
cttccataga	ctcagagctg	gctcaaatg	aattgcaaat	gttcatacct	ccggtcttgg	53640
caagtgaagg	ttgtgctggg	cctggcttgc	tttagtgact	tgattggact	caattataat	53700
gaacagcatc	attcacacat	gagtgaggca	tagactaaaa	tgttgttagc	ttggtgtttt	53760
cttcagtaac	atcagtgcac	acccacacc	ccataaatct	ccctttttta	aatcacaaat	53820
tctaaatcag	ttaaagggtaa	attaatgcag	atttatagtg	gtaaagtgcg	gacattttatc	53880
atctctgttt	tcaagtcaac	cttagagtag	gtcctgggca	gtgtttttca	aactctcatg	53940
gggtgaagaa	tactgaaat	ggcttgctga	aactcagatt	gctgggtccc	tctttgagag	54000
agtctgattc	agtggggatg	aggtgagaat	ttgcatttct	gacaagcacc	taggtgatgc	54060
tgatgctgct	ggtctatgga	gctcaccttg	atctaggcag	ccattttctc	gatgcctgga	54120
ttcatagcaa	ggcttgacac	acttcagtga	caagcacctc	accaccttcc	tgggcagctc	54180
tttcccttga	gagagctcta	tcaatttgaa	aattccttct	tttatggagc	caaggctcctc	54240
attttgattg	tgagccattg	gcttgaattt	ggtaacctgg	aaccacacag	attatccata	54300
gaaataccag	caggtatgga	tttaaaagtga	tagaaagcag	tgacctccct	tagggactaa	54360
ggacatttgc	caagaccaat	gggctgctca	ttgctttctt	gatgttgtgc	tcaaaattgg	54420
accaagtcta	ggttctcatg	gccagagctg	tggtgcaagt	tgaaatgctg	agagctgaga	54480
agcctggggg	ggagatgaca	gagcccaagc	ctttcttctg	tttaccattt	gtgcattcag	54540
ggcacatttg	agcatgagtg	aactgttagc	caaagatcca	ggaatccttc	tttcaacaca	54600

agatccttagg	cagctgaagt	aacacccact	gccaattctg	agaatcttca	acaagactca	54660
gatggtttag	ctttgaacac	atggggcacag	acaaaacaag	ttccctgctt	tcttgatgct	54720
tgaactatag	tcagggtctc	agctcagtc	tggcctgatg	tattccttag	ggaaactgaa	54780
tccatggcca	acaaacatgg	ccaatgcagg	accacctcca	ggcccatgg	gagattccct	54840
gaagtcagag	gtcaagatac	ggttttctga	tgggaggagt	gtagtctcac	ctgatttgct	54900
gggctgggca	ttgcagcagg	gctgcagcta	ttgacatgag	ttttaggaga	ccagagcagt	54960
taggaccagt	ctcaaggaga	tgtgagagct	ccttcttgctg	ccttttgcca	agggttaca	55020
cctatttgct	ccagatcagg	agactgaata	caagattgat	taacgtgagg	tcaccagat	55080
gcaacagctt	cactttccag	ggcatgtttc	cctccttatt	tgttatgcaa	tttgtccttc	55140
ctgttcttgc	ctccctgaaa	gaaaacaagt	ggaaatccca	tttccataaa	gaccttctta	55200
gaacaaggga	gtgatggaga	aacaagtgga	taacatgaaa	cagaggaggc	tttcttgatt	55260
ccttctgagc	ccagaagatg	tgactaccac	tatgcattta	ctcgctccca	tgctgacca	55320
gttactcatt	cattcaacttg	ttcatgcatt	tattctttga	cttagtctgc	cactaacctt	55380
ctgattttatc	acttaccac	tcattcatcc	atccatccat	ccatccatct	actcaacct	55440
ccaccacct	aatcatctta	tccatccttt	taaccagcta	cccaatcata	atccagccat	55500
ccactcatcc	atccatttac	ctaacaatcc	aatcattcat	ctacaccact	gcccagtcca	55560
atcattcgta	caataaacat	ttatttggac	tcacatgtgc	cgggttcttg	ggattcaggt	55620
ttgaaaaata	taggatttta	cttctaagga	gctcatgatc	tagtgggaaa	gacaagtaaa	55680
gaaagaggat	aaatcccat	ccttaaacad	aagtttgaga	agcatatggc	tttattttct	55740
atatcccat	tttttgttta	gagcccatat	cttttttagcc	tggcaaagaa	ctttcgtgtt	55800
tcaagggtt	cactttcccc	ttagggatat	gggaagattc	ctggggctac	gtagttccag	55860
ggatttgagg	ggtggaacca	tctggcattt	aagttatagg	ccttctcatg	tttcagctga	55920
gtcctccttg	agtctgacta	ccttgacctt	agccttagtt	ttcacttggg	acacagcctt	55980
ctttcagcaa	ggctaccat	ggctgcctct	gcctaaagt	gtgatttctc	accttggctg	56040
cacaatttta	tcactctggg	agctttaaaa	aaaatactca	tttcaggcct	accttgacc	56100
aactaagtca	gaaactccaa	gaataggatc	tgagctttaa	catttttacc	tataacttcc	56160
cccagggtat	ttgaatgtgt	agccaagggt	gagaaggaa	agcgaggaaa	cctatataac	56220
accccatcc	ctgtctctac	ctttcttttc	tgctcctcca	acctggacaa	ggggatgggg	56280
tgtttctttt	tagtttgagg	taatctcttc	ctttgtgtgt	ttctgaataa	ggtacgttgt	56340
ctgtgtccca	catctgttcc	cactaagata	aagaatggtc	agaggttctg	ctttctgccc	56400
agccacatcc	cttcctaggc	aatgtgctta	ggaaagaaaa	tatgcttaaa	ggggggtaaa	56460
gaaaaaaagg	aagagataaa	cataagggag	agatggagg	agagggagat	gagggagggg	56520
agagcaagaa	gagggagggg	ggatgggaag	agagaaaaag	agaggggggg	aggggagagg	56580
gggagagaga	gagagagaga	gagagagaga	gagagagaga	gagactgaga	tttctaata	56640
tcctgccagt	cagataggtg	catgcagcaa	ccagtagcaa	tggtgtgatg	gacacaggac	56700
tgatggggaa	aggggagagc	acaaagggtg	gtgtacttag	ttctgtctgg	ttcatgaacc	56760
acgccttgat	ctaggcaatc	ctttgccaat	gcctgtattc	atagcaacac	tcgcacaact	56820
tcaatgacag	gtacctcacc	acctctctag	gctcttttcc	tttagagagc	tctatatatg	56880
ggaaagtctt	tcattttatg	gagtcaggag	tctttccttg	aaggagtcag	gagaggtggc	56940
ttttagatag	aggaggcatc	tggtgctatg	aggacctagt	ctttgccctt	ggctttcatc	57000
atagtgtat	cccactgtg	gctgactctc	accttgggtt	ctgagcttct	ctaggggtgtg	57060
acctgtgtcc	gtttgctggt	ctagccctgg	attctggctt	cagggccttg	cctagagctg	57120
gaactttag	catgtgcttt	gggtaaagga	aggtgggaaa	gagcatgact	ggctccctgg	57180
gaaagggtc	tgtgccccac	cagcccgcca	cgggattggg	gccagagcga	ggctctcacc	57240
tgaacttatc	cattgcccag	gtggtgtgga	tcacagccac	gctgccttac	ttcgtgtgtg	57300
tcgtgtcct	ggcccatggc	gtcacgctgc	ccggagcctc	caatggcatc	aatgcctacc	57360
tgacatcga	cttctaccgc	ttgaaagagg	ccacggtcag	tgctcrgtga	ccaccaagcc	57420
ttgggccagg	cttgtgggag	ggttttcagg	agaaggatg	gatggaaaa	ctgggtccag	57480
ctctgccaca	aatgtgcagt	gtagccttgg	acaggatcct	tcctgtctg	aggtgcagct	57540
tccccatctg	accaatgcgg	atttgcacct	gacagtctcc	ataagccac	ccatgtctgg	57600
aggcctggga	ttctgtggtt	gcactgtgtg	gtcttcacag	actactcttt	ttgaggagag	57660
aaattccctg	tgaagaggac	atgatgtctt	gggaccttgc	tcttgccctg	tgcccacag	57720
tccttagtcc	accccagcca	ttccctgccc	ctttctact	cttgatccc	caaacctagt	57780
ctttgccacc	atcctgtgat	gtcagcacia	ggatagtctt	agccaccagg	gaggccctgc	57840
caactctctt	ccccaacacc	ctcatccaac	cactccccct	gtccagaggc	ccaaactatg	57900
gtgaaagtgg	gtgaatttgg	tagtggagtc	cagtgcagag	cagtgatgg	gggagcagag	57960
acaatcacag	aggtactcag	taccttgagc	atcttcagat	aactgctgag	attacttcta	58020
gcctcctctt	gcagggcccc	tcagtggaga	cacctcaaca	tgctatctta	caattctcca	58080
gggtttcttt	atttgaaccc	ataataatcc	tggcaggccc	cagcagcaca	ggatgaagag	58140
ggatgcaccc	caatatacat	ctccatagtt	gtaatgctcc	aacacactgc	aatgttatag	58200
accgtaaac	aagagaaaac	ctattttcat	agtaacagcc	agaaagataa	cagagcataa	58260
gacatgaatc	agcctcgtac	attgcaaaat	aagtcagact	tctatttgtt	ctgtgactgt	58320
ttatgccaaa	cctttcagat	gtgtagaagc	taagccctca	gtgcagtctc	aaggagcaga	58380

tctgtcttcc	cccatcagat	catgctgccc	tctgtttgca	caggcatctc	tgaaatctga	58440
attgcaaggc	tgggcgcggt	ggctcacgcc	tgtaatccca	gcactttggg	aggctgaggc	58500
gggcggatca	cttgagggtca	ggagttcaag	accagcctgg	ccaacatggg	gaaaccccg	58560
ctctactaaa	agtacaaaaa	ttagcggggc	acggtggcac	gcacttgtaa	ccccagccac	58620
tcaggatgct	tgaacccagg	gagtgagggt	tgcatgagc	caagatcatg	ccactgcact	58680
ccagcctggg	tgacagagtg	agaccctgct	taaaaaaaaa	aaaaatctga	attgcagctt	58740
agtctgagtg	tgtgagggtat	aattatcccc	attatacaga	tgaggaaaca	gacagagaga	58800
agtgaacttg	accagggcta	gaacatgagg	cagagaagtt	aaaaaggaat	tcagatcttc	58860
aggcctccgg	ccatgtgcct	ttatcaccca	acggattaaa	tacgtaagcc	ccattggccc	58920
ccaaggagtc	accattgtct	atggcttgta	gaagcctcct	aggaatggtc	ctcgttttct	58980
gaaaatgcca	tctccgtaac	tcctaagatg	gccataaccc	tctgttcttg	ccccattcac	59040
actctagcct	agaacttttc	attttggtta	ctttctttga	aaatcagggc	atgaaattga	59100
gtgaatgagt	tcctacaggg	tgagctcact	cacgactacc	caaggctggg	agatgctaga	59160
gaggccagc	ctctctctgc	agttgttttg	tacaggatgc	aggggagggg	gttggcaggg	59220
ctgcccattc	ctgggttcaga	ccatgtttcc	tctggtctca	gagcatcccc	agggttttct	59280
agcccttccg	gaccagtgag	gtgttccagt	gttgtaggaa	gcagaggtcg	atggcttttg	59340
tctgctgggt	tcagggtatgg	attgatgccg	caactcagat	atttttttcc	ttgggggctg	59400
gatttgaggt	attgattgca	tttgccagtt	acaacaaatt	tgacaacaac	tgttacaggt	59460
aagattcttc	tcagaattct	gagaagctct	aaatcctggg	gattgactct	tgtggggtgg	59520
cagagagggc	tctggtctgg	aagccaactc	tccttgggca	agccaaattt	tcttcttggt	59580
aaccatcctg	ggcattctat	aaactgcgac	atggcctctg	agggctctga	tgaccacatt	59640
tcatttcagg	atgcctctta	aacaaatgtg	agggttgga	ctgggaaaat	tgagggttacc	59700
accactgaga	gatgggtagt	tatgacagag	gagaactgtg	aagatttcag	tatggactct	59760
gtccatcaga	tgcccaggca	ggcaggggtg	gaatatcgca	gctgctgagg	gcctggcagg	59820
gtcagaagtg	agactgcagg	ggagactgag	actcagaaga	ccatgatcta	gctcagttca	59880
ggaagcagtc	aatgctacct	cctgctggcc	cagtgcgtgtg	gggacttcag	gcacaggcac	59940
aaatttgggg	ccacttccat	tacactccat	ccaaggctta	aggcagaatc	acagtgtctt	60000
tggtacatga	cagagtccag	tgaattcata	ccagcgggac	aggctatagg	gaggtaagga	60060
aatgggggtga	tcagccccct	gatagaagac	aagccagtgc	atggagggtga	atttgagatg	60120
agccttgagg	gatagttagg	attatgctag	gcagacgtgg	agtggactgc	atgcactggg	60180
gggagaagcg	ggacaacaca	ggcaaagtga	aggaagtggg	ttgttttatgg	accaatttat	60240
ggtttggtca	gagtacacct	tgggagtcac	ggaagataaa	tatataagga	agggtgggtc	60300
ttcttggtcaa	agctcttgaa	tgacaggatg	aggagtggg	aggcactggg	gagcagccat	60360
ggaagggttg	ttgaagggaag	ctggtgactc	aatccctggg	caggagtaga	ctctgggtatc	60420
aggctgttgc	atccataagc	agttagccta	cttctgcac	cagtgatggg	gaggccctgt	60480
atccatgtgg	cagcaggagc	cactgaaggg	gggatggcct	ttgaggctgg	ggccaggctg	60540
cagggttctat	agccagccca	gcagtcaaaa	cacagggttg	agggtgtcaa	gggacttgac	60600
ctcactgtgc	ttcttcccc	agggatgccc	tgctgaccag	cagcatcaac	tgtatcacca	60660
gcttcgtctc	tgggttcgcc	atcttctcca	tccttggtta	catggcccat	gaacacaagg	60720
tcaacattga	ggatgtggcc	acagaagggtg	gggtgggcagc	ccacctgggc	cccagccac	60780
tgaggcggga	gctgagaagc	ccaccttatt	cttggtcgca	tggctcttcc	gtggctgtag	60840
gaatactggg	ttgtccatgg	agggtgtcaa	accacctatg	tgattgactt	tcctttgagg	60900
ttattagtgg	gcattccagg	cagtcacagt	ccccatgcac	gtaggagaac	ctctctctga	60960
gtcagggttg	aaggaacgga	ttttggactg	tcctctctgt	accagccctg	ggctaagcac	61020
ttgacatacc	tccacttagt	tctcacaagg	ctgccgggca	agtgtcaata	gactcacttt	61080
acgaatggga	agactgagat	gcaagctaaa	tacattgtct	ggcgtcacc	agctagttag	61140
caattgtgca	atagtattca	caccccaatc	aatccagctc	tggagcttgt	gtccttccct	61200
gcagcttccc	atatccttat	ggccacagag	aagctgagac	ctggggaagg	gctacctcta	61260
atgcactccg	aggaccccaa	gcttttagtga	gtaagagtgg	atcccttata	gagtatagta	61320
ggtgggggtt	gcagcatgta	gcctgtagct	gtccaggcag	ggaactgctc	tccagactgg	61380
ctgttggggg	tcaacctctc	cgatgcacag	gtgagctgta	agttcatgct	gatttcatct	61440
gttatctcta	aacctgtgtt	ctgtccgccc	acacatgacc	kaacaattgg	gccccagat	61500
actcccctat	catgtgcagc	tcagaccaat	gggttcagcc	attgatgagg	tccttgatgt	61560
ttcttacagg	agctggccta	gtgttcatcc	gttatccaga	ggccatttct	accctgtctg	61620
gatctacatt	ctgggctgtt	gtgtttttcg	tcattgctcct	ggcgtggggc	cttgacagct	61680
cagtgagtga	ccctgcttag	gatacctatc	ccccatccca	ctgggcctga	cccccttccc	61740
caacacacag	tgctgggcct	gaagtcccca	ctattcaaac	accagggtta	cagttgtttc	61800
ccagaaggcc	ctattttaaat	tcagacaaaa	aaaagtgagt	cctcactcaa	aaagataaga	61860
cttaggccaa	agccaagaac	cataggaacc	cctttgacat	cttggaaatc	caaaagaaga	61920
ggcttcagat	aagccagccc	cacactgtcc	tcttgacaggt	ggggaaatga	ttcagaggca	61980
acacagataa	aatcttgtgc	tctaacaag	cattttctca	ttatatttta	ttatcaataa	62040
tcaataggcc	aggcatgggtg	gctcactcct	ataatcccag	ggctgtggaa	ggctgagggtg	62100
gaaggattgc	ttgaggccag	gatgtcaaga	ccagactggg	caacataggg	agacccccat	62160

ctctataaaa	aatttaaaaa	attagctgag	catgggtgttg	tatgcctgta	gccctagcta	62220
ctcaggaggc	tgagggtggga	ggatcacatg	agcccaggag	ttggaggctg	cagtgcagcta	62280
tgattataacc	actgcacttc	aactcgggtg	gagtgagacc	tggtttctaa	aaaacacctc	62340
aaaacccaaa	cgaacaaaca	aaaacatttt	gaacccagta	gtttcttaca	tcctttttatt	62400
ttatccaaat	gtaagattgg	atttactgac	atcttttttaa	atctatgtct	acccttagta	62460
cctcatgcct	ggacatttgc	aaaaaatctt	atggaagggc	tggcacttgg	ttttcctccc	62520
actgcctttt	gctttcagtc	agcagatctg	ccaggagcag	ggagttgaga	aggattttga	62580
ggctgcttct	gggcttataa	tgaagaatac	tgattttgat	taacagtgtc	tgccaagagg	62640
aggggagagg	agaggagagt	ggtagcttgc	attcttcttg	tctgccctca	cattgtcctc	62700
ataaggaagc	aatctgcccc	tagcagtggg	atatgagacc	ctttcagact	ctaagagtct	62760
ggagtttgaa	gtgaccactt	tgcttgatca	ttagaaaggc	agccaaaaat	ccttatcaaa	62820
aactgctgcc	tgaagttccc	atcactagaa	gctcttctgc	aggagttggt	tccagagaca	62880
cttattgaca	tgtaaacgta	tgacatgggt	tttgggtgtt	tactgcttcc	actccactat	62940
cagcttatct	gtaccactc	aggctgagtg	agtgtcagga	gacaggtagc	tgttgcgtag	63000
gggagacagg	tgttgactta	accctcaccc	tctcccagct	agtttctgag	ttctgagttt	63060
gcctgagaac	aggacagaaa	tgtgacgaga	ggatggggaa	ggaaggacgt	gctgatttct	63120
cgagagaggc	aaggcagcct	acatgagtcc	tgggctgcag	gaggctctag	gaaccctggg	63180
gcctgagact	gaggtccagg	gagaccctaa	ttcctgcacc	ccaccctccc	tggttccctc	63240
cagatgggag	gcatggaggc	tgtcatcacr	ggcctggcag	atgacttcca	ggtcctgaag	63300
cgacaccgga	aactcttcac	atttggcgct	accttcagca	ctttccttct	cgccctgttc	63360
tgcataacca	aggtgagtag	gggctgggct	ctgggtcacc	tgggggcctc	tgaggccgca	63420
tttcaataaa	gtcaaactt	cctagcctta	gaactggggc	tgagctcagg	gagaacaatg	63480
caggatccag	catcctcaat	tcagcgccct	gaccacttag	ggtaggccc	agtagcttcc	63540
ttccatctct	gatgctgagg	attccattca	gcctctgtta	ttgccttatt	gacttgaggg	63600
gcagcaaaaag	tccttttggg	acccatctaa	ctctttattg	gctgaaactg	aggtgactgt	63660
aacgtcaata	caacagcacc	acagccctat	gccctggggt	ttcaaataga	gctccgagca	63720
agtgggacag	ggggcaggta	agagttgaca	gacacaacaa	tcagttccca	cgtttgacca	63780
aagagggcct	cttggcttct	tctctccctg	tgccagggtg	gaatttacgt	cttgaccctc	63840
ctggacacct	ttgctgcggg	cacctccatc	ctttttgctg	tcctcatgga	agccatcgga	63900
gtttcctggg	tttatgggat	gtgagtgtgt	ggaaaagcct	cagctcccag	tcctcctaga	63960
atcctgcacc	tggaggtgtg	cagggaggcc	ttccatttcc	aggacagcca	cctaaaattc	64020
cagagtcag	caagtcactt	attgggaaca	aatctyaatc	ctcggtcat	ctttggatga	64080
acctgccctt	aacaggaggc	tgcaaaggcc	cctgggcac	aactcctaaa	agaggaaccc	64140
ttagggaaaat	gctgaccccc	aagtcataata	attcatccta	ccaggggggt	gtcagattta	64200
gcaaacacaa	cacgggttgc	ctagttaaac	ttgaatttca	gataaataac	aaataattat	64260
ttagtataag	tatagctcaa	atattgcatc	ggacataact	accctaattt	ttttcattat	64320
ttatgtgaaa	ttcaaactta	actgggtatc	ttgtattttt	tctggcaaac	ttattctgga	64380
acagaactga	gagaatattt	tacaaaccct	taaagtgtgt	aattgtttgt	ttttcccccac	64440
caagtgtcac	accaacatgt	tagtcctgtt	ctcactctgc	tgccactcag	aaagagattc	64500
aatggaagag	tctgggctct	cctatcagat	tgaagtcagg	gaatgtgctg	tatgcatagt	64560
tgttgttatt	ttcagagcaa	gagtaaccaa	gaggaaagag	ctgggctttg	gagtcaggcc	64620
aactggctct	ggaatttggg	gcaaatcccc	tcacctcttt	gagcccaggt	ttccctctga	64680
caggtgacat	ggggtgacac	atgaaagggt	atactgtcct	agagtttgtc	ctctccctca	64740
ttctgcatta	caaagggtccc	atccccaggt	ctccctagtt	ccakkkkatc	agcatcttgc	64800
ctcactgccc	tgtctccac	ctggggccag	aacctcatgg	gaggacctgg	ccctggctat	64860
catggggggc	atggtaacag	gcctgccttg	tgtgtgcaca	ggagtggaca	ggttcagcaa	64920
cgacatccag	cagatgatgg	ggttcaggcc	gggtctatac	tggagactgt	gctggaagtt	64980
cgtcagtcct	gccttccctc	tgggtgtgtag	tgtctgcagg	gaagycctgc	atgtggggag	65040
ggggctgtgt	ccaggatgga	gctgggtgag	gatatttgct	tcttagggga	ggaggctctg	65100
ggatccagag	gcctgggtca	tgcagagggg	tcacttggga	tgttggccc	tgtggataac	65160
gtggtagaca	tccaccttac	taggggggtc	tccagctggg	gccaggctcc	cgggggctgt	65220
tatgcctttct	ccaaagtcac	cttctgttct	tcctcttttc	ttgtccctg	tcatatctgc	65280
ctccttttga	ttatcacttg	cttcttgaat	ttcttcttat	ttctccatct	ctttctcttt	65340
tcactcctt	ccttatttcc	tccttttgct	gtgatgtctc	cttctcttca	ttctctccc	65400
acctttcttc	caacctcttc	tctctttcct	ttcttgtctc	tcttctgtcc	tgtcttccct	65460
tctctccctt	ctctgcccac	ctctagtctg	tggttgtggg	cagcatcatc	aacttcaagc	65520
cactcaccta	cgacgactac	atcttcccgc	cctgggccaa	ctgggtgggg	tggggcatcg	65580
ccctgtcctc	catggtcctg	gtgcccatct	acgtcatcta	taagttcctc	agcacgcagg	65640
gctctctttg	ggaggtgagc	tctggctctc	cccaggggaa	caggggtggga	gggggctgag	65700
ggggaagacg	ggacgactct	cattcctgtt	gggggtgggg	aagggacaga	aggacacaga	65760
cactaggggc	aaacggaccc	acctcattgg	ccaggttatt	ttcccccatg	agcctcagtt	65820
tccacatctg	tatattgagg	ataatattac	gtaccccaaa	acaaaaaaga	agtacttagc	65880
acagtgtctg	gcgcacagga	ggtgttcagt	acatgttact	tgggggtgag	ctcagccctg	65940

gagttcacta	aggattgatt	agacagactg	cctgaaccca	gctcactgtg	atgtctctgt	66000
ctaagatttg	tcatttccca	agatgtccca	gctctcccca	tccaagccca	ctgtgatctg	66060
ctccttctgg	ttttcacctg	cctctttcca	gaacctaata	atctgatcag	cctaaaccag	66120
agatttctga	actatttctt	tctatgcatt	ctgcatatat	gtcaatattt	atacatatgt	66180
atatatgtac	atgtgtgtgt	atatacatat	atgtatatat	acacacacac	acacatttat	66240
ataaatattt	aggaaactgc	cctttattct	gaaattatgt	cactcctatt	tgattaaaaat	66300
atcctttctt	tcataaacta	atagtataaa	tcttttccct	atataccttac	tttacaaaac	66360
aaagatgatt	tcattccctc	attcctttat	ccactcactt	ggaagggtatt	tattgggacg	66420
cagatatatg	ctgggtagta	ttcgaggcac	tagacaaaaa	ttcctgccct	tatggagttc	66480
acattctaata	caagggcagg	taaacaataa	gaggatggaa	ggcatccttg	ggagccacaa	66540
ggaaactcaa	ggaagggtgt	aacagacaga	cagtcctccat	cctcattctt	tgtgatacat	66600
ttcctgtctg	tgaaatccct	aagtctgggt	ccgggtcact	gggaggatca	gtgttcagtgt	66660
acctcattct	agacatggga	actgggacct	gagccttcta	ttcttcacac	tttgggagtg	66720
gagaggcttc	ctgctaccag	tgatcaattg	ttgggttcaga	acacatggct	tgagacccca	66780
caagtgcctc	cactgcagga	gggctttcct	gattccctgc	agggccagag	gcttccttcc	66840
acactctccc	tgctgcactt	tctccattct	gggtctaaga	tgatgtgtgt	gtttgttcat	66900
tgccagtccc	ttacatgggc	ggtaagctcc	cccaaagtag	agactgtgtg	ggtctccttc	66960
aagtctggat	ccatagggcc	tagcccatg	tctgaccaca	gtaggcagct	caagaaacag	67020
tgtctggatg	agtgactcaa	tggaccagct	ccacaaacaa	agctggagggt	gtcttgtaca	67080
gaccccaaat	gctatccatg	tggggctgca	ggatcaataa	gcagggtggcc	ctcatctgsr	67140
ggtgcagcca	ggctggccaga	aggggtgtccc	tggggccaagc	tgaggcctcc	tcccttctc	67200
ttcctttcag	agactggcct	atggcatcac	gccagagaac	gagcaccacc	tggtggctca	67260
gagggacatc	agacagttcc	aggtgggtga	agcctagacc	cctgggggtgg	agattacaag	67320
ggcggggcct	ggctgttccc	tgctgtgyac	tgcccaaggc	tagacatcac	atccagaaaa	67380
cccagaaacc	cagtgtgagc	tgccctttcc	ccttggaaac	atcgggatgg	gggacaggga	67440
ggctcacctt	gagcccatgg	cctcaggctt	gccctgtgac	tttggggagg	ttctgctgcc	67500
ctttctgggc	ctctgtgaca	attaggggat	caacttgcac	gttccctgag	gtccgtgaag	67560
gaaggggggtg	tttttctgcc	ttctctctac	ctcctgctgc	ccccgccagc	tgcccttgc	67620
tcctttctgt	cccaccatg	tcataagtc	ctcgtgtct	ttctctgcag	ttgcaacact	67680
ggctggccat	ctgagcctgc	ctggaggaga	aggaggaacc	cccatgccaa	tgtccaggctc	67740
acaggcatcc	gctgcgctcc	cacctcggac	accatcttgg	gattcctccc	ctggaagttg	67800
tcctttctga	tcctctcttc	ttttcccatt	tacaaatgat	ttcgtgactg	tagtttttgt	67860
tcaccttctg	tgcatctggc	ctgggggctg	ttagctcaga	ggagaggagc	aaacaggaaa	67920
atgacttctg	ttctgtcccc	gctgttttgg	gggaagtctc	tcycactttg	ggatcctgct	67980
gaagctaggt	tcataagggtc	ggaaatcccc	accacatttg	cctagacttt	gggcacagga	68040
gttcttagtc	caccaaatac	gagagaggat	gggcttttga	tcagataccc	cccccaaaa	68100
aaaaaaaaaa	acaaaaacta	aagcaaaaat	caaacaaaat	ctggctgagt	ttagtgggggt	68160
ggttggggaa	ggtacataga	ccctcctctt	gcccacccta	gacagccctc	tcagtgtctga	68220
acctcagcct	gggagttaga	tttatttgtc	tctaaataga	agtcagtga	tagatgcttt	68280
gagggatttt	gagtagaaac	attcatagtt	aattttact	ctggccaatc	tgagtttgat	68340
gtgtgtgttc	tggaacattc	ctccagcttt	tggtgggtcag	atggcccaga	gatattggggg	68400
acaggaggaa	gagggtaaat	gaaccacagt	gagcagggtc	taggagggtac	ctgcatcaga	68460
caagctgggtg	gaggccacgt	ggcaaggcac	atctactgag	gcctcatgct	gctcttgctc	68520
tgtaagacac	ggagcccaga	aaccatctg	cacttcttga	gacctgcctg	gggaaacggg	68580
ggcagggacc	aagtgaggcc	tcatagtgtg	cttcaccgtg	ctgtcctcac	aaggccaggt	68640
gggtgcccaa	agggagcctg	acaggctgtt	gtgttaattt	attgttcttg	cacacctgca	68700
cagcctccct	ctggggatcc	cacctggagt	ggaccagggg	tcttgagaaa	tgagaggttg	68760
gctgcaaaaa	ctctcatgca	ctagatgtgg	caccttggag	ggcagggtga	gacaagcagc	68820
ccagaaatac	tctctcaagt	ggaggggaga	attttgagag	tggatggaac	agtttggttg	68880
tttcagagaa	tttctaggtt	tctacttgga	tctacttctg	atacaaaactt	gcacttggtg	68940
ccctctgggtg	gtgttttagtt	ttagtccgt	aagagaaatg	attcctagtt	tgctaaattg	69000
gtggcatctt	tgggaggggt	ttctgtttat	gggttagagtc	tcttacaccc	ttgttgagg	69060
gattcttatt	ctgactgtgg	gagctcctgt	tgcaggatct	tgggaaaaaa	taaagaagcc	69120
gctgcattcg	cacgtcaaga	aggtgctttg	cctcaaattg	gggtgtgtgt	gagcctgggtg	69180
gttctctgat	gaagaggatt	atgaggggac	caggggtggg	cagggagatg	gttttgtctc	69240
ccagggtcct	gaggtttcct	tgctgggtcg	gggtcctcag	gtcattctat	agataaaaaga	69300
gggaaaatca	ggagactttg	aatctttctg	tataaaaagg	tcagctgaat	gcctgagaca	69360
gcccagggtg	caggtgtcct	ggagccctgt	gaacagtga	gcttaagaat	ggagaacaat	69420
caggtcgggg	tctgggcccc	attagtgtg	ttatatcctc	ccataaaaagg	taacttcttc	69480
ctaggtgtta	ccatttttct	ttctgttttt	tgttttctgt	tttgtttgtt	tgtttgtttg	69540
tttgtaataa	agcactttaa	tgacatttac	ctgccatctg	cccagtgagg	actgcagggc	69600
tatagcttct	atctcccat	ttcccagggtg	agagaaccaa	ggcccagcat	tttagtcaact	69660
cttgctcaag	gttttttagc	aactaacaga	tcgagttggg	ccttcaattc	acatccactg	69720

actctcagcc	cagattatatt	tgaatatcc	ctgcacaata	gggttcaccc	caccacaggac	69780
tgtcattttt	aaaaaactca	ttcaaaaccgc	aaaggaaaat	ttcttagcaa	aagaacaatg	69840
tgttgaggga	tggaagggg	cgagagaatg	ccatttatatt	tcctctagct	ggtttccaga	69900
gaggaaatta	tttagctgct	ctcttttgat	gaaaataatc	actctttgga	atagttggat	69960
gtgaaaagct	gagtctactt	ggttgaaatg	agagcaaaca	gtcagcaaag	ccttttgcatt	70020
tagagcaggg	tcgtgcttcc	gagagagcct	gccatttccct	ccttgccatc	tgcatgtggc	70080
cccttctgcc	tccagacatt	tgtcccgggg	tgaatcggag	atgtgggtgct	agctgaacca	70140
acaccaaacc	aacgcagtgg	tgtgccttg	cggcggaagt	tggtcctga	atctgggatg	70200
ggaacctggc	tccaagcctg	gggtcccctg	gaggggtggg	gtaccacaga	agcccttgga	70260
agttctcggg	gaggtgcttg	gagatcattt	gggtttacct	ttccaccac	atttaattgga	70320
gagagagtat	gggctttatg	ttaagtcac	tttgacttcc	ttttttagc	ttgtttttaa	70380
tagcagaggt	caccggggac	aagggtgctg	tgtactgtat	atgacacttg	acgcttttga	70440
tattttttca	ggtttttaaa	gaattattat	ttttcatgaa	atgtaaaata	tcagtttgag	70500
aacatcacat	ttacgtctac	tcaatgtcta	gttatattagc	acccaccttt	tagctttcat	70560
tctagatgaa	aacgagacaa	gggagaagga	gagctacca	ctcttgccag	atatcctgct	70620
gaacagaaat	ccctgaagct	gccttaattc	tcaaaaggag	ttaccgctca	gctgggagcc	70680
agttcctgct	atatgatctg	ttttctagcc	tcgctaattg	gagactgaag	cattcttacc	70740
aaagaaatca	tttccctagta	aagaagccca	ttgaactcac	tttatttgtt	tatttcttct	70800
gaaagccacc	gaagagagaa	aaacagagaa	gggtgtgagt	gtggcgga	aagcacagca	70860
tatagtttta	cagacttggg	tctgcagctg	actagctggg	tggtcctggg	atagtggtct	70920
catcttttgg	ggcttcaaga	ttctttgtct	ttaaaatcag	gggttatatc	agatcatcaa	70980
agttccatt	ccattaaaga	aaaccctgca	tgtatccata	atgatgctct	cctgttaaat	71040
ttacaatgaa	ggaaacacat	cacttaactg	taagaatttc	ccaaaatgaa	ctgatgacca	71100
gtgatctctc	tatcagagaa	atgtcagatt	tctagcctcc	agaactttga	tttttctgga	71160
cattcaatag	ttcctcttct	tcagatattt	ttcaactgat	gccagaaaca	cttgggtatt	71220
gttttttaac	caacccttct	gttttgaggc	tttgagggt	aacacatttt	cataccctgt	71280
gagtcaccag	atccacagct	ctgctgtggt	ctcagaagcc	actgaaacat	tggtgaatgt	71340
gaagtccact	ttgggggtgc	tgccctcacc	cctctgtctc	tctgcttccg	tgtaaaataa	71400
gactgtttca	attgtgtcct	ctctgtgtca	tggactgttc	caatgtcatg	cagatttctg	71460
tgtctgatat	ggatttttaa	agttgttctc	tttgtggaat	ataagtgtac	agaataataa	71520
ataatgtttc	ctgggctgtg	tatctggtag	cagagttctg	aatgctttct	tccatgaagg	71580
tggaaatgcta	caaattatgt	aaggagggtg	gggtgatcta	tgatcagctt	ccaactagta	71640
aagaagagcg	tctggtcata	gtgacccacc	ttttaatcaa	ataactcttt	ttataaccta	71700
tggaaaagga	gatttgaagg	agttaaatct	gtaatcttag	ccttgagatt	aacatatatt	71760
tttaaataaa	aagagggcac	caagtatac	cagggttagt	ttagtttagt	tttcatttct	71820
aaggctgttt	caaggagctc	agaacctcct	gttgattga	attaaataca	caatttgggtg	71880
catgtgtgaa	tttttctggg	gagagggata	cattcacatt	tagaccttag	aagatctaag	71940
tctttgtttg	gggaagatgt	aagctgagta	ttgtcattgt	ttggagaaga	tgtgaactta	72000
taggttaatta	tttttaatgc	aagccagcaa	atagatagtg	ataccaatgt	aaaaggggtg	72060
ttgtcaaata	actgttcagt	caatgtcttc	aaatatctaa	aggctgtcag	agagtgtgtg	72120
gtgggcccac	gtgctgaaat	gggtccaatg	gtagggaagtc	caggaagaca	gcttgcaaga	72180
ttctaccaga	atagagaatg	ggctgttgct	ggaagtggta	actccagctc	tagagatatg	72240
caagcagata	gcaggcagtg	tctcctgggg	atgcaatgtc	aggtggaatt	ggggggagg	72300
aggttgcaca	acctctaaga	ttccttccat	ttggagtccc	tagggttgtt	tttttcttct	72360
tttcttcttc	tttttttttt	tttttttttt	tttgacagtc	ataagcctgc	cttgtacagc	72420
agcactggga	gatgcaaata	cattcatgcc	aaggaccctg	gggtaggagt	ggtttggcct	72480
cacaaattag	agttgggaag	atatcccaga	gaggctatta	tcattctgat	cattttgttt	72540
caaccagaa	ttggagtggg	gctttattat	agtgaatcaa	acagaagaca	gctgcacttc	72600
tggtcattccc	ttgtgcctga	cgagatctgg	taagcagtg	tcctgtggga	ggaggggagg	72660
gaggctggtc	cagagaagga	aagggcagct	gttttgtggg	gggtgatggg	aatctgggtg	72720
cccaggcttc	caccctgtcc	cctaggctga	caacacagta	ggagaagtcg	gagcagcaca	72780
gataagcctc	accttaggca	cttagtgggc	ttctgaattt	tccccaattt	aattgcaccc	72840
catcctactt	ctggagattg	gatagcttca	tttttatctc	ctcccaaag	gcactgatac	72900
acgtactctc	tatctggggc	tcaatttgtt	cctctacagc	ggatcgggag	tggtcagaac	72960
taagtgttca	tgaatgggtt	tcaaaatttt	tcagaatctt	ctgagattaa	attcaacttt	73020
ctgtttgaat	gaatttgtgc	tcatttttgg	ggaaaaagga	tcatacatt	catcaagttt	73080
tcaaatattt	aaaaccaca	agtatatatt	acttttgggg	gcctctctct	tctgatgata	73140
catggcatcg	gtctctgccc	ttcaccacca	actaaatgag	gatgacaata	gaccttattt	73200
ctgaatctca	gtcaccgcc	attatgttga	ccttgttttt	ttgtctgttt	gtttctgaga	73260
cagggtctca	ctgtgtcgcc	caggctggag	tacagtgggtg	cgatgacagc	tcacagcagt	73320
cttgacctcc	tgggctcaaa	gtgatcctcc	cgcctcagcc	tcctgagtag	atgggattat	73380
aagtgcagtc	caccacagtt	gtctaatttt	atttttggta	gaaacagtga	ctcactagat	73440
tgcccaggct	ggtctcaaac	tcctgacctc	aagcaaacct	cctgccttag	cttctgagt	73500



agctgggatac	acaggtgcag	gccactgggc	ctggcttgac	ttttcatatc	aatcatccca	73560
cagcaaatac	ctcattttat	cccgtgacaa	tgagcctgca	agataggcag	caacaggaac	73620
accgtgcccc	ctggacagat	gagacaactg	aggctggagc	tgagaagtga	cccgcctaag	73680
gtcacgcagc	tactgaaggg	caaagtcagg	tcccccatg	cctgggtcaa	tgctcttcac	73740
attatattca	ccgccctatg	gaaataaggt	agagtgggga	ccagacaagt	cctgacgggt	73800
accacagaac	tgtgggaaga	gactgcaggg	ctataaggac	ttggtcacct	aacaggagct	73860
tgttgacagg	tactgggaac	attgcttcgt	cacacagtct	caaacaggac	tggaaaggatc	73920
aatgctgtta	gggatcaatg	ctggttaggga	tcaatgctct	ggaaaagtgc	tggcccccca	73980
gtgtccactt	gagaccaact	actctgatgt	gatgattgag	tcattgttga	aaagtcatgt	74040
ctaagccttg	gctctccag	ctgtgaaatg	agaatgttgg	attggatgat	tctctaaagt	74100
cctttctgtt	tctgactcta	tgagatacac	tcaggagacc	ggcatgaagt	tgatgggcta	74160
attcatatga	agatgtaaat	gactactttg	tcaggcagac	agtgcagat	aaagggtggga	74220
gttgctgctt	tttgcttcac	ctataagttt	agtgcggggc	ttggtaaact	atttctgtaa	74280
aggctctctg	cacaacttct	cagctgctgt	tgtagcatga	aagtaacctt	atttataagt	74340
atcagggtgg	gggttggtt	tggcctgagg	tctgtgggtt	gcagatctct	ggtaggtgg	74400
aaagagtga	gggtctggag	ttggactaga	cctgggtttg	agtctcagct	ttaccactga	74460
ctgctgtgaa	atcttgagca	agttatgtaa	aacttccgaa	ggctttcttg	tttctgaaga	74520
gtgagaataa	gattcccaca	agagagtttt	caggaagggtg	aaacaagggtg	atgtacactt	74580
acagcaactc	tctggggctg	cagtacctgg	attcaagacc	tggttccatc	actccacagt	74640
gtgaatccct	gggcaagcca	cataacttcc	ctttgacctc	gtttatcatt	cataaattggg	74700
aaagacagta	gtgacccttg	ctagggtcat	ggggagaatt	aaatgttaat	attgtattca	74760
gaatagtacc	acctacacag	tttatccttt	tgtatatattg	gttcattgtca	gctataggat	74820
gaatgtatat	ttctctctct	catcacctct	gcccatttca	aaggcatccc	agctaccact	74880
gtgttttcac	gaagccaaat	cagtgtctgt	ttctctgctc	tcttgatcc	cctccttagg	74940
atggtgacct	ccttaggatg	atgtccttga	acttgggtct	gggtagccaa	atccaagttt	75000
ccctgggcct	gagtgcattg	aaccacctgg	gcagaagttc	aagcttctgg	aaatcccagg	75060
ctccacagac	cttgccctct	gcaggaaccg	gcttccctgt	aagccctcag	ctgtcagccc	75120
ccattagacc	actggcatgg	gagatattac	tctaggctgg	ccctggctct	ggctatgacc	75180
tggaaagggg	ggagaccaga	gggagactcc	tcgaagagct	ggcacttgct	tgggtcctgg	75240
agtctgtgct	atcagctacc	ggctctgcca	gcctcaggcc	tggggaaagc	tgggtcgggg	75300
cagactagca	gggcatgagg	gtaagggttg	ggctgcagta	catcgaggag	gaccaccctg	75360
tccccagaga	aggcccagca	agggtcacag	cctggaatgc	ccaggagcca	caaagccacc	75420
atctctgcag	cagagggtag	ttgttaggtg	gggagcactc	cacacacccc	tgcatctcca	75480
ggctgcaatc	cagacccag	ccccggaggg	gcagacagga	gtcagaagaa	gagaggccta	75540
acacagcagt	agcacctggt	cacagtcagc	ccagcaacag	ggcacctgcc	tgccgtccac	75600
ctcgagccat	ttccaggacc	ctgctaaacc	tcttttcttg	caccacggga	accaaactgc	75660
ctcctttag	tcgcctttga	cccctgaccc	acatctgcag	tcacttgggtg	gtaacaatcc	75720
cctatcatgg	ggagaaggga	cagggtaggg	ctggcattcg	aggcataccc	actcacataa	75780
gagcattgca	gctctggcct	gtcaaatgga	ctgcagagcc	aaaccaggga	gtgtcagaga	75840
caagatttag	ggatctgggg	tccacagtta	catttgggga	acccttgccc	ttgagttttg	75900
gaattggaag	gacaacaaag	cacaaagagt	gtgtggcttc	atcaaaacag	ctgagaggat	75960
gaggccacat	cctggccaca	caagccctga	agttccagga	ggaccaaggc	tttaggagca	76020
tcagcacctt	ggacaaggcc	aattggctga	tctgccttta	attagcaaac	agggttggtt	76080
accttttgtc	agttactatt	ctgagtgtct	tacaaatatc	agtcactgaa	ccctcctaac	76140
gactccatga	gatagcatga	ttattcgcac	ttataaatgg	gggaaactga	gacacaaaga	76200
gctgaaataa	ctagttgttg	gaactgggat	ttgaaccggg	taagtctggc	tccagtctgt	76260
gtctttaacc	attgatctgc	ccccttccct	ggttcccggc	cacatggaca	tgacatgggtc	76320
aggctgggtg	ggacatgagt	cctcctctac	ttccatccct	tcttcaattg	caaatgcata	76380
atactaaata	aataacttat	gtgtatacat	atgtaagtgg	tacacatata	tgtaatttaa	76440
cacacatata	tgtgttatac	acatatatgc	ctatttttaa	caaaaatatg	taaaagttaa	76500
tatatatgta	tacgtgtgtg	tgtctataca	tatatatata	catatatata	catatatata	76560
catatatata	catatatata	tacatatata	tacatatata	tatacatata	tatacatata	76620
tatacatata	tatatataca	tatatatata	cacatatata	tatacatata	tatatataca	76680
tatatatata	cacatatata	tatacatata	tatatatata	cacatatata	tatatattta	76740
agtgcctaca	atgtgatagg	aagcaaaaca	cttgctctag	atcacatagt	aagagggaat	76800
tcagtttgga	cagaggctcc	ctatctccta	ggaaaagtat	ctatcctggc	tttctccaga	76860
agccccccag	tctgtactc	tctggttctt	tatgccaaat	acagggttag	tctgggetca	76920
ctagccaaaa	gcaaaaagat	taggcacata	tatgttagga	tgcaagtgc	tgcatctaac	76980
agaaatgtaa	ctatagtttc	ttcataaatg	gacttttctt	atcctcttgt	aacaaacagg	77040
caatgggtca	gggagaagggt	gttgacaggg	aagaagtggg	agaagtaact	ttggtcctag	77100
agaaggactt	caacaggggc	ccctgcctgg	atgtgtccag	aagccccaga	tgggtctgga	77160
gctgctttaa	aaagtaataa	aaaaattgga	tgcttccag	cttcttgttc	cactatccat	77220
agcatgtggt	actcatcctc	atggagaaaa	gatagtgaag	ccacctgcag	atgccttgcc	77280

caccttttcag	gcaggaggaa	gggggaggga	gagaaaaggt	aaaggcagaa	gacagttgag	77340
tcatctcttg	tcatgctgga	ggagcatggc	ttccccagaa	cccctccgca	gtctgcctac	77400
accccatctg	ccaaatctgt	gcaacacaga	acccgtgact	ataagagagt	ctggagaagt	77460
aagaactttt	gctgggtacg	ttgctgcctt	gaacagaatc	atggttctct	tagggagagg	77520
atgggaagga	cattgaggag	atgctgatcg	ctgcctccct	ctctgcagct	tcctcacccc	77580
aggttccctc	atctgctgag	aacaagaggg	tccctgtgga	aagcacccctg	gacagaaagg	77640
ccacagataa	gggcatctat	gttctatggc	ctgatattag	ttactccctt	gggctcaagt	77700
tgtggggact	caggactcag	gtcttgacag	aggaagacag	acagacctgg	ggttggcatt	77760
cacagaggga	ccactgagct	ggcaggtaga	tatgtccatt	gagcagagta	tttctgcccc	77820
ttctaggttc	cctctcctct	tccctggcct	gacaggtgcg	ttagtaacaa	cggaggggaga	77880
tttctaattg	ataatatgag	cactacgacc	accaggtggc	accaacacac	acttctgctg	77940
ctaagcagag	gctgaaccca	gacccttctc	agagcctgtc	tgaatcctca	acactctctg	78000
gaaccagggg	agtgaaaagc	agttttgaat	aatgaaaag	atccatcttg	ttttgttact	78060
atcatatctt	ggttgacttc	attcgttcat	tcgtttattc	attgatcaga	atcatacatg	78120
gtcccactat	gttccaggaa	agaacaatgg	aaaacagaga	aggaatatct	ctgcccggga	78180
ggagctctca	gtctaattggg	gagagggatt	gtgtgttgat	aacgaaacat	ttattgagca	78240
cctattgcat	gctcatggaa	agccctttag	tggctcctca	tttccttcaa	ggtaaattca	78300
agtcctcagc	ctctctgtct	tcatctcacc	ccacctctct	gcaccatcac	cctacactag	78360
ctgcacataa	tccaagcaca	ccctgtctcc	ctgagcctca	gccttaggct	cttccccctc	78420
tttcatctct	ctgaacctga	ataacttctg	tttgcactc	aagatatcag	accctaaaaa	78480
atgcctttcc	taacctatcc	atcaccagt	ttgccacatt	tatttaaatg	atcttccagg	78540
ggaccagcaa	atthttgagac	aggaggcaat	aactgcttat	tcatatttgt	atgcctgggtg	78600
cttagacaag	gatctggcac	atgtaagcct	taaggggatg	gttgggttta	tagagatgaa	78660
tgagacaagg	tcatctcata	acctagcaga	gaaatcatgc	acagagctcc	atgtggggag	78720
atcagagagg	gtcctccata	gcaggtgggtg	ctagagttgc	gtcttaggga	aattccagggt	78780
catgagaaca	gtgaaagtgg	cagcacagag	gcatgaatca	gtagcagaga	gtacaatatc	78840
tacagaaatt	tgcagggtcc	aagcagaggg	gctgtagaag	agcataaaat	tcagaatatg	78900
gagacatcct	gtgctgagat	aaggcagtgg	aactttttcc	agaaggcaaa	agggagccaa	78960
gggtttttag	tgggtggaat	gatataatca	taattgggtg	tagatgggtg	attagtgaac	79020
gattgtgggtg	tagcgaacta	ccccaaact	tataaagaca	accatgtatt	taactcgtaa	79080
atctgtggcc	catctaggaa	gttctgcaga	tactgaccaa	gctccgcac	ttgattgggt	79140
ttcctcatgt	gtctgtagct	ggcaggccag	ttggaaactg	gctgggtctta	gatcgctcc	79200
cctgggatgt	tttcttcca	tgcagtgtct	cattccccag	ggaaatcatg	tgggttcaag	79260
ggagttagtg	gacatgagta	aggcctctta	aggccttggc	tgagaactgg	ctcaggcacc	79320
gtcacgtctg	ccatacatta	ttttgaaacc	acatgtaaaa	gctgatatat	agagagggtga	79380
aaacaattgt	ggccattcag	atggtctact	ctgcctctgt	agtgtggaga	gtagtgatag	79440
agagaccaat	taggaatctt	acaccagccc	agggtggagg	caaagggtgg	gtttaaaca	79500
aatatthttat	ttttttaagt	tcaaatttaa	cttttaattg	acatatagta	ttaggttctt	79560
tcaaatgtaa	ttgcagttht	tgtactgttg	aaatgtgtcg	tttgatattg	gaatacatcc	79620
ttaaataaat	gtggttatgc	tatacatgat	tttaattgcac	atatttcgct	tttaattttt	79680
tgctaattgac	ttattacttg	ctgtttattt	catatttatt	ttaggctatg	gaaataatgt	79740
tagacaaaaa	gcaaatthga	atgatttttt	tttagttgaa	aatgggttgt	aaagcagtgg	79800
agacaactca	caacatcaac	aacacatttg	gcccagggaac	tgctaattgaa	catacgggtg	79860
agtgggtggt	caagaagtht	tgcaaaggag	acatgaacct	tgaagaccag	gagtgtagtg	79920
accagccatc	agaagttaac	actgaccaat	tgagaacaat	catcgaagct	gatcctctta	79980
cagctacggg	agaagtgtgt	gaagaactca	acttgaccat	tctatgatcg	ttcggcgtht	80040
gatgcaaat	ggaaagggtga	aaaacctcaa	taagtgggtt	cttaatgagc	tgagcaaaaa	80100
tttaaaaaaa	gtatttttga	agtgtcatct	tctcttattc	tatgcaacaa	caatgaacaa	80160
tttctcaact	ggattgtgac	atgtgatgaa	aagtggattt	tatacggcaa	ctgggtgacaa	80220
ctagggtcagt	ggttggactt	agaagaagct	ccaaagcact	tcacaaagcc	aaacttgcac	80280
caaaaaacaa	aaggctcatgg	tactgttttg	gtgatctgct	gccagtctga	tccactactg	80340
ttttctgaat	cccagtgaac	ccatttatatc	tgagaagtat	gctcagcaaa	tcgatgagat	80400
gcactgaaaa	ctgcaatgcc	tgcgaccagc	attgggtcaac	agaaagggtc	caattctcca	80460
caacaaccaa	ctgcacatcg	cacaaccaac	acttcaaaag	ttgaatgaat	tgggctatga	80520
agttttgcct	catccgccat	atttacctga	cctctagcca	attgtctacc	atttcttcaa	80580
ggatcttgac	aactttttgc	ggagaaaatg	cttccacaaa	cagcaggatg	cagaaaaatgc	80640
tttccaagag	ttcatcgaat	cccgaagtat	ggattttttac	gctacaggaa	taaacaaact	80700
tatttctcat	tggcaaaaaa	gtattaattg	taatgggttt	tattttgatt	aataagtgtg	80760
tttgagccta	gttataatga	tttaaaatgc	acaatccaaa	accacaatta	cttttgcacc	80820
aaccttaata	ttgtacatac	ttatgggggc	acgtatgtat	gtttcactac	acataatgta	80880
cagtgtatcag	atcagggttaa	ttagaatagc	tatcatctca	aacatttaat	atttctttgt	80940
gttgggaata	ttcagtattc	tcttagctat	ttggaactgc	atagtacatt	attgttaact	81000
atagtcattc	taaagtgtca	tagaacatta	gaatgtattc	ctcttattta	actgtaattt	81060



tgtctccctt	aacaaatttc	tcactatctt	tgcctttccc	tacccttccc	agcctctagc	81120
atcctctgtt	ctagtttttt	cttttatgag	atcaactttt	taaagcttct	caggatgagt	81180
gagaccaagc	tttgtttgac	tttgtgttcc	taaaacaaag	gttttaataa	aacaatacaa	81240
aagggtgggc	aggcctaaag	taccccaaca	ttaaaggccc	ccaaagaagt	ctgatctatt	81300
taccctaaaa	gccagaaagg	aaagattaca	atgagaaacc	cgaccaaaaa	ttgcttgggg	81360
ctatgattag	gcaggttaat	caactgacaa	aaggggccaag	gtccctttgc	taaacacctt	81420
gctggaaacc	caagctttgt	gcacatgagt	gggtgaaatg	gtcaggagtt	ggagaagaga	81480
aactccaggg	ctccttgata	ccaaagcccc	tatgtgctgt	ggtgaagccc	cagtggtggg	81540
tatatacaga	attgtatata	gaatatataa	ttgtaaaggc	tgatagggtt	atgaaagttg	81600
gaatatttga	acaggcttta	tgtaagaaag	cagtgctctc	tttgcttgag	tgttttgtgg	81660
gaatggatat	tgctgtgctg	gagaacactt	cccttaccta	gtattataaa	actgaaatct	81720
gttgatatag	tcctaattgga	gactatagtt	aggaatagaa	gagttgaggg	aattaagggtg	81780
aacatttgga	tgaaaactaa	tatgtttggg	caggctttat	gtgaagtgtc	tgcatctcct	81840
ttacatgatt	gtattatggg	actagacatt	gtatctgact	ggggaatgtt	ccccctacct	81900
agtactgtaa	aacagaaggc	atatatatcc	aacctccaag	caatattaat	tgaacacact	81960
aaatgagaac	cagtaagatt	gtctgagggc	agacagtgtg	gactggaagc	tggagcactg	82020
gtaggaacaa	attctcagcg	tgatagtcct	ggcggggcgg	gggcgggggg	aggggacata	82080
aaccgggact	tatggcaaaa	gcctgtgagt	gcctcccagt	gatgaacact	gggactttga	82140
actagagaat	ttccacctga	gggtcaatta	ttacctgtgt	attggacatt	aattgaagct	82200
acctcagtga	ctgaaggaca	taaaacgata	ttaaatcctg	aaatacccat	gatattcttg	82260
gtgatgtcag	agaaacactc	tactgggggt	agggggaagg	cagtggttcag	aggtattcca	82320
tgaaaatgag	ttcaatggaa	atagaattca	gtggaaatgg	tttatacagg	atcatgctat	82380
ctaggagtgc	aaggaggaga	cactcacaaa	cagagagtct	ctttcacctc	aggactgatt	82440
ccagagctgt	gtgaggagct	tctgaattat	attagttgta	cagtgcccta	taaaccattc	82500
ttactgagc	actaagagct	gcttggtctg	tggacagcaa	ttccaagggtg	aacgaacatc	82560
ctgtttggaa	ggccaccact	ttgtttgaag	aaagcaaaaa	caaatcagct	caatgggttg	82620
aattgcatgc	tgtttaccta	gcatgatgga	agaattgaac	agtgggaaaa	gcccccatgt	82680
tggggccagt	ggcctggcca	cacactcagg	caagagggtg	atggaaacct	ggcctagtaa	82740
aagggtgtct	acagggggca	cagtcctacg	ggaatttgag	gggtgcatta	aagtaggaca	82800
tgtcaatgcc	cttcagaaga	atcgctttcc	agatttgaaa	ggtagttgga	attggcaaat	82860
agatgtccct	gtgtgcttgc	ttaagggtga	cacctgggtc	catgaaatga	actgacactg	82920
gggtagggca	gccacgcagc	tggaatgaat	ctaggcatat	tccttttgca	tcctctgagg	82980
cacaaaatgc	caataagaac	tgttctgttt	gccagcagga	gacagagggt	ccagagggct	83040
atgtggcaga	ccctggtggg	aaggccctga	acatagctgg	caagtgagac	tgatgggtgg	83100
agccctggca	tgggggtgct	aaaaaggggt	cttgaccaga	atagatgctg	tctctagact	83160
gggttttgct	tacctggtgg	aagatgcaaa	tactcagaat	gccataaaaag	aagtgggaata	83220
gaagatattg	caccaatttg	gatggcagat	tcacatttct	tcaggccaag	aaatacacaa	83280
tatagcctat	aatgtccaac	aatgggcaga	gagatctcct	cctcagaata	atagtttgat	83340
agaaaatttg	acagacaac	taaaacattg	gttgtctgaa	atggagggag	ataaattgcat	83400
gaaaggctgg	cttgcacatc	ttcacaagtg	tatgtctaca	ctcagcagga	ggagatgaag	83460
aagtgcctcc	actagataga	ctcctctgtt	ttcctgggtg	atctgggaaa	gaagagatgg	83520
ggagaatgct	ggtgtgacta	tgcaattctt	agtagggaaa	gaatatgctg	atactatgac	83580
tattttttta	tcttcttcac	actatatcaa	cttttttttt	ctttttctta	tctgatgcag	83640
tggttataga	accagggtcg	attccaacga	caacaaaaat	gtgtaaattc	ctaaggccct	83700
gatggggcag	attgtgctct	gatcccatct	gtaaaaattg	gggttcatag	taaattgcatt	83760
tatattttac	caggtggtag	aaacacccca	ctagtctctg	acctgtgtaa	ctttacccta	83820
tctgaatggg	agtggactaa	gtgggaggca	cttgctagac	tagcattgct	gcctgcaatc	83880
tgggagcaga	cagtggccaa	aactaatgta	ccttcgaaa	gatggaaaag	ttaggcaaaa	83940
atggggagaa	ggagggaag	tagctaagg	caaagggaatg	aataaatggg	ttgtgtgatg	84000
acggaaatcc	aatatatatt	aacatctcaa	aagaggctca	gagcaagtga	tgatattgtc	84060
tcttagctcc	attatacaga	tgccataaaag	gctaaagctg	tatgtttgca	gagtccagtc	84120
ttgcttttgg	aaccagcaa	gatctctcca	acaaggctac	cagcccaagt	gctctctccc	84180
tgggagacat	tttcatacaa	tatagcgatg	aagtgagact	aattattaat	gatggaatgg	84240
gattctagta	atgcgccagt	atttttttga	gttctatatt	gtttgctgta	aagggtttct	84300
ggccagagtg	acccagaggg	atgggctgtg	acatcataag	aaacacatat	tagggccctg	84360
gcctcagcca	gggacccctg	cagtctggaa	catccaacaa	aagaaacaca	ggcacagcac	84420
cagtcagcag	aggggcttcc	tccaagggtc	aggagtgtac	ctggtaaggg	ggttaccttt	84480
ctcctccact	gcaatgcaga	gtatggctgc	aaatgaaagg	aaatacagag	aagccatgct	84540
gctaagagcc	tatctactgc	ccattaccct	taagcactc	tgatcttttt	aagatctagt	84600
ggatcatagc	ctaaactata	acatcaaaaa	tatttttgata	ttatgccctc	ctgtgaaacc	84660
aagggcaaga	atttagccac	aaataaagac	cctgaacaga	accttgacct	tctgaaaaca	84720
cccagaagcc	aactgacaat	actcaactta	caccacagta	aaatgaacac	aaaccctccc	84780
agatgagaaa	gaatcggtgc	aagaactctg	gcaactcaa	aagccagagt	gtccccctac	84840

ctccaaatga	gtccactaga	tttccaggaa	tggctcttaa	ccagactgaa	atgacaggca	84900
tagaactcag	aatgcagatg	gcaagaaagc	tcatcaagat	ttaggagaaa	gttgaaacct	84960
aacccaagga	atccagtaaa	acaatccaag	acctgaaaga	caaaatagcc	gttttaacaa	85020
agaaccaaac	tgaacttcca	gagctaaaaa	attcactaca	ataattctat	aatataatta	85080
aaagtattat	caacagaata	gaccaagatg	aggaaagaat	ctcagagctc	aaaggccagt	85140
acttcacatc	gacacagtca	gacgaaagtt	aaaaaaat	tattttcaag	agaattaaat	85200
cgtttattga	ttacacgtga	taatggatga	tacacaagct	tcattcccat	ctataatttt	85260
atctggtacc	attattcaat	ttagatata	tgcataagat	gtgccaacaa	tcacttttat	85320
aaccattcca	tgattttgct	tgggtaatcc	cttttaatgg	tgaacttcag	gtcacaacag	85380
taactatcag	ttcaactaca	ccaaggtttc	caaagacaat	ggcttctcca	cccaagcagg	85440
ttgtatataa	attccaaata	gaacctggca	tcacctgaa	ggaattctaa	cttcacactg	85500
ttggggaaat	ttaccaagat	ggcttcagag	tagactaact	ttacacagca	cattaaaaaa	85560
aaagacattt	attcagcatc	acgatcagac	tattacattt	agcaatcaac	agcatgggtg	85620
caaaaaaaaa	aatctacatt	aaaacccttt	gttggaatgc	tttacacttt	ccacagaaca	85680
gaaactaaaa	taacctgtta	tacaattagt	cacaaatata	gtccttgagt	tttttgccca	85740
tacacatgag	tattttgtcta	aaacatgtct	tctttgtagc	agctaggccc	tgccaccact	85800
gtgcttggct	gagttcacaa	atctgtcgta	acctgtagct	tccctgtcac	ttctctggct	85860
ctcctctcct	gctaagcttt	gtttccta	taaaatcttc	aatgaacaaa	acttccaaga	85920
agtatgtaaa	gagaccaaat	ctgcaattca	ttggcattcc	tgagagaaaa	aaagagaata	85980
agcaaccttg	caaaatatat	gtggggatat	agtccatgaa	agtttctcta	atctcactag	86040
agagggttaac	atgcaaattc	gggaaatata	gagaactcgc	tagatgctat	acaacatgac	86100
catcctcaag	gaacatagtc	atcagattca	cgaacatcaa	cccaaaagaa	aaaatcttaa	86160
aggcagctag	agagaagggt	caagtcacat	acagagagaa	ccccatcagg	ctagcagcag	86220
acctatcagc	agaaatctta	cacctcagaa	gatattgggg	gtctattttt	agtgtcctta	86280
aaggaaaaga	atttcaacca	agaattcata	ttccttcaaa	ctaaacttca	taagtgaagg	86340
agaaataaaa	tcttctcag	ataagcaaat	gctgagggac	attgtttcaa	ctaaaccagc	86400
cttacaagag	gtcattaagg	gagtgctaaa	catggaaatca	aaagagtgat	acttgttacc	86460
acaaaaacac	actaagaata	tagcccgag	gtactataaa	gcaactacac	aaccaagtct	86520
acataacaac	aagctagcaa	cacagtcaca	ggctcaaaat	ctcatatacc	tattctaacc	86580
ctgaatgtaa	atgggctaaa	tgctccact	taaaagatat	agagtggcaa	gccagataaa	86640
aagacaagac	ccaaccatct	gctgtcttca	agagactcat	ctcacatgta	atgacaccca	86700
caggttcaaa	gtaaagggat	ggagaaatat	ctaccatgca	aatggaaaaac	taaaaagaac	86760
cagtcactat	ttttatgtca	gataaaatag	atgttaaacc	gatttctatt	agaaggaca	86820
aagaagggtg	ttacgttatg	ctaaaatgta	caattcaaca	agaaaaatta	actatcctaa	86880
atatatacac	accaacatt	ggagcacccc	aattcatgaa	acaattcttc	ttggactaca	86940
aaaagactta	gataaccaca	caataagagt	gggagctctc	aacattccac	tgacagcatt	87000
agacagatca	ttgaggcaga	aaacaaacga	ggaaactcta	gacttaaaact	tgactcttgg	87060
ccagttagac	ctaatagaca	tctatagaac	actccacca	acaatggcag	aacaaatact	87120
cttctcacct	gcacacagag	ttccgctggt	gtcgtccagg	ctggagtgca	atgggtgcgat	87180
cttggtcac	tgcaacctcc	gcttcccagg	ttcaagtgat	tcttctgcct	cagcctcctg	87240
agtatctctg	ggattatgac	acccatcatc	acggctggct	aattttgttt	tattgtttgt	87300
ttgtttgttt	gtttgttgtt	gttgttgttg	tttgtatatt	tactagagac	cgggtttcac	87360
cacactggcc	aggctggtct	caaactcctg	acctcaaaag	atctgcctgc	cttgggtctcc	87420
caaagtgctg	ggattacagg	tatgagccac	cacacctgac	cacacagaac	atattctaag	87480
attaactaca	cgtcagtc	taaagcaagt	gttaaaattt	tttttgtaa	gttgaaatca	87540
taccaagcac	actctcggaa	cacagtgc	taaacataaa	aatattatca	agaactctc	87600
tcaaaactgc	ataaatacat	ggaaattaaa	caacttactc	ctgaataaact	cctgggtgaa	87660
tatcaaattt	aaggcataaa	tcaaaaaatt	ctttgaaatt	attgaaaata	gggatgcaac	87720
ttaccaaaat	ctctgggatg	cagctaaagc	agtgttaaga	ggaaagttaa	gagcatgaaa	87780
tgcttctatc	agaaggttag	aaagatctca	aattaacaat	gtaagtgtgc	acctaaagga	87840
actagaaaaa	gagaacaaac	caaccccaaa	gctagcaaaa	gaaaactaaa	attagagaag	87900
aatttgacac	tgagttgcaa	aaatccatac	aatgatcaa	taaaactaca	agttgggtat	87960
tagtaaaaaat	aaaccagatc	aataggcccc	taactagatt	aacaaaatca	agaagatcc	88020
aaataagcac	aatcagaaat	gacaaaaatg	atgttacacc	tgatcccaca	gaaatataaa	88080
agatcctcag	ataatattat	gaataactct	atgtgcacaa	attagaaaaat	ctggagaaaa	88140
taaataaaatt	cctggaaata	atctcctaag	attgaactcag	gaagagattg	aaatcctgaa	88200
gagactaata	tggaactctg	aaattgaatc	agttacaaca	acaacaaaaa	aaccttacca	88260
atcaaaaaaa	gtcctggatc	agattaatcc	acagccaaat	tctaccacat	gtacaaagaa	88320
gaactgagac	caattctact	gaaactatcc	caagaaaatc	caagaggagg	gactcctctc	88380
taactcattc	tatgaagcca	gcatcagcct	aatgccaaaa	tctggaagag	tcacaatgaa	88440
aaaaaaaaaac	ttctggctaa	tatccctgat	gaacatagac	acaaaaatcc	tcaacaaaat	88500
accaggaaac	caaatgcagc	ggcacatcaa	aatgttaata	aacgatgatc	aagtaggctt	88560
catccctgag	atgcaataat	tggttcaaca	agtacaaatc	aataaatgtg	attcaccaca	88620

ttaacagaat	ttaaagcaaa	aacaatatgt	tcatctcaat	agacaaagaa	agaatttctt	88680
ataaaatctg	acatcctttc	atgttaaaaa	ccctcaacag	actcagcatt	aaaggagcac	88740
atctcaaaac	aataaaagcc	atctatgaca	aacccacagc	caacatcata	ctgaatgggc	88800
aaatctggaa	gcattcccct	tgagatatgg	aacaagacat	aaatgccaac	tctcaccact	88860
cctattaaac	atagccctgg	aagtcctaac	tagagcaatc	aggcaagaaa	aagaaataaa	88920
aggcatctaa	acaggaaaag	aagaagtcaa	actatcttca	ctgacaatat	aattctatac	88980
ttagagaacc	ctaaagaatc	caccaaagg	ctactagaac	tgacaaatta	ttttagtaag	89040
gtttcaggat	acaaagtcaa	tgtacaaaaa	ttactagcat	ttctatacat	caataacact	89100
caggctgaga	gtcaaataca	gaacacaatc	ccatttgcaa	caaccacaaa	taaatgaaat	89160
acctaggaat	acagctgacc	aaggaaagtga	aagatctctg	caaggagaac	tacaaaactg	89220
ctcaaacaaa	tcagagatga	cacaaataaa	tggaaaaaca	ttcaatgctc	atggatagga	89280
aaaatcaatt	tcattaaaaat	ggccatgctt	cctaaagcaa	tttacagatt	caatgctatt	89340
tccatcaaac	tacctgcacc	aattcttcac	agagttagaa	aaaacaattc	taaaattcat	89400
atccaacca	aagagccaga	atcatcatag	caatcctaag	caaaaagaac	aaagctggag	89460
gcatcacatt	acccaacttc	agactatact	ataaggctat	agtaaccaa	atagcatggt	89520
actgggtaca	aaatggactc	atagaccaat	ggaacagaag	agaaaactca	gaataaaagc	89580
cacaaacctt	aaacctctg	atcttcgaca	aggccaacaa	aaacaagcaa	tggggaagg	89640
actccctatt	cagtaaatgg	tgctgggata	actggccagc	catatgcaga	agaatgaaac	89700
aattgaaaca	cagccatgcc	catttggtata	ggtatcgtcc	atggctgtct	ttactatcac	89760
agcagttgcc	aaagagaaca	tggcctgcaa	agtccaaaat	atttactatc	tggcacttta	89820
tagaaaaagt	ttgctgatac	tctaatttgg	atcactgagt	gaccacatgg	aagacaacca	89880
cattgttgac	ctgaacaaca	acactctact	tctttacata	aatgaaaaat	aagccattga	89940
aattctgggc	ctaattgcta	ccatagttta	tcctgggtctc	actaataatt	cttccctcagc	90000
agtcacaggg	tgattgactg	atgaatgtac	atggcccaat	catcagttgt	ttgagccatt	90060
gaggtggact	agttatgccc	atgggagtac	agctctctcc	tctacgaccc	accacgagcc	90120
caaaatttcc	tccagatact	ctgaccagtc	agtcctagga	cctgattgac	cccaggggag	90180
ctgacccccct	aagtataaca	cagcatcatg	ggcagcatca	tgggcctggg	aaggtgtaaa	90240
cataatccaa	tttctgccc	ttgaactgaa	tgtaacagg	aagacgttcc	ctgaagcaga	90300
aggaaatgac	cttgatgacg	atgacccttg	ccaaaggtag	gtacccttgc	cttgtcacct	90360
acctgggtgg	catgacgggtg	atcaaggctg	gccctgcttt	catgtaacta	actggccttc	90420
gatgggttcc	ttttcccat	gagtgacttt	tttcagttat	acacttttgt	aaactagaag	90480
tgtttttact	ggcattttct	tatgtacttt	tttattttta	ccatcatttt	aatttaaaaa	90540
atgcagtcac	acatttttcca	tgcatacctc	taatttatgg	caggttatag	aggtcctgca	90600
tttatggcaa	tgggtataaag	tctccttttt	gagtgagcat	gttgaagtaa	aaagagtgc	90660
ttcattttaa	gaaaactgct	catggaagta	cagatgat	gctgataagg	caaaaaacca	90720
tgatattagt	atgagactaa	ctgaggttcc	agaaacactg	cgtatgccca	ggctgcagtg	90780
gagaatgtca	tagaatcctg	gattcataga	gtgtggagcc	atgggtgaagg	gtgcgtgaga	90840
gggtccctcc	cccagagcca	caccctgtct	ttccacaagg	aattcccaaa	tgtcacccag	90900
tggattcaga	cttctgtctc	ccagttcagt	gttctccacc	acaaaatcta	cacctgatca	90960
atcccatagt	tcagagacaa	agctgagtga	ggggcccgaga	aagacatgtg	tttgcgtgtg	91020
ccaatgcctg	ctctaacatg	tgttttccac	atatctgctg	agcaaactga	tggaggtgga	91080
gaagcttggg	agagttcatt	tgaaggcccc	agatatgccc	actctcccaa	gtcctaccca	91140
acctcctatg	taagccaggg	gtggcttttg	catgtgtcca	tggggatggt	cgcctcaaa	91200
tgatgcagga	aggagtcaag	gcagtcctct	gatgggctga	tcctttgtct	tggaaatcctt	91260
aagatcattg	tagatcctta	agaacattcc	agaactctca	cagcattctg	gagtcattta	91320
tttaacacat	gtttattgag	cacctactgt	gggccaggca	tgcttctggg	tccttggggg	91380
ccattagtga	acaaagcaaa	ggtccttaga	ttcacggagc	gtgcattcta	gcagggggag	91440
acagataaga	agaacatgca	aattactcca	tggatcatgt	gatatgttag	aacgggataa	91500
gtgccttgga	aacaaagaag	cagttaagca	gatgaggag	atcagaagga	aggatcccat	91560
gaattccgct	gtcttgaatt	ttgacatagt	aggggagagg	agtgggccag	gaggtgtgtg	91620
agtggcaagt	gtactgaggt	gtccagtcgg	caagtgtcca	actctcaggt	gtgccagct	91680
ccctaattgct	gaggagaaaa	atggcaggtg	tgtccattca	ccctggccaa	gctgggaaga	91740
aaagcccaaa	ggttctaatt	ggcctcacca	cctctcccca	gggtacaaag	gaccctacag	91800
gcatcagaga	agaccccat	catctcagca	gccaggcatt	tggagggttt	ccagcagccc	91860
acctctagct	gccttctttt	ctttcctttt	ttaaaaaata	atatttactg	tttttatttt	91920
ctgactgcaa	atgtaatgca	tacttattac	aaaaaaggta	aagtattatg	atttaaaattt	91980
tgtttgtatt	ccagtttttc	tgctgtgtgc	tatactttct	tcctttaaaa	tggaaatgta	92040
agttcagata	atgttgatgc	ttgctttgct	cattaagtat	atcatgagca	tcattctatg	92100
ccattaaata	gcatagcctg	atattagcag	ctgcatcaca	tttggtattg	caccacaatt	92160
aatttcccca	agctttttatc	tggggtcatt	aggttacata	tgaagttttt	gataatatag	92220
agagcactgt	gatgaatatt	ttatagtga	acctttatgc	ccattcataa	ttatttttagg	92280
ataagtcccc	agaaatgaca	tttctgagtc	gaaaagtgtg	tatcttttgt	taaaattcct	92340
tgccaaaata	ttccaactac	acttctccca	ttgaaggatg	aaaatctcca	ttcatcagat	92400

tttttgctgt	gcttggggtt	attaaaattg	tttttggtta	tccgataggc	aaaatgataa	92460
taataatagc	aatattat	tcctatttag	tttgcat	tctgaagacc	agtgaagttg	92520
agttctttt	ccctttcttc	acattggaat	gttggtttta	ttattattat	tattataatt	92580
attattgttg	ttatgccact	tgtacttggt	gatctgcagg	aaaacctccc	aagatggaaa	92640
gcatgaaatt	gtctttgctg	gctctgattc	ttgacagctg	tgtcatccca	gagcctgagt	92700
gcctcagttt	cctcatgtac	ctagtggggg	ccatgaggcc	tgccttctgg	tactttgagg	92760
tctgggactg	ttgcttataa	tatacttggt	tataagcacc	acatggcatg	gatctacctg	92820
gctatgtaaa	cttgggcagg	ttctctaacc	tctctgggct	tcagttttct	catttgtaaa	92880
atggaaataa	tggaacctat	gtaatcagag	cttaatgagg	cttaaatgag	ttaatacata	92940
aagggctact	gaaacagtgc	ctggaacact	gggaggacgc	aataactatt	accaatgttc	93000
atctatgttg	tatccttgag	atctttcatc	agggcaacca	acagcacttg	cctgggatag	93060
gcagatggta	gaatcttggc	atgtcagggc	tgcaagactc	atgcagaaat	caatcctctc	93120
acatagacct	ggcagattgg	gacccagaat	gtgaaaggaa	ttcacccaag	gtcaccctgt	93180
aaatgtgtgg	gagagacaaa	actagagcac	agttctgacg	ttgtcccaca	aagattttac	93240
ccctaagata	ttgttgga	tgtcacctcc	aagggaggat	cagtgatttg	gtggtctccc	93300
ctcctcaatg	ctgggagttc	caaagtttcc	gggaagaaaa	gagctgtgaa	gcccttctca	93360
ctctgcttgg	tcttaggaga	ccttagtgag	tcccagcgct	cccacctgaa	gccctgata	93420
gcctcctacc	cactacaatg	tcgtgagtc	gtaaatatca	agtccatttt	caggcttaaa	93480
cctcccagtc	caaggcgctg	ccatagaaga	cacctcgctt	agatctggct	gaacctcagg	93540
gggtcttctt	tccccctccg	caggtgcacc	caagatccca	aggtagggca	gtttctctca	93600
gaactattga	ccaaccgaaa	ggaaaacatt	cctttcaagc	tttctgaaga	ctgtctttac	93660
ctcaatattt	acactcctgc	tgacttgacc	aagaaaaaca	ggctgctggg	aagttgtggg	93720
atcccctggg	caagacgtgt	cagtgccagt	acccagata	ttctagtgtg	gatcggaagg	93780
ggatgaaggc	agcttgggga	gggagctgca	caggccaggga	ttgtttcagg	acccagggc	93840
ctctacagga	aacacaggtt	ttccacacgt	cagtttcccc	tcgtgacata	gggactctgg	93900
gggagtttgc	tgtgcctctt	taatgaacat	cttaattggt	ccaagttccc	tcagtataa	93960
agaaggatga	gaatgattac	ctttagttac	atctgataaa	atctgatacc	cagattggta	94020
tcagagtggg	taagacatga	ttttcaataa	tgttagcggt	cgaaggaact	tagagaaaag	94080
ccaacacctc	aactcttctt	tttcagatag	agaaaccgag	gcccagacag	ggaaggggag	94140
gtcaccaggt	aggatagttt	tggtcaagt	cttctgatct	tcaaactagt	gcttttgaca	94200
cagagtaggg	cattgagatt	gtatgtggcc	tttctccagc	acaccaacat	ccatctgggg	94260
taactttcac	tgtccgggta	tgggtgttgg	gggcagagcc	tgggacaatc	ccagaagctc	94320
ttccttttgc	ctttggccaa	atatctggga	tttttttgta	cctaatttcc	ctccctaatt	94380
gtgttggcaa	aggggatga	cccaatgtgt	cagcatatgc	caaataaaca	aacggcagga	94440
gatggggctg	gctgccagct	gcaggggttg	gagtgtctgc	tggcaaagaa	ggccacccca	94500
aggtgaaaga	ggaagggtg	tcaggtccag	tagctgtccc	aggggcaccg	tgagcatggg	94560
cctaggagtg	gcggagcagg	tctgcgaaca	tgggactaga	agttggccct	acatgtgctt	94620
cgtgagacac	aggaagtggg	agaaagggtt	actcattaat	tcattcattc	ttctattgtg	94680
tactcagggc	cccatataca	cagttagacc	tggggcttca	cggaaaggag	gaacatgaac	94740
gcactccaca	ctgcccctgc	cttcaaggat	cttgcccttt	gtggggtaga	ggcatatcct	94800
cctttcagca	tgttattgca	ggtcagcact	cgggctcagt	cttcacacaa	agatgaatgc	94860
acactcaatc	cctccacagg	aggcaggcag	ggattagagg	tgtgggagaa	acaggagctc	94920
tgggaacctg	aaggcaggaa	aacctccagg	aatggccaca	ggttctagaa	ctacacgtgc	94980
ttagaacagc	acttcgtaca	tagtttatgt	tatgagttct	tttatatttc	tgataataa	95040
ttattacaat	actattat	tagccactct	cacttcttcc	ccactatgtg	gacttttaaa	95100
atgcaagaac	cttgagttag	gaattgtacc	tactctcatc	ctcgggtatt	agcagagtcc	95160
ctggcacata	gtaagtcttc	agacagtgtt	agtccattga	ttgaaggcat	cctgaagagg	95220
gtgggtttta	ggctgggctc	tgcaggggtg	ataggatttg	gggatgcaga	ggcataaagg	95280
aggcatttga	ggaagagaca	ccatcacagg	catgtgtgct	tctcgagaca	atcattcatg	95340
cacagagaag	tttacttcac	catgaaagag	ttaactgaga	tgaagctgag	atacaagggc	95400
tgccccatgg	gtacgcggag	tgcttgaaca	gtccaggctt	gaggggtgat	ggagtgaagg	95460
ggagaacatg	aatccttagc	gtttgctatg	cccattgatg	tgttctcagc	gtgaagagcc	95520
ttgcgaggag	gaggcactgg	agactgggta	gaaaggaaag	ggcagccagg	gtatgtgcag	95580
tgggggtggg	gcttggggcc	cagttgggag	aattatggag	gagagagact	gccttttgca	95640
accttgctgg	gcacttggtg	aatttgggta	acaacctccc	tcagttgtga	ccaacaggca	95700
ggtcaccaa	caagatgccc	tctgagtgtc	ccctggcctt	gtgtcctgta	acgagtatgt	95760
tgttcccccc	ctgcccagg	gatgggtgtg	atccacagag	gggggctgat	ggtgggcacc	95820
gcatcaacct	ctgatgggag	ggtactcgca	gcccataaaa	acgtgggtgg	ggtgaccatt	95880
cagcactgcc	tgggcatctg	gggattcttc	aggtaagaaa	ttagactctc	ctcactgcac	95940
ctttggcccc	caacatgagg	ctgctaggac	cagctctggg	catgtcagcc	ctcaggagac	96000
cttaactggg	ttctcatttg	tagcagacaa	gcaccttcac	aattggacac	tacctaccct	96060
ctcaactccc	agccacacta	gtccactagc	ctctgagctt	ttgtatgtgg	tgttccctct	96120
gcctggaatg	cttagtctac	ctaaagaatt	cctcttcac	ctgcaagacc	cagcccccag	96180

ttagctccac	tgaaagactc	atctcctttt	catctgtgct	gctcccacac	attgcatttc	96240
tctgtcatgg	cagctagcat	gcagcccagc	tgttgaaggt	tgacacatct	gacttctcat	96300
ggaaaggagg	gaaggggcag	agtcatacag	ggagttcagg	gcataattgtg	ggtgaaggaa	96360
tgggcgctgc	agaaggtggg	gtgtgggagc	atctgactcc	ttcctggagg	agtgttggga	96420
cccactcacc	ccattttctg	cttgaaatct	ggcaagtgtg	ggaagcaaag	atggagtcct	96480
cctcatcagg	tctccatggg	gacagaagtc	cccattggcgt	ggaggaatth	ggtagctttg	96540
agagcttggt	tggggaaagc	attcaaaactt	aaagggctgg	tacattggag	gagagaaaat	96600
ggggatgcca	agaattttta	gaatttttga	gaatgttttt	agaattcatt	ggttataagc	96660
aacagtttcc	cagtgaccag	atttaagtca	agacggacga	ttggctaggt	gtgggtggctc	96720
atgcctgtaa	tttctgagag	tgatgtggcc	ctcactcctg	ctctggtgga	gaaggggtgac	96780
gtcaagcccc	tggctgaggt	aggtctcccc	ctggatgccc	ccaacccctt	ggctctgtgc	96840
ttctgaattc	tcagaggtta	ttcttgccat	gggttctagc	tgatgttctc	ctagaatcac	96900
tgaagcgatt	gggaggtaga	ggcggaagcc	ttgcttgagc	ccaggagtta	gagaccagcc	96960
agggcaacaa	agtgaatcc	tgtctctaca	aaaagcaaaa	aattaagctg	ggcatggtgg	97020
tgcaagactg	tgggcccac	tacatgggag	gctgaagtgg	gaggatcacc	tgagcccagg	97080
aggtctatgc	tgcaagtgc	tgtgtttgca	ccactgcact	ccagcttggg	aacaaagcaa	97140
gacctgtgcc	caaaatcttc	tcttgaaaag	gagaatttat	ttttcaagga	aatagagatc	97200
tgggaggatg	ggctttgtgc	aaaaacagga	agcagaaatt	acaaaatgat	gggaatccta	97260
gactctgtta	ctcttgttct	ctctctgtct	cttctctctc	gtctgtctgt	ctttctctct	97320
ctctctcacc	ctctacttct	ccctgtccct	gtttatttat	ttgagaaaca	ctctgggcat	97380
tgattctgtc	cgagatcctg	cacggggctc	tgggggcatg	tgcgcttgcc	ctgactcccc	97440
gactgtggag	cctgcctgct	ctccctctgt	gcccttcttt	ctggctgcac	tttgtctcca	97500
atctgcatga	gcaccctatc	tgcccttgag	cttaaggact	ctccttgggt	ccagaaagta	97560
gtcaggctgt	ctttcctggt	gtgaaaaatg	agtgtttttt	acattagcag	ctctccaccc	97620
caattccagg	tcacttaaga	gagaggctca	ctgtcccgtc	tttgcttcga	tgtccctgaa	97680
ctcttagaaa	agtaggaaac	cagagtatgc	tggggcaaat	gaccccaatg	cctagggtcag	97740
gcagaaggga	ccctgtccct	cgggagggct	ttttaaatth	ttatatthtt	tacattthtt	97800
taaagtga	aagaggttct	tgggtatta	attattgtta	ctttgtggct	tgactcagga	97860
caaaggtgca	gagaccatcg	ccatggcca	aattctggatc	tatgcctgca	tgccccttga	97920
gctaaggatg	acttttttta	atcatatgaa	attcaaatth	cattgtccat	aaaggaagtt	97980
ttcctcgaa	acagtgcac	ccattcattt	acottgtgtc	tctggctgtg	tttcatgcca	98040
acagcagtct	tgaagttgca	gcagagacca	catggcccac	aaagcctcaa	atatttacta	98100
tttggctctt	gatgggcaca	ttgctgacct	gtggcctaaa	gagtcatgtt	tgattactgc	98160
ttgggactct	agtacacaaa	tgtgcagggtg	gaaactcctg	gctgtgccac	agatgcctca	98220
ctcagctgag	aaacccccatc	tatgtcttgc	aaggggacgag	accctgtttt	tcttttagaac	98280
tcaccattaa	agcacatttg	ctactttctg	aagtggctct	gtgtgaatca	tcttatctag	98340
gcctcctgca	attctgcaca	tctttattgt	gtggaagaca	tggcactctc	ccacatgtat	98400
taactcatga	ggtagggtgca	gtcattatta	ccatccatga	gtggagaaac	caaggcccag	98460
acaaatcgga	tggactgcct	gtggcctaag	ggctggtaag	tggagcagcc	aggatttggga	98520
agcagacaag	taaattcaag	attccatcat	ctcaacccca	gctccacctc	acctttcttg	98580
acacattcag	cttgagatga	ttatgtccat	ttcaatagag	ataaggtagc	agagataaga	98640
gactgggtaa	ttggctcata	ctacaattgt	gattagtaat	agaggcaatg	ctctgcggaa	98700
tccagaacct	acacatgtgg	gtctagagtt	tcttctgtctg	ccccctgcca	cttgtagaag	98760
tcaggcttag	ttaggataga	acatcttttt	ccatattgat	ggaggggaag	gacttcgctc	98820
ttgaactctg	ttgttgcttg	tgatctttgc	agcaaatgtc	taacactgtt	gggtgtgaaa	98880
ccaccaactc	agctgtcatg	gctcactgtc	tgcggcagaa	gatggaagag	gagctcttgg	98940
agacgacatt	gaaaatggta	ggttgectgt	tcccgtagcc	caaaccctgt	aaacttggtc	99000
ccagacttct	tcatttcagc	tgtcctcttg	ccctgggaca	gttacctggg	gcaatttctc	99060
aagtctcagg	agtctcagta	tctgaatggg	gaatctaatt	tgtccttttt	tttattgaaa	99120
aatgacacaa	atgtaaaaac	aaagtccaaa	aataacatga	taaaaaaact	gaccaaaattt	99180
actatttgac	caaattttta	tattttgcca	ttcttgtttt	cagatgtatt	tttgagaaac	99240
taaacattac	atattccag	gggacaccat	cattctgaat	tttggggatg	gagttattaa	99300
gctcaaagat	tttcagaaag	atgtcacaag	ttatcttgggt	tgacttagaa	actgtctgta	99360
ttagacctgg	tagtgggtcca	gttttctaga	ttttctgaga	ctctgactca	gttgtcatte	99420
taggatagtc	gttcgtccac	tcaatcatta	atccatctac	tatgatcttc	ttatgcatct	99480
atgtgttcac	taattcatcc	cattcattga	tatatthttt	tcaatcta	atcaacctgt	99540
tcataacttt	ttatttttct	atthttcaatc	tatccactgt	tcatgcatca	tccagccacc	99600
atatacttta	actctatcac	cccattctct	caaaaccaac	aatccagtta	tcacctatct	99660
gttagatttt	accactatt	catgtatcca	tccaatccaa	ctgtactcca	gctattgggtg	99720
aagccatcca	tccctccatt	tatccaccca	catatccatg	ctaagtatgt	aggggtgggtg	99780
gttagaggta	gtgaaacaga	catgaagtgg	acatagtccc	tgtcacata	tacttttcag	99840
gttgagtatg	gtggcagcac	agaggggaag	cattcattgt	agtcatcagg	ggtgtctcac	99900
agagaagggtg	gacgagccga	atttgagacc	agacagcgga	attcggaat	tcatgccctt	99960

aaccctgact	ccaccttata	tttcttgaga	aattcagcat	tgagatcatt	gtgcccattt	100020
taataagagg	aacagagaca	gagaaatttt	gtaattggct	catgtcacag	ttccagttag	100080
tcagaggcaa	cacagttcca	gttaggaccc	agaacccaca	cctgtgggtc	tagaataatc	100140
tctgccattc	ctgctgtcct	cacatattag	gacttgggga	cctttatgat	tgacggacag	100200
ctgtggcagt	ctctcaacac	aggggaagccc	agcaggacaa	acacccagat	gacacagcac	100260
ccagggccat	tgggaactat	tcccttttgag	ggagaagggt	gtgaattcca	agctcatgag	100320
tagcctgata	tctggaatcc	ctccttggtac	ctgaggctac	tccctgggtcc	cagggtccggc	100380
tgctaccact	ggactctgct	tgtgtttaca	tgggttgagt	ccaatgtggt	cttggagcct	100440
aggtcttggt	tcaagctcta	aatgaccaa	gtgttcaagg	aattaaaaca	caactgcttt	100500
ctaatagcctg	gaaggaggca	aacattccag	caattctgca	tgtggcatca	gaggaccacg	100560
cttaaaagga	aaaacttggt	aactttggga	aaatccagcc	ctaagatcct	gggacatcct	100620
tctgagattt	tctgagatct	tgtgggagcg	cctccatgat	tacccactgc	ctccagtaca	100680
cacacatgca	gacacacaga	gaaacacaca	cacatagaca	cacacacaca	gagaaacaca	100740
cacacagaca	cacagagaca	cacacaaaca	cacacacaga	cacacacaca	gagaaacaca	100800
cagacacaga	cagagacaca	cacaaacaca	cacacagaca	aacacacaca	caaacacaca	100860
cacacacaca	cagacactcc	tggctagtgg	gactacaatc	cttaatggag	agacctgcac	100920
tggttacttc	ctgccaacag	gccagacacg	tgagctacag	tgcagcgata	caatcactgc	100980
aatcttcattg	aacacacacc	aaagagaagc	atggggtagg	gtaagtcca	gtgagttgta	101040
tgagtcagag	ctgtgtaaatg	ggagatgaga	aaactcccc	aagggtgcctt	gaatggaaaa	101100
aggaatgtgt	tggataaaca	tccttgtgtt	aactgaaaa	ctcaggagtt	gacagtttca	101160
ggcatggctg	gatccagatg	cctattgaat	gttattgaga	atctaccatt	ctctatcctt	101220
cagctttgga	caactctgtg	ttgacttcac	tcttcagcag	atacatcttc	tgggaagggt	101280
aaagacaaca	gcactctaga	gttatatcct	atctgcttcg	aaacccctcg	tccaaacaa	101340
tcctacaaaa	gttctggggt	aaactctatt	ggattgacat	ggatgtatac	ctatccctga	101400
actaatcccc	gcaatcaggg	aaatggagcg	ccccaggcca	catatagatg	cctgaattca	101460
tggagtata	gggaaagaaa	gagatccctg	aaaaagaatg	ggggtattct	tccctgggga	101520
acaggaaggg	gagagggatg	ggggacaggg	aaggctccaa	aagcaggtgt	cctatccaga	101580
gctgtagcaa	tgctggctca	gagttcctgg	cccactcctc	ccgtgccagt	gcccactcct	101640
tcgttctatg	acttcaccct	gtgctcagcg	ccagcagagc	cagagtcagg	cccactcctc	101700
ctgggcccag	ccagctcggc	accaggaggg	agaacctgac	acctctgctg	cccactcac	101760
ccagctcagt	gttctcctgg	gaagcctctt	accacacatc	tctgcttttg	tcttcacaga	101820
atctctgaac	tctagactta	catggagacc	ccagagaggt	aaggacattt	tgtttctcga	101880
ttgcgggttt	tgagtcttag	cacctttaag	ctccaattaa	ctataagtga	agaatcctc	101940
tctcgggtaa	ttataggaac	tctgtgtgct	tgatgctga	ggcccagaga	ggggcagcta	102000
ctcacctggg	taacacagcc	aggaagacta	gtggctggcc	tggaaacccat	tttccctgact	102060
cccagtcag	tgctcccagg	catcacctct	gtatgccctg	ggctctgccc	actcccctgc	102120
ttttttacat	tttctgctcc	ccaaaatggc	actatgggag	gaggttgaa	cagaacattc	102180
cactatcggg	aggcagagat	aacagggtatg	attagccacg	gagaggggaa	gcctgaatct	102240
cagtcacagg	acactcaact	ctcccagca	cacaggagtc	tccaaacaata	tccctcgtgat	102300
ctcctcaacca	ccccacctc	ccaatgggtt	gctgactttc	ggtgacatca	cctctgacga	102360
atcttacaat	cctgtcctct	ctgctgcctt	aatggaggctc	acagcactct	cctaaatgg	102420
catgggagg	gtacatgaga	atcattccag	caaaagactt	attaacactt	tctatatcc	102480
aagaacttgt	ttaaggagct	gtgatatagg	agtaaaccaa	gaaagactcc	ttgccttttt	102540
gggaccttct	attacagtgt	agggagagtg	caataaaaa	gcaattctag	tatgtattct	102600
gttggtatgg	gtgcatgcat	taggggtaga	gtttgcaggt	ggattcaatt	taagtgcgag	102660
gatcagggaa	tggctcaata	agaagggtggc	atttgagcca	agctctggag	gaggcatgaa	102720
gccagctgtc	aggaaacctg	gggaagccta	ttccaggcag	agggaacagc	cactgcaaag	102780
accccgatgg	aagtggcagg	tccagctgga	gaggatggag	tgtggggaca	gactggcctg	102840
aggctgaaga	ggtaatggga	agtgggagag	ggatcattta	aagtagttgc	atttggtatc	102900
tgagcaagat	gggaagcctt	tggaggtttt	gaacagagga	gtcacatgat	cttagatttc	102960
acaaaggctct	ctgcccctgg	tgatcaaata	gactgttagga	aacgggcaga	gtggatgcag	103020
ctgaccagct	ggcggggccac	tgcattgcca	taatccaggc	aatggctcct	ggctgcttaa	103080
ggctgtagta	gtggggatgg	gaggaatgg	tggagtctgg	atatctttga	aggaatagct	103140
gagaggatc	gctgatggac	aggatgctag	gggtaaagaa	gggagaggag	tggaggatgt	103200
cctgagtttt	cgggcagaag	caaagtcata	cccacacagg	gcagccactt	gaaaactcta	103260
agtggacaac	aatcacttgt	cattgttgct	gtggtcagtc	ttcccacttg	gctgccacc	103320
aaccagggca	atcctgtctc	tctcctcaac	ttttatcctt	ttctacttca	tatcctctac	103380
ccaattccgt	gtctcatgg	gcagccagat	tggccttctc	taacagagtt	agagtgcgtc	103440
acccccactt	cttaaaagcc	tgaccttctc	tatgagacaa	attcccttcc	ctccatggag	103500
ttagtccttc	aaaacacacc	tgcgtgcgca	ctatgtgcc	gactatacag	aaggtaggct	103560
ctgcacctgt	cctccctctc	aaaacctgcc	ccacgataat	ttccaagcc	cagaactcct	103620
gagtgtttct	ggaatttacc	ctgcatagt	atatctatgt	ccctttgctc	acgtggttcc	103680
cgtttttttag	aaattctcac	tcctttcctc	acttgtcaat	accagtcact	gccagagacc	103740



cactgcaggc	aggcggcacc	tcctccacgt	agcctgcct	gcattcttct	tgcagagaag	103800
ctgctcctct	tgctggcctc	ccacggcagc	cctgcctgaa	ctgcacagcc	tctcaaggag	103860
gccggacttg	caccccaatc	ctgttcctga	ttgtcagcca	tattggatta	ggatctgcac	103920
ctgtccagc	tggttctggt	ccacttcaca	gaacatttcc	cccaggcagc	ccgaactagc	103980
tcgtcattca	ttggcttttg	tagagcagaa	caaaggctct	ggaagccata	gggtctcaaa	104040
aaagctagga	attgtccagt	tgcatctgat	atctgggagg	gaaaatacca	gcccataagg	104100
gcatgggagc	tgggaagatg	gcccagaagg	actgggggtc	tattgaaagg	ggaccacag	104160
caacctgact	aacaggtaat	acttacagtt	attcagccct	tccagacacc	aggtgctgcg	104220
ctaagtattt	tgcatgtgtt	cagccattta	attcctcaca	ataactcacc	tcttagatga	104280
gaaaactgag	gcccaaacag	gtgaaactcc	cagccagtaa	gtagcagagc	caggcttcag	104340
atccagttaa	tctggtttca	aagtccatac	tctgttttaa	ctgtaccag	aaccagctgc	104400
cctgatggca	atgcgtgaat	caggctctcg	ctaactctgt	accatacaaa	aattattcat	104460
caaaggtaaa	acctaaaatt	aggacatgga	tcaatatact	gtgagttcat	cactgattct	104520
tttattcatg	attttctctc	taataggga	tctcgtccta	gtctaggctc	cttgagtgat	104580
gagggttccg	tacatcctca	aagccacca	tggtcaata	acagctctca	tttaaataga	104640
gatatagtag	acaatctctc	ctcattaatc	attgattctg	cgtttataaa	ttcacctgct	104700
tcctaaaatg	tccttataac	ccccaaatcg	atactggtgg	cactttcatg	gtcacacaca	104760
ggcagggtaca	gagtagggga	atctggattt	gcattggtgg	cacgttccat	ctgagatccg	104820
gcaaggcaac	ctctgtcttc	ttgtttcatc	tctcaagcta	acaagtgtcc	tcttcgtggt	104880
caattttagt	ccatgtgttc	tgcatttttg	tgctttttct	ggtgatgtca	ctgttcagag	104940
ttgcccgcaa	gagtagcgct	gctgtctagt	gttctctgagc	taagcaggct	gtgctgtgcc	105000
ttaccgggaa	ggcgctgtg	tgagataagc	ttgggcagtg	ctgctggcca	tgctgtcggt	105060
gttgaaaaat	ccacaaaact	gcacatacag	gaaaaggagg	aggaaattgg	ccagttcata	105120
catgaggctg	tgatgggaag	tgctaaaagta	acacactactg	tgtgtgatgc	agctgtggaa	105180
agatggaaaa	gaaactgcat	tgaggagatc	atgagatgat	gaaggaattt	ttaaaaagca	105240
ggatggacag	cactgtttgtg	agggtgaaaa	caggaaattt	acactcatct	taccagggtg	105300
caaaaaatgg	gaagggtctt	tcagctggtg	ttttattaaa	agtaatccta	cttataatta	105360
actctttgta	agacttatgt	attatataaa	gtgtctttca	acagaaaccc	acacataaaa	105420
gaaggttgat	gaaaatgttg	tggccagagg	tttgcaagaa	cctaaccag	tatttcccct	105480
ttgagtgatg	accctgtatt	ctctaattca	gcactcgtgg	gagctttgtc	ggaagcaact	105540
gctgggacta	ccgaaaacaa	ctgtggacac	agagagggaa	atgcatgtac	ttcaaatgta	105600
agtatataga	catgtaattt	tatatagata	atacatgtat	ttcagtctga	gtgaagattt	105660
cttcctctcc	tcgtcacctg	accagtgtca	gcctctgctc	gaagttctgc	ccctgagtca	105720
cacatctatc	ctccttagtt	aggaccctgt	gtgtgcatac	ccatggccca	aagtcacgcc	105780
ggtctagggt	gctgggtctca	ccctcagaca	ggcagagttg	gggacacggt	tgtgacctag	105840
ggtgggaatc	acaggcgctg	tggtgtctct	tccccagag	ttacccccac	acaccacagg	105900
tgattgatgg	agtggtgctg	ccaaaaacac	cagaggagct	tcaagctgaa	aggaagtctc	105960
acactgtccc	ctacattgtc	ggatttaaca	ggaagggaatt	tggtggtttt	cttccaacag	106020
tgagaaggcg	caggcctctt	ggagggactc	acccaccccc	atcagccctc	ccacctctga	106080
tcccaggagt	gcttccctct	ccaagcactg	ctctgagttc	tgggcagctg	ttcccttcag	106140
caggaggtaa	cattttccatg	gaaaccttct	ccaggagggc	acagttgtca	ccgggatata	106200
agggccctgg	gatccccctc	ccccagactc	tctgattgtc	ttcctattga	agaatcctga	106260
agtgctgtg	ctggggaggac	cagtagataa	aataactgtg	cagatgggaa	aactgagggg	106320
gcctaggagg	ggaaaggagt	tgaggagtcc	ggagaggcag	tcgggggctt	cctggcttcc	106380
cactttgggc	tgggtatgca	tagttccccc	ataaatcact	catgctcttc	atcacctcat	106440
tgaaaagatc	caaaaaagtg	gcttcttttg	atttccatt	gacttctagg	gaacagtaga	106500
caccagggtc	tacttgaggg	atgacgggtc	gaggagggtg	aggatggaca	agttacctaa	106560
tcgggtgctg	tgctcaatac	ctgggtgacaa	aataatccat	acagcaaaact	ccagagacac	106620
aatttaccga	tgtaacaaac	ctgcacctgt	acccccaacc	ctaaaaataa	aattgggaat	106680
aaaaagtggg	agaaagaaag	attgacttct	aaaattgaaa	aagcgttctc	cttccagctg	106740
aggacacaca	aagctgacca	tgattaaagc	agtaggacag	aatttattca	gtaacacaa	106800
tgacacagag	aaagaagagt	ccagtatgga	ttggactcaa	atccccaaaa	ctaactcctg	106860
gcactgtttt	aaaggctgag	tggtgcaaaag	gataggcact	gtgtgctgtg	gagagggact	106920
tggtccatgt	gactagaccg	cctggatgtc	ttcatcctgg	ctcacctggg	gcagaaacaa	106980
actcctctta	tcgtcaggac	aggaagccat	gcattagact	gcaggaagaa	cccactgaag	107040
tcaggctcta	ctctttccac	agggactggg	aagatcagga	gtcagctccc	tgaatgtttg	107100
cattgcaaag	agaaggctct	aaggccctca	aggaaatggg	gttgggtggt	aaattccatc	107160
ccaaagggca	gagaaagtgt	ttatcattgc	aggcttctaa	actaactgct	ctagttgggt	107220
tcaggggcct	gactgcttct	ctccagggtt	tggtcggagc	agagtaaat	gttctggcag	107280
agttgagcct	tcccaggcaa	gcattgttaag	gatactggag	tcattctagg	gacacagcct	107340
taagctgcta	gaagcgatgc	tagagtttct	tcgagctctc	gagtcagag	gtttgggcag	107400
agttgttttg	tgtgaagaga	tatgaagttc	gccccctcaga	aggatttcag	aggttatacc	107460
aaagacaaa	gcatgaagg	caggctctaa	ggctttcagt	gtcatctgtg	acagggtggg	107520

gtactagggg	ggtctgcac	ctcttcccc	gaacctctc	ttccacactg	gcttggcaga	107580
caccttccct	caccatgtca	ctggccactg	taggtatccc	agcctgacac	acacacaaaa	107640
cacacacaca	cacacacaca	cactgcaaaa	cactgccaca	gcttctccac	atTTTTTTTT	107700
tttttgaat	ctttgcaatg	cttgagtttc	tggatataag	cccatttgat	tcattgattt	107760
tggccatttc	agtataaaacc	catgccctta	aaagcccaaa	atattggagg	actttcagtc	107820
tgcatgtgatt	tgggtgggtc	gtcagtttgt	ttcttctcgt	taattcccaa	tgattcataa	107880
atgcttaact	tttttttttt	ttttaacagt	tgatgagcta	tctactctcc	gaagggaaac	107940
tggaccagaa	gacagccatg	tcactcttct	ggaagtccca	tccttttgtt	gtaagagtct	108000
aggaatcacg	ggaattggct	aggaccacaca	gagcgacaag	gattgcccac	attatagagc	108060
aattaaatgg	ccgaatgaag	actggggcct	cagggtttct	ccatctttc	cacctttccc	108120
acttcacttt	ccaccctagc	ggggagttgc	acagggttg	tgggattcac	cattgaggca	108180
gcccttctctg	gtgggctgga	gaagctacat	cgctcaccag	ggggtgggtg	tcactttatt	108240
gatctatttt	agcgcatctc	taaggaattg	attccagaag	ccattgagaa	gtacttagga	108300
ggaacagatg	accctgtcaa	gaagaaagac	ctgttctctg	acttaatggg	ggacgtactg	108360
ttcgggtgcc	catctgtgac	tgtggcccg	aaccacagag	gtgagtccta	gaggtcgaa	108420
aggggagggg	tatgggaccc	accagcttct	gtatctgact	cacctacctc	ccagcataga	108480
cagatgtgga	aacagccgag	ggtcaggcct	caaaggctga	ttccatatgg	catgggatga	108540
ggtgctgtct	tattttgggt	tatgccagta	gcagcctgtg	aaaaaaaaaa	ccagaggcaa	108600
gcggtttttt	taagggtggg	atcccagata	tcagcagtag	ggcgggtggg	aagtgagaga	108660
ggaaagagat	ggaatccaat	ccaagggtgc	ttgacaagg	agtatcctct	gtggacaact	108720
ggagctggga	aactcaagga	aacactgaga	atacagcact	caggggcac	ccatctgagc	108780
accaaggag	ctgggggtatt	tatccaccag	ctcccacttg	tcattgtttg	aaggctcttg	108840
caaggagtgt	tttattccct	gtgactttga	cctgtgcac	acaagggcag	agtagtctct	108900
tgtgaccaga	caaaggcctc	aggccgggag	ctgcagatgc	tggaggtaga	agtcaggctg	108960
gcatgccag	gaagagggga	tatgggtgag	acactgacag	catctgctgc	aagggctcca	109020
tgcctggagt	tatcgtggga	catagggctg	ctgtaggaca	aatattgaaa	gatgagtctt	109080
ggaagggttt	taagggtccaa	gttggtgca	aacaagcttg	ttaagcattg	gagctggaag	109140
aacaatggga	gtcctgcaca	ggatccagag	gattgtccag	gaccaagaag	gccccaaagta	109200
agagctatgg	tgggtgtggg	ggaggtgtgc	ggaagaatgg	caatgtctga	ggctggcttt	109260
tgtctatctc	ggtgtgtgca	ggaacatgca	agcacagtgc	caggacagg	tctatgcagg	109320
accttctacc	actgacccaa	ggctgtgtgg	tggggcatg	aggttaggga	tgctgtgggt	109380
cacctctaga	gaagtgtctt	ctcctgggtg	ccaactagag	gaggtccaca	ggactcctct	109440
tttcttcca	gctctcattc	gcctagtctg	caagccagga	aatgtcctct	ctctaaccat	109500
gctggaaagg	tttttaaatt	tggaaactca	taagctaaag	ctaaagctat	agctaaagct	109560
gatgtcgag	gtgccagac	acacctttgc	acagggaagg	gcagggtgctc	ataactctca	109620
cttcttcaca	aagtctgat	aaaaccctat	aaccaggacc	actggagttg	aatcatttct	109680
gtcttaaat	tggctttgct	ccatgttctg	catctgatct	atatatagt	ttccatctc	109740
catcttccaa	tgggttgagc	aatactgaac	ctctgttttt	catctgattt	cccacaactt	109800
tgagttcaga	gttttttgtt	gttgtgttg	ttgtgtttg	ccaggactac	acagatctta	109860
tcaactttca	cttattgttg	tgtctcactc	tttttgataa	aaacaacatt	tctgaacata	109920
aagttaatat	gttaaagtta	atatgaagaa	agtttcaaaa	atatggaaac	acgtaaagaa	109980
gaaactacat	atcactccta	attccccac	ctggaggcaa	gtggtataaa	tttttttgta	110040
ctttcttcta	aagatttttc	atgtcctata	tactttaaaa	atcaatttta	tatttcgctt	110100
ttgttcatag	aacactatgt	tgtgaggatt	ttctcaatat	tcatataaac	tcatcaaac	110160
attccttatt	ccatgaaatg	gctgtgttaa	atagacttta	atattcctat	cctattagat	110220
gttttagcctg	gctgctcaca	ttctgatact	acaataacac	tgagttcagc	ctaattgtta	110280
taagtctcta	accacatgtc	tagtaatttt	cttggaattc	tttttagaag	tgaataacta	110340
ggctggacca	aagaaatatt	tttgaactct	tggcaataaa	tgcaaatttg	cattccagtg	110400
cataagaacg	tggatttctt	aatttacttt	ctcatttggg	ataccaagg	taaaagttaa	110460
tgctgccaat	ttgccccacc	aaaaagaagc	acatcaccct	gtattctttt	gcatgtcttt	110520
catgacatgt	ctttcattgt	ctctgcttct	cttctgtg	ctatttgtca	ttgccccaaa	110580
ctgtgcccta	ctttctctg	aagacttgtg	ttgtgactgt	aggaattcta	tgaatatcaa	110640
tcacttttag	caaaaagggt	tgacaaagta	cattttggg	agcatgctgc	ctataataat	110700
ttctatcatt	cacaaaagct	ctttctctta	tatttggctc	tgagttcctt	tggaaaatgt	110760
ttgaatggca	aaggcaagg	caaaccctcc	tttttagcaag	ttttgcttga	ccttgaagca	110820
gccatttaac	aggtggatta	cagagccaca	gaaggatggc	atcttcccaa	gtgcgcttcc	110880
tgctgagcca	aggggtgcag	gcaggaggct	gacaaagatg	agtgaataga	ttattcttca	110940
ttcttacatt	gaaatgacat	gtcgggggtg	ggcgtgaggt	tagggatg	tgagctcctg	111000
ttgttaaate	cttttgtggc	tgaatattta	agaatgttaa	gaaatgatgg	ctggaggtgg	111060
tggctcatac	ctatactctc	agcccttttg	gagactgaag	tgggaggatt	gtgagagcct	111120
aggatttcaa	gatcagcctg	ggcaacatag	tgagatcctg	tctctacaac	aaaattgttt	111180
tcaaaaagtg	atgatactat	attacaaaat	aacatatata	atatcatccc	aagtttata	111240
acataaaaaga	gagatatgtt	aaaaataaaa	agaagcgttc	tctgtggtag	agttaccagt	111300



gatgttttaa	atttgatttt	taaaatgggt	tttcaaaatg	atttttaaat	tatataggag	111360
gtggaaaatt	caaagtgtctg	aggcacagga	ccaggtggcc	catgatgtag	cccagaaggg	111420
ccagtgtatt	gtggctccaa	tgagccaatc	attgggaaac	tggcatcttc	ttcgggctgg	111480
aacaggagag	ctttgtgtgt	gggagagaag	gcaagcaaaa	agaagagagg	caagggaaaa	111540
gcaaggtcac	ccttgctcag	ccccttcttt	ggctctgcat	gactttactg	ccttaacacc	111600
ctaactactcc	caggccaggg	aggcagcaag	acacatggag	acagtggatg	ataaagcagt	111660
gagtcccgca	gattcctgag	acacaagagg	cagattgttc	cctctctgca	tatgtttgta	111720
tttaagtagc	ctcatgttca	gacaagcaac	ttggatttgc	ttcagtcttc	tcaggatggg	111780
tgagaaaaac	actggaagtg	ctcaaaatga	gggagaacag	aagacacctg	tcagagtggg	111840
gatggcgctc	aagtgaacga	agtctgttat	caatgaatta	catccagtgt	aaccagatgt	111900
agagagattg	tcttgtgtga	gaatgtacca	gcaggcaaa	gggtttacga	ggcagagtca	111960
gtgtccctgc	actggcagtt	attttgaatg	aattgaccca	gggtttccac	attcatlcat	112020
taaacatttg	ttcattgaac	aaatatctgg	ctctaattcc	agttccacct	caaccagcta	112080
tgcagccggg	agcatgtcgc	tgagctttcc	tgtgactctg	tttctctact	gtgtgacag	112140
ccagaggttt	cctgcagagt	tgagacctt	ggtagcctcc	aggtgtgtgt	ctggcaacat	112200
gaactgtgca	tgaatccttg	tcttctcaga	tgctggagca	cccacctaca	tgtatgagtt	112260
tcagtaccgt	ccaagcttct	catcagacat	gaaacccaag	acggtgatag	gagaccacgg	112320
ggatgagctc	ttctccgtcc	ttggggcccc	atctttaa	gataatggct	ccttgctctc	112380
cgtgagcttg	gagttaggag	atctgggttc	ctgtcttggt	gtgggtggct	tcagcaagtt	112440
tcttctctct	tggtcttagt	ttactgatc	ctcataacag	ggttgaatgt	cactgggttg	112500
tccccagctc	tcctccact	ctaactatg	tgaggcgga	tgtgtattca	tgtgcccttt	112560
gcacagccac	tcagaatcct	gctctgtgac	atcaacaaga	cgggtgtgtg	tgggggagtc	112620
ttctgaagga	ttcactatac	aggggtgaat	gtcattaggt	tgtccccag	cttccctctg	112680
ctctaataca	catgacgggg	gatgtgtatc	catgtacctt	ctgcacagaa	actcagaatc	112740
ctggcctgtg	acatcaacaa	gacaggcggg	aggggtgtct	ctgcaggatt	cagtatgaca	112800
gagttgaatg	tcacggggtt	gtccccccac	ctcctccgc	tctaactac	ctgagggagg	112860
atgtgtattc	atgtgccctc	tgacagggcg	ttcagaatcc	tgttctgtga	catcaacaag	112920
acaagtgttt	ggggggtctc	ctgcaggatt	cactatgaca	gggttgaatg	tcattgggtt	112980
gtccccagc	ttcctcctgc	tctaatacac	attagggagg	atgtgcatcc	atgtacctc	113040
tgccacagac	actcagaatc	ctgggctatg	tcatcaacaa	gacagggtgt	gggacacatg	113100
cagggtgtgt	ctaggttgag	aagccaccaa	taactttccc	tctccaggga	gcgctgagaa	113160
tgtgagtgag	ggtgagatta	gagttggtgt	taacctgag	tcagggtctaa	tgtgtgtcgg	113220
tttgtctttc	tgctgtgtct	taacaaaaac	tcataaacct	ttacatttat	tacattta	113280
aattgttagt	ttagaaatca	caggattatg	aattacgatt	tatagtcagc	aggattcact	113340
gtgacaggat	tgaatgtcat	tggcttgtcc	cccagtttcc	tctgtctcta	acacacatga	113400
gggaggatgt	atatcatgtg	ccctctgcca	cgacactcca	gaatcctggg	ccgtgtcatc	113460
aacaagatag	gcggaggggac	acatgcaggg	ccctgtctta	ggttgagaaa	ccaccaatca	113520
atctccctct	cccagaagtg	ctgagaatat	gagtgagggt	gagattagaa	ttgggtgtta	113580
ccctgagtc	ggtctaattg	gtgtcggttt	gtgttctctg	ctttatgtct	ctaacaaaac	113640
ctcataaacc	tttaaattta	atataattaa	taattgttaa	tttagaaatc	acaggatgta	113700
tgaatttgga	atgggagagg	agactttatt	ttttagtggt	tttatagtca	gcaaagttgc	113760
tatccctcaa	ctggggaagg	tgctctggc	tcaagccaca	aacaggctca	tcgaacgagg	113820
aggggttggg	tagaagcttt	atacgaacag	attggctaaa	catacatgtt	caacacgtta	113880
cagggggagc	aatggatatt	catgaagaca	gtcctgacac	atgtgtatta	aacaaacatg	113940
catgtaacat	tgcccatgtt	cacctggtgg	tggagacct	atattttaa	gtattacaat	114000
tagggcttat	aaatccaagg	gtcttctcag	gacacaaagc	ccagcaagtg	agcagcctct	114060
gtacaccggc	caggtccagt	ccatggctgg	tgatgttctt	atctggagaa	aataactgaa	114120
atcagtctct	tatgcaatca	aagccgtagt	taaggctggt	gggcagggtt	ctgttcttcc	114180
gagtatccaa	gctgcagcca	ttttaattgt	tttcattttg	cttaactcca	ggccagtact	114240
ggtttagctg	tagacaaaaa	gaagcacctt	gcagcaggga	gaacagagtg	gattccttaa	114300
gggtagagat	gcaggcctga	acccttgccc	ggcatggcct	tcgatctttt	tttaatttgg	114360
tgtcttattg	ccacaaggag	tgtgttctgt	cagaatgatc	acctttattt	tattgtctgt	114420
actcgtccgg	tggtgtctaa	accacaaaaa	agggggagta	tgatgaggcg	tgtctgacct	114480
cctgtctgtt	tccaggcagg	aaactcagttt	aggggttttc	tggggtcccc	ttagcccgag	114540
gagggtctgt	tcagtgaagt	gggggtgtta	ggattttatt	tttagtttac	attatacaat	114600
atttttaaaa	atcctttcat	gatgtcttct	aagccttaac	tctcagctgt	tacagatcac	114660
atgggactca	ccccatggct	gctcaggatg	caccatcgcc	actgggcatg	tcccaattat	114720
gcacccttag	caggcttgag	ttctgttata	tttcagaatg	tgaattgtgg	gtgtgtgcaa	114780
gagagagcaa	ccctgggagg	tggggcaagc	acatggaatg	atgcatgccc	attgctgagc	114840
cctaggtcag	ccatgcttaa	aggtaaagta	cacacaaatc	caccaggatc	ttctaaatgt	114900
gcagacctca	gctcagtggt	tgtggagcat	gcgccaagac	tatgtttcta	gcagggttgc	114960
acgtgaagtt	gacaatgcag	gtccgaggac	cacactttga	gtaacaaagg	ctttttttct	115020
tcttccccac	agagggtgcc	tcagaagagg	agatcagact	tagcaagatg	gtgatgaaat	115080

tctgggcca	ctttgctgc	aatgggtgag	gctcttgcca	aagacacagc	acagctggtg	115140
aggggtgggg	gcggggcatg	cctattggga	aggggcagct	tctaagggtc	tagcgatcaa	115200
acttctgacc	ctgtgaccat	agcactctga	caatgagagc	tctctacaaa	tggagaggcc	115260
gcccccgag	atagtgaact	ccccgtctct	ggagatatac	aagcctcttg	acggagataa	115320
cttgggctc	ctcacacatc	tctgaagatt	gttggggaca	cacagcagct	ttggggcaat	115380
tctatttgat	tttgtttcca	gaaaccccaa	tgggaagggt	ctgccgcact	ggccagagta	115440
caaccaggag	gaagggtacc	tgacagattg	tgctaaccac	caggcagccc	agaagctgaa	115500
ggacaaggaa	gtagctttct	ggaccaaact	cttcgcgaag	aaggcagtg	agaagccacc	115560
ccagatagaa	cacattgctc	tgtgaacgga	aggtccatcc	agcctcggga	acctggagga	115620
gcaaagactg	gggtcttttg	ccaaagggat	tgacaggttc	gaaggcatct	taccatggct	115680
ggggaattgt	ctgggtgggtg	ggggtagggg	gcagagggtc	tgaaggagca	agttttttat	115740
ttgtgacctc	agctttggca	ataaaagatc	ttttgaaagc	caaatacactg	cttgtgtctt	115800
gtattagaga	ttaatccatc	ctcctcagag	acagaacgat	gatgaaagag	gcaatgtgag	115860
aaggaagctg	gctttgctgg	ggatggcctg	gcctcaggac	gagtacagtc	cagagggtctg	115920
ggatcatggac	agtgtctcag	ggagctcttg	gcctactgca	tgcttctctg	cccccagaag	115980
tttccaacaa	taggattttg	gattgccaga	gtgcagcatc	cctatcctcc	atattggatct	116040
gcctattgaa	atggaaatgg	cccaggctga	gaatttgctc	ggatcaggga	agagagagag	116100
gtgccgagct	gatcccgtag	cactgttgga	tgccctttat	tgactcttgc	acagggtctgc	116160
cacaccttcc	tcagtattga	cactagcctc	ctagaccctc	ccctgaggct	gtctctttca	116220
acagctggtc	taaactccct	ctgtaacctg	gaccacttct	gttgccggga	ctgaccacct	116280
tagagcaagt	ctccagagg	tcacctaact	actgtgtctt	tcagaatctc	aggggtgatt	116340
tctggattct	gctagaatgt	ggaaaactct	aaagagtgtc	actcctgcct	tatcagcaag	116400
agaaaaagct	ggattgtcct	caaaatcata	acttttccta	ttgccaggga	gaaagattgg	116460
ggtagatagt	cagactagag	agggccaggc	atgggtggctc	aagcctgtaa	tccagcactt	116520
tgggaggccg	aggcaggcag	atgataaggt	gagaagatcg	agaccatcat	ggctaacaca	116580
atgaaacccc	gtctctacta	aaaatacaaa	aaattagctg	gggtgtgggtg	tggggcgctg	116640
tagtcccagc	tactcgggag	gctgaggcaa	gagaattgca	tgaacccggg	aggcagtgct	116700
tgcatgagc	cgagatcatg	ccactgcact	ccagcctagg	tgacagagca	agactccacc	116760
taaaaaaaaa	aaaaaaatc	gccctgggca	gagctgcagg	ggagggtggg	aagccgactc	116820
aggccctgca	cctgggtagc	tgccccacct	gggtgctgccc	caggtaacgc	atgtacagga	116880
tgagcctccc	ttccccagc	agggacagat	cccactcagt	cctgccccgc	atgctctcct	116940
aaaagtttgt	atcaagactg	tgctcatta	ttccctgcga	tgggaagggc	tggggagaaa	117000
aaaacctacc	ttaccacttg	attgtgtcaa	atacaagggt	aattcattgc	aaagagcttg	117060
ctgtgctcca	tgaacgggtg	ggagctcaag	tctgaaatta	aaggatgggt	aggaaggggg	117120
atggccagcc	acaacgtggt	ggaagtgtga	ccctgagcag	tgggggcaag	ggggccagcc	117180
cacgggcagc	agggtctggt	ttggcaaggt	tgctggagca	caccgtgggt	gcctggagga	117240
cagcttttct	accttgacat	gtaggaaaca	gacttctctc	tttataggaa	gataatgcca	117300
taaaatgtct	gtctacctat	ctgtctatct	attatctatc	taccatctat	caattatcta	117360
tctatcatct	attacctatc	taacttatct	atttcattaa	ttacatttat	ttatgtaatt	117420
gtattttcaag	ctctattttac	ctcctgaact	tttcatgtga	gagactacat	tttattcaat	117480
atatgcttta	ggtaagtttc	agttggattt	ctcttagtac	atatgacaga	gtcctgatta	117540
aaatcattgc	tgcatttgat	cattttatatt	ctatcctgta	actataattt	atgtgatcac	117600
cagtaatttt	atctgtatca	atcttgtctc	ctgtattaga	taacagggtc	ttaaggctctg	117660
gtacaacatc	ttcagttttt	tattgaacat	aacatacata	taagaaatat	atatatatac	117720
acatacacac	aaacacacac	atgctatgta	tattattatga	cttgataact	tcactaactg	117780
atcacactgt	gtaattagga	cccagatcaa	gacacaatat	taccagcatc	ccagaagcca	117840
catggagctc	aattccaggc	cctgctcact	tccccctcct	tgctatctca	cccaaaatgg	117900
tcaccacagt	cctgatgtct	agcagcaata	tttctttttc	caggttttgt	gcttttatatg	117960
aacagaatca	catactcttg	catctgggtt	ctttccctca	atattatgtt	tatgagattc	118020
acgtgtattg	ttgtatatgg	ctgtagtttg	tcactcattgc	tgtatagtca	ttcattgtat	118080
ggatatgtca	taattttactg	gtgtagggca	cttgagagaat	gtattagtct	gctcgggctt	118140
ctgtaacaaa	ataccacaga	ctgggtggct	taattaactg	aaattcgcat	ttgcatagtt	118200
ctcaaggcta	gaagttccag	aacaggacac	aatgagaagg	cagcagctcg	caaacaagga	118260
ggagagccct	caccaggaaa	tcagtcagct	taatcaacta	aaatttgcat	ttgcatagtt	118320
ctctaggcta	taagatccag	aacaggacac	agtgagaagg	cagcagctcg	caaacaagga	118380
agagaggcct	caccaggaaa	tgagtcagct	taatcaactg	aaatttgcat	ttgcaaaaaa	118440
ggaagagagc	cctcaccagg	aaatgagtca	gcttaaatcaa	ctaaaatttg	cgtttgcata	118500
gttctctaga	ctagaagtcc	cagaccagga	cacagtgagg	aggcagcag	ctgcaaacaa	118560
ggaagagagt	cctcaccagg	aaatgagtca	gcttaaatcaa	ctaaaatttg	cgtttgcata	118620
gttctctagg	ctataagttc	cagaacagga	cacagtgagg	aggcagcag	ctgcaaacaa	118680
ggaagagagc	cctcaccagg	aaatgagtca	gcttaaatcaa	ctgaaatttg	catttgcata	118740
gttctctagg	ttagaagtcc	cagaccagga	cacagtgagg	aggcagcag	ctgcaaacaa	118800
ggaagagagc	cctcaccagg	aaatgagtca	gcttaaatcaa	ctgaaattcg	catttgcata	118860

gttctcagagg	ctagaagttc	cagaccagga	cacagtgagg	aggcagcagt	ctgcaaccaa	118920
ggaagagagc	ccccaccagg	aaatgagtc	gtttaatcaa	ctaaaatttg	catttgcata	118980
gttctctagg	ctataagttc	cagaacagga	cacagtgaga	aggcagcagc	ctacaaacaa	119040
ggaagagaac	cctcaccagg	aaatgagtc	gcttaatcaa	ctgaaattcg	catttgcata	119100
gttctcagagg	ctagaagttc	cagaccagga	cacagtgagg	aggcagcagt	ctgcaaacaa	119160
ggaagagagc	cctcaccagg	aaatcagtc	gctgttctca	tttaattgtt	tcactttaga	119220
agatcatgca	agggacaaaa	tctccagaat	ctttcctggg	cggggtcaca	gctggggtgg	119280
gaaagttgta	gcccctctga	aacttcccgc	atagctgtcc	ttctatggag	gccaggagcg	119340
catcggggaa	ggtacagtcc	acagtccccc	tccatcccac	cagtccaggc	ccaaggggtc	119400
ttcacatcca	caaaacacca	ttttcataga	tcaatagcac	acacaccaag	atgcgcaaat	119460
tcaaacacaga	tacccaatg	gcactcactt	attgaatttg	caaggatttt	taccactact	119520
cttttgggtg	tagtgccatg	tggaagaat	atagaaaacc	aggaagtatt	cagcactgat	119580
gtgacagatc	agtagctcct	gggatttggg	cagaattttg	tgagctccag	ctttttggag	119640
aagcttatgt	catttaccgt	tgctgagtc	tgtgtaagcc	ccaaagccaa	gctttcacaa	119700
gctaggactt	aggcagcttt	gaaaaggaga	agtttatctt	ctaccctctc	aaagaggggtg	119760
taggaggttc	cccttgagag	taaccactgg	tccctccaga	tggtctggct	gcttctgcca	119820
ggctctactt	tcagaaatgc	ccttcattgt	gcaattatca	gaattaaagc	ctttcagtgt	119880
ctcctcattg	tccagggatg	aagtctgttc	tccttggtt	ggcattgaag	ctctctgtct	119940
tccattcccc	cttccattgc	aactggcctc	cccaagaagc	ccctgaatct	gccttggttc	120000
aatgctaatt	cttctctctg	ctctccaaat	tttgccatc	tctcaatacc	tggtaccatc	120060
aagagtcac	acagcttttg	gcatttaacat	atatgaatat	tgatagttct	cagggcaaga	120120
aaacacacag	aacatgcac	tctatggagg	ccactctatt	cacctggatg	cttataatgt	120180
aatctgtagt	ttgagtttcc	agggtctctt	ccagattata	attcaatctt	cacttttctg	120240
tgtctaaatt	tttaccattgc	tttctgaatc	atcttttttc	ccattttatt	cttaacaggc	120300
taaaggaagg	cttaatagag	tagcccta	gaataggatc	tggttttata	atcgggcttt	120360
tgtgatttga	atcaaagaaa	tgcaaaaact	tagtgtttat	cagagtgtgc	tgcaacttatt	120420
cctggagtta	tgcaagatca	ttttagatgg	cacacaaaact	aaaaaccact	tatagaatgg	120480
ctgtttat	attttgctgt	gtattaggga	aaaaaccctt	actatcaagt	ccatggttta	120540
atggatatta	cctgtgacaa	ggattgctgg	cagtctgtta	aaatctgtcc	caccttcctt	120600
ggtacacagc	cagattacat	tttccagcct	tcattgcaat	tagattgaac	acgtgaataa	120660
gttctcacca	atgtcctctg	agtgggagtg	gagagtgc	cagccaggcc	tggtccatc	120720
aaatgctcca	tggtcacact	tctgctcctg	ccctctccag	gtgacaggca	attgacacct	120780
atggcaactt	tagaaacat	gagtgaagga	aggcaagcc	accatagcct	agatcaggac	120840
tgagtaaaact	acagcctgag	ggccaaatct	ggcctactgt	ctttttaaaa	ataaagtttt	120900
attgaagcac	agtcatgccc	attggcgtag	gtattgttta	tggtccgcct	tactaccaca	120960
gcagtcgcca	cagacagccc	atggcctgca	aagtcctgaa	tccttactat	ctggcccttt	121020
atagagaaaag	tttgctgata	tcctaatttt	gatctctgaa	tgacctatg	gacaacagcc	121080
accttggtga	cctgaacaac	gttctagtc	tttacctatg	cgaaaaataa	gccgttgaaa	121140
ttctgggcct	atgtgctacc	atagtttacc	ctactctcac	taataattct	tgctcagcag	121200
tcacaggggtg	attgactgat	gaatgtacat	ggcccgattt	ccggttggtt	gcgccattga	121260
gggtgactag	ttatgcccc	gggagtacag	ctctctcctc	taagaccac	caccaggcca	121320
aaatttcttc	cagatgctct	gaccagttag	tcttaggacc	tgattgacct	caggtagctt	121380
gacccctaa	atataacata	gcacatggg	ctggggaagg	tgtaaacata	atacaatttc	121440
tgcccattga	actgaatgtt	aacaggaaga	cattccctga	agcagaagaa	aatgaccttg	121500
gtgatgatga	cccttgccaa	aggtaggtga	cccttgccaa	aggtagttaa	cccttgccct	121560
gtcacctacc	tggtggtcct	gatggtgatc	agttctttca	tgtaactaac	tggtcctcaa	121620
tggttcactt	ttcccattga	gtgacttttt	tcaattatat	gcttttgtaa	attagaagtg	121680
tttttactgg	catttcttta	tgacgttttt	tattttttacc	atcattttta	tttaaaaaat	121740
gcagttacac	attttccatg	catacctcta	atttatggca	ggttatacag	gtcttgacgt	121800
tatggaaatg	gtataaagtc	tcctttttga	gtgagcatgt	taaagtaaaa	agagtgcctc	121860
atttaaagaa	aactgttcat	agaagtacag	acgatatgct	gatgaggcaa	aaaaccatga	121920
tattagtgtg	agaataagtg	aggttccaga	aacactgcac	atgtccaggc	tgagtgagg	121980
aatgtcgtag	aatcctggat	tcataagatg	tggaagccag	gtgaaggggtg	catgagagag	122040
ccccctcccc	atagccaccc	cctgccttcc	cacaagggaat	tcccaaatgt	cacccagttg	122100
attctcagac	ttctgtctcc	catttcagtg	ttctccacca	caaaatctac	acctgatcga	122160
tcccacagtt	cagagacaaa	gctgagtgag	gggtccagca	ggacatgggc	ttgctgtgcc	122220
caatgcctgc	tctaataatta	gctttccata	tatctgctga	gtaaaactgat	ggaggtggag	122280
agggttgggg	gagttcattt	gaagccccc	gatatgcccc	ctctcccaag	tcctaccccc	122340
tgcttagaag	ttaaggccag	ttcctcagat	tttactttcc	acgtcatata	gttccacatg	122400
ggaaaccaga	gggattcccc	agggaaaagc	aatgacccaa	atcaactgcc	gcttaaacaa	122460
gagacgtact	gcttacagct	gaagtgatgc	aggggagtt	tatgtattaa	gcaaaaatga	122520
gatctactgg	aaggcttggt	aggctccagc	ttcaccatc	acaatctgca	gaatcatcat	122580
gaaccagaaa	tggtgcagtc	caggagtggc	caaaaaattc	tctgtttgca	caattggctg	122640

gtgtcacaag caggagtgtg attgcgcagt ggttcaggag aagaactaat ccttacatct 122700  
 tatattttgt gaatacagca ccacaaaatc ttcataaggcg aagagccagg actgtttctc 122760  
 aggttgcaaa ggtcagctga ctaaggcaac agggcaggat gggttaacagg cacgtgcatg 122820  
 tgtgcacatg tgtgtgctg tgtgtgtgtg gctgagttag tgggactagc tttgctttct 122880  
 acttaggagg accaccaga ttgtcccttg tggatagaga tagggatgct ttttattagc 122940  
 atgcagttta tcaaccagg ttctgtcctg gataaaagta agggaggagac cctaagctca 123000  
 ggtcaacttt tgtagagctg gttagtcttg gggactgatt ctcagtctgt cagagcatcc 123060  
 tcattcccat cacagaatgc ccctcaccag cctgcacgtg gctagaatga gtgctaata 123120  
 gcatcccttt ttgaatttgg gtctccagaa gcttcatttc agatacaact cacggccttg 123180  
 ggcaagaatc cattagcagg tctgggactg tcatgtgctt tatggctgct cgttgcccaa 123240  
 tctttcctga tgtcaatcgt ggtctggact ggacaagggc aggccttgcca agtgacattg 123300  
 ggaaagttaga acatggctcc ccaagtacct ggtacctggc tctcatcttc ctctcttttt 123360  
 ctttcttttc ttttctttct ttctttttct ttctttccct ttctctctct ctctctcttc 123420  
 ctctctctcc ttcttagtct tcttcttctt tcttctctct tcttctctct ttctctcttc 123480  
 ctctctctct ttcttctctt ctctctcttc ttcttctctt tttctcttta ttcttgtagc 123540  
 gatagggtct tactatgttt ccaggttggt tcttgaactc ctctctcaag caatccccc 123600  
 accttggcct cccaaagtcc taggattacc aagcgggaag ggttgccaca gtgcccagcc 123720  
 tcccctggct atttctatcc cttcagccct accatgtca gcctgggtca atgagctgac 123780  
 aaggcaatgt gccttagata aggtaccac actgtgctgg aaggcagaaa cctcaagtag tgggtctgac 123840  
 gagaaatggc tgccagccac agtgctgctg caaacctctc ccatctctgg gccttagttt 123900  
 tttgccactg agttgctgtg tggccttagg agcctatgta ttagtctact taggctgcca 123960  
 cttttgggaa taaataacgg aattgagttg acaacagaaa tcaatttaag attgtgagac 124020  
 gaagaaaata tcacagactg ggtggcttaa ctgagactga gttcctgcat acaaaactct 124080  
 agcattaatc tcatggggtt attttgagaa agtaagctct ttgtcaatga atgtatgaag 124140  
 cggcatagtg tttgccacac aataagtaaa aacactgaca agattacagc caggaaatgg 124200  
 aaataaaagt ggaaaatgca aataagtaaa tccaatattt tcccatgcaa ataaagacat 124260  
 ctgttgtaat tctaattagc tatatagcct cctatctaga ttttcaaaaa tatttcatta 124320  
 atgttactac caaacggga ccatattata agtttacctt tttaaagtgt acaatctagt 124380  
 ttttattgaa atataagtca catgtcataa acatcatcac tatttaatcc caggacattt 124440  
 ggtgttttagt atattcccaa agttgcacta ttagcagtea ctctcatcc cgtctcttt 124500  
 ttaccacccc caagataaaa ctcatgccc tgtctctgta gatttgacta ttctggaaat 124560  
 ccccttcccc agacctgtc aaacactttc ccttttgggt ctggcttctt tctttacca 124620  
 tacacataaa aagcatcata tgacatgtgg catgttcttc ttatggctgg atgatatgcc 124680  
 taatgatttc cagcttcacac ttattttaca cattcatcag gtcatggaca tgtgggttgt 124740  
 tctgcacgaa tacaccacac gaatgacact gctcttgggt tacaagtttt ttatggacat 124800  
 gccactttt tgactaggat gacacctagg aggggaattg ctgggtcata tggaaactct 124860  
 gctttcagtt ctgttcggta ctgcctacac cgcacaacag ttataacct gttatttttt 124920  
 atgttgtaatt tttggaggaa cttcattgtt aataagtagc tgtgcacatc actattttga 124980  
 cctttcaca cgcatcctgt tagccagcgg tatcacagtg tgtttagtga attcctatt 125040  
 gtgaatacat catatttctt atgaaagagg ttttagtgac tctctgtgt cccagcagc 125100  
 gttggacatt taataatccc ggtgtgccc gagcactctg tatccctta atttggtgat 125160  
 ttgtaaatga cagttttcca cactactgc tctccaccc tatatgtgt gtctacaatg 125220  
 ttcacattgc cttgacatca aacctatgtc tgaattgacc tttgtatcca ttatacatgg 125280  
 gtgaacccct tgagaagctg taaatgttca cagaatggat ggttacatga atggatggat 125340  
 ccagggtgct ggcattttg gagagatgga atcattttta cattctgtcc aaaaattctc 125400  
 gattaaagcc aggagctatt acctgagatt ggaagtgtgt gagaaggctt ggctagtgg 125460  
 gctttggaag gtagtgattt tcaggcatca gaaagtggac tggataaaat ttaggatcgc 125520  
 caggatactg tgaagctaata aacgctatga aacacaagcc ctgggagctg agatagtcc 125580  
 ttccaagctt gaaatcctgg tgagggtgtga gtggctctaa cattttccag ttgtttctga 125640  
 taacttacc agctgagctg tcaaagcttc cctttgccta aagcatctg cctgctgggt cgggcctttg 125700  
 ggacctcaga tcaaagcttc aggttagagt cctgcaaggg tgacaccgtt atgccacaag 125760  
 ggggacctca agtttacagc tctctgtaat ctgagagtag agtccagatt ggtttgatga 125820  
 cagttgggag actgtgagtg ggcgtggctt gagggccac tggagacca gggagatctg 125880  
 aagagggtaa gggcttttct gatctctccc aattagagga cagagtcctc ctgagctgca 125940  
 gggaaaggga gggggccagg gtggcgccag ggctggagac ccttccagc atgtggctcc 126000  
 ggggtaact gggggccagg ggaactgtcg ccgctggctt ttctgaagtc aaatatgcgg 126060  
 cggagaccte ctcgctgctt ccgctggctt aactgggctg agatgcgtag aaaggcaaag 126120  
 cctggccact gaaatccttg ttctgggccc cgacctccgt acttggaatt ggacttgag 126180  
 ggcaactttt tccggctccg tggcggggcg gagacacagg gaggtgaaac atgctgagac 126240  
 acacaaaagg tgcggctccg ggccgcgcg gacacacagg gaggtgaaac atgctgagac 126300  
 cagctgagcc cagccagcct aagaaggccg gacatgggc cacctcactc cgcacacaag 126360  
 cgccctgcac tgcttgcccc

agaaatthag	gcagctcagt	ttattgtccc	ataattcgct	ccgttatggc	tcgataacgg	126480
atagcggtc	aggagaatat	taagagcatc	gactctggag	ccagagtgcc	tgggttcgag	126540
tcccgcgtg	gcgcttcctc	gctgtgtgta	cttaggcaag	agactgagct	attctgtgct	126600
tgggttaccc	cctctctgaa	acagagggtg	cagtgtctacc	tacctcactg	ggctttgggtg	126660
aggaggaaat	gggtgggttg	ttctaaagca	ctcttggaag	cgcttggtat	gtagaaagca	126720
tgaaaaaggg	gtggataaat	ttaaaggcgc	tgtttaaaaa	cgtagtgtat	gaatagaaaa	126780
tttgagctgt	ggtcaggcca	ctatatcagg	acctcttgcc	attaaaaaga	cagtttctta	126840
ctcatgttct	caacaggagg	gggacaccag	tgcgcggggc	acaaggggaa	gcagcagagc	126900
ctggggaggg	gacagggcgg	atctgaggcc	aaggggcttt	tactgtggct	tccaaggata	126960
gaagaggaaa	ggcagggcag	gcaggctgag	gactggcaag	ttgggatact	tcaggggctc	127020
tggggcacag	gggctgttcc	taattgtttt	gtacctagcc	ctggcatgat	tagggcaggt	127080
gggtagtggc	cagggcattg	caacccgatc	aaagaggcag	ttgggggtgtg	ggctctgggg	127140
tggctggagc	ctgggaggga	cagtttctcc	aaggtcaaca	aggcctcaga	tgccagagta	127200
tcagaatata	gaaaacaaaa	cacatgttac	atagaggggg	gcagcgaggg	gcctcgaaat	127260
acccccatgc	cattttatag	acagagaaac	tgagactcac	acagggaaat	gtacttgccc	127320
agggtcaacc	cgaaaatcat	gcctaggtct	gtctctgggt	cctgaatcct	gacagcccag	127380
ccccgtctgc	atcctgtctt	ccttctggca	gcctgacact	gcgagagctc	tggaaactgtg	127440
gggaagggca	gagaagagag	gaagcctatt	tggaaactgaa	tgttccttta	cctctgggta	127500
ctcctggcaa	tgccatccat	ttccttcctt	aggaagacca	tacaggctgc	ctccacttcc	127560
tcagtttctt	cctctgtaaa	atgggcatgt	tgtatgcctac	ccagcaaggc	ttatttgaag	127620
atggatttaa	acaaactgga	atgcattgct	ggcacatagt	agggtgcccac	catgttcgtg	127680
cttcataata	catcagcagc	aactgttctt	gttctcacac	ttgtttctgc	ctcccccat	127740
tcacccactt	tttcaccctt	ggcaatctgg	ctgccatcca	cctcatcctg	ttgaagggaa	127800
tccttgagct	gagcatgacc	agcccagtg	tttcttctct	gacttgactc	tcctccacct	127860
ccctgaagtc	ctcagcaatc	ttagctgggt	cctcgccctc	ttgctccctg	ggcttcaaag	127920
acatgggaac	gttctctctc	ccctattctg	atggatcttt	ggtcttgccc	gtagtggctc	127980
ctgtgtttga	cctttgtttt	tttttctctt	ccctctcaca	ctggcatctt	caatgaagcc	128040
atacacatcc	accgtatgta	ccctcacagt	ccaggagaag	attctgccct	gtccctcac	128100
caaggcttct	tccagctttg	aagtgcgctc	atcctgtggc	atcatcttgc	ctggatatcc	128160
cactcacatc	tccaccgagc	ctgtgtaaac	agggatccag	cattacaagc	cagctctttg	128220
gtcttctttc	ccttccattt	ccccacctc	tggtcaggga	ccaagtcttt	tcttttctct	128280
tcttttcttt	ccttccctcc	ctcactccca	ctgcctgccc	tgcctgctcg	cctgctgccc	128340
tgcctgcect	ccttccctcc	ttccttctct	ccttccctcc	ttccttctct	ccttcttctc	128400
ttccttctct	ccttccctcc	ttccttccat	ccttccctct	ttccttctct	tcttctctct	128460
ttctctctct	ctggaggagc	caggattaca	ggcacatgct	accacacca	gctaattttt	128520
ctattttcag	tagagagggg	gtttcaccat	gttgccagg	ctggctctga	actcctgacc	128580
tcaaatgatc	tgcttgcctt	ggcctcccaa	agtgtggga	ttacaggtga	tccactgtgc	128640
ctggtctcca	agcttttcaa	aatacctttt	agacatcatc	atattttctac	atattttttc	128700
tttttttatt	taaaatttta	aaataattaa	gatggggggg	aggatttcag	gtgaagaccg	128760
gaaatcccat	acagtgtctga	aaaggtggaa	atcaccaaga	aaacaggcca	catgtaatgc	128820
caccacccat	tgctatgtcg	ataaacatgc	ttccaaggaa	gttcattctca	gtattatttg	128880
taattagcaa	caacaacaaa	agaaaagaag	ctaaatattg	acattgcagg	gttggtctatt	128940
aataagatga	gacatggatg	ctgtgtgtga	actgggcttt	ccataatggg	tttccattgt	129000
gattggatat	tcccccttaa	gaccaaactc	gaattgttct	gttctgctct	agccccacac	129060
tttgaggag	gtgttgacgt	cttgtctgta	tccaaagcag	agcagctggg	aggacaagag	129120
gctggaaatc	atttccctag	agggaaagctc	agagaaactg	aggtgactgg	agccagatag	129180
gacctgaggg	gtgggcagca	agatcaagtg	tctgaaaggc	cacaggctgc	agatcagatc	129240
aggccagtat	agtcccatga	caggtagaac	cagaactgat	gcggaggctg	tgggaaatga	129300
atttcagctc	agtgaggaaa	cattgtccgt	tgggcaagaa	tggagcagac	ctgcccaggg	129360
ccaccagaag	aatcttctct	gacctgatca	catcctttat	ctggaacggg	tctgtctgct	129420
tattttgtcca	ttaaagaaaa	ctcaagcgct	tagcctggca	ttctaagccc	tccctgacat	129480
gtgcggtctc	attccaggaa	tattttccac	tccccccaga	ctccacctgg	tgcatgtggg	129540
ccatgcccc	ttccccaggc	aggctctgca	ttctgtgctc	ctgagcctca	gcaaattccc	129600
ttctctctgc	tgtgtaccac	tctctgcttc	tcatctcccc	tcattcagtc	ctccccctgc	129660
gcaagtccca	gctcctccat	gatgcccgc	atcagaaggc	cttgccccct	cttctaattc	129720
ctagactgcc	ttatgggtac	ctctcccagg	acatggccac	ttccttccca	gctgtagccc	129780
cagggtgtata	tgtgaccctt	ccctataatg	gtcagtgcct	gtgagaatat	gggacacccc	129840
tttttcatcc	tctcatccag	catgcggctc	agtgccagga	ttctaattgga	taaatgtttc	129900
cagagacttc	taagggggaa	gctaaaatgtc	tgttctcttc	ctagtagctc	tccttcttgc	129960
atttattttt	agctggatgt	ttttatgcct	ccaattctag	tttgccatt	aaaccagctc	130020
aatgggttag	ggaggacatt	gatcgtcatc	cctattgtac	atcaagagaa	actgaggcct	130080
agaggggtta	ggtgacttat	ttaaggtcac	tcacttagaa	agcggcaaac	tccactgga	130140
atctgggtcc	agccttttgc	ctctgatgca	tctgtattta	ttctccatgt	ccagcagggc	130200

atccgtcctc	gccacctgtg	gtggacaccg	tgcattggcaa	agtgtctggg	aagttcgtca	130260
gcttagaagg	atttgcacag	cctgtggcca	ttttcctggg	aatccctttt	gccaagccgc	130320
ctcttgacc	cctgaggttt	actccaccgc	agcctgcaga	accatggagc	tttgtgaaga	130380
atgccacctc	gtacctcct	atgtaagctg	cggcatgtgt	ccttggggat	gtttacctca	130440
aagtgatgca	ggaaggagtc	aaggcagtc	cctgatgggc	tgatcctttg	ctctggactc	130500
cttaagatct	ttgtagatcc	ttaagaacat	tccagaactc	tcacagcatt	ctggagtcca	130560
ttatttaaca	catgtttatt	gagcacctgc	tgtgtgccag	gcgtgttctg	ggttcttggg	130620
atccattagt	gaaaaagcaa	agatccctag	gttcctggag	cgtgcattct	agcaggggga	130680
gacagataag	aacaatatgc	aaattactcc	gtggattatg	tgatatgata	gaacagggaa	130740
agtgccttgg	aaacaaagaa	gcagttaagc	aggtgagggg	gatcagaagg	aaggatccca	130800
tgaattctgc	tgtcttgaat	tttgacatag	tcggggagag	gagtgggcca	ggaggtgtgt	130860
gggtggcaag	tgtactgagg	tgtccactcg	gcaagtgtct	aactctcagg	tgtgcctatt	130920
cctgaggaga	acaatggaag	gtgtgtccat	tcaccctggc	caagctggga	agaaaagccc	130980
aaaggttcta	attggcctca	ccatcactcc	ccaggttagg	aaggacccta	cagacatcag	131040
agcagaccct	gctcatctca	gcagccaggt	gttcggaggc	tttccagcag	cccaccagtg	131100
gccgccttct	tttcttccct	tttttaaaaa	ataatgttta	ctgtttttat	tttctgagtg	131160
caaatgtaat	atatacttat	tacagaaaat	ttaggaaata	cagagaaagg	aaagtaagaa	131220
aattaagatc	acatacaata	ttccaccacc	cagagagaac	aactatcagt	attttagatg	131280
gtaaagtatt	atgatgtaat	atattgtttg	tattccagtt	tttttgctg	tgatataact	131340
ttctttcttt	aaaagggaa	gctatatatt	gataatttgg	atgcctgctt	tgctcattta	131400
taagtatact	atgagcataa	ttccatgcca	ttaaatagca	cagcctggta	ttaaaagctg	131460
cattacattg	ggtattgaac	cataattaat	ttcccgaagc	ttttatttgg	ggtcattaag	131520
ttatatatga	tgtttttaat	aatataacat	catgaatgtg	aaacatttat	gcacattcat	131580
gaatagttta	ggataacttc	tcagaaatga	cattttctgag	tcaaagagta	tatatctctt	131640
gtttgatttc	cctcccaaaa	tattccaact	acactcctcc	cattgacgta	tgaacatctc	131700
catttggcag	actcttggca	atgcttggga	ttattaaaaa	tatttttggc	tattgtatag	131760
gcaaaaataat	aataacaata	ccagcaatat	tattttcctc	tttaatttgc	atttatctga	131820
agaccagtga	gttctttttt	cctttcttca	cattggaaatg	tattattatt	attattatta	131880
ttattattat	tgttattcct	cttgcaactg	gtgatcttag	gaaaatttcc	caggatggaa	131940
tcaagaagtc	atctttgctg	gctctgattc	tgtcacttga	gagctgtgtc	atcccagagt	132000
ctgagtgcct	cagtttctct	atgtacctag	tggggggcgt	gatgactgcc	ttttggtaca	132060
ttgaggtctg	ggactgttgc	ttataatata	cttgtgtata	agcaccacat	ggcatggatc	132120
tacctggcta	tgtaaccttg	gtcaggttct	ctaaccctgc	taggcttcag	ttttctcatc	132180
tgtaaaatgg	agataataga	acctacctaa	tgggactagt	ctgaggctta	aatgagttaa	132240
tatacaaaag	gtacttaaaa	cagtgcctgg	aacactggga	gaactaaata	actattacca	132300
gtgttcatct	atgttgcatc	cttgagatct	ttcatcaggg	caacacaaca	gcaactgcct	132360
gggagaggca	ggtggtagaa	tcttggcatg	tcagggtctg	aagactcatg	tagaaatcac	132420
tccgctcact	tgacactggc	ggattgggac	gcagagtgtg	aaaggaattc	acccaaggct	132480
acccataaaa	tgcatgggag	agacaaaact	agagcacaat	tctcctgatg	ttgtccca	132540
aagatatcac	ccctgagcta	ttgtgagaaa	tgtcacctcc	cagggaggat	cagtgtatta	132600
gtggtctccc	ctccttgatg	ctgggagttc	caaaggctct	ggaaagggaa	gaggtgtgaa	132660
gcccttctca	ctctgcttgg	tcttaggaga	ccttagtgag	tcccagcgcc	cccactgaa	132720
gcccttgata	gcctcctacc	cactacaatg	tcgtgagctg	gtaactatca	agtcatttc	132780
caggcttaaa	cctccagtc	caaggcgctg	cctgagaaaa	cacctcgctt	agatctggct	132840
gaacttcagg	ggttcttctt	tccccctccc	caggtgcacc	caagatccca	aggcggggca	132900
gttactctca	gagctattta	caaaccgaaa	ggagaacatt	cctctcaagc	tttctgaaga	132960
ctgtctttac	ctcaatattt	acactcctgc	tgacttgacc	aagaaaaaca	ggctgccggg	133020
aagttgtggg	accccttggg	caaggcgtgt	cagtgccagt	accccgcatc	ttctggggca	133080
gaatgggaagg	gagtgaaagg	agcttgggga	gggagctgca	caggccagga	ttgtttcaga	133140
gacccagggg	cctccacagg	aaacactggg	tttccacaca	tcagtttacc	ctcgtgacat	133200
aggcactctg	ggggagtttg	ttttgcatct	ttaatgaaca	tcttaattgt	tccaagttcc	133260
ctcatgctaa	tagaaggatg	agaatgatta	cttttagtta	ctagattaaa	aatctgatac	133320
caagattggg	taagacatga	ttttcaatgt	tagtggtgga	aagaacttag	agaaaagcca	133380
acacccaac	tcttcttttt	caaatagaga	aactgaggcc	cagacaggga	aggggaggtc	133440
accagtagg	gtagtttttg	ctcaagtctt	ctgatcttca	catcagtgct	tttgacatgg	133500
agtagggcat	tgagcttgta	tgtggccttt	ctccagcaca	gcaacattca	tctggggtaa	133560
ctttcactgt	ccaggtacgg	atgttggggg	cggagcctgg	acaatcccag	aagctcttcc	133620
ttttgccttt	ggccaaatag	ctgggatttc	ttttgtacc	taatttccct	ccctaattgt	133680
cttggcaagg	ctgatgacc	cagtgagtc	gaatttccca	aataaatgaa	gggcaggaca	133740
tggggcagcc	cgcagctgc	aagttggagg	gtggggaggg	tctgctggca	aaggaggcac	133800
ccagggtgaa	aaaacaaagg	gtgttgtgtc	tagccagctc	cccaggggca	ccgtgggcat	133860
gggtgcctatg	agtgggggag	caggtctgcg	aacgtggaac	taaaagttgg	tctacatgt	133920
gctttgtgag	acacaggaag	tgagagaaag	gtttactcat	tcattcattc	attcattcat	133980

tcattcattc	ttctattgtg	tactcagtg	cccatataca	cagttagacc	tggggcttca	134040
gggaaaggag	gaacatgaat	ccactccaca	cagcccctgc	cttcaaggat	cttgccttct	134100
gggctgtaga	gacatatcct	cccttcagca	ctttatttga	ggccagccct	caggctcagt	134160
cttcacacaa	agatgaatgc	acactcaatc	cctccccagg	aggcaggcag	ggattagagt	134220
tgtgggagaa	acaagggctc	tgggaacctg	gagtcaggag	aacctccagg	aatggccaca	134280
ggctctagaa	ctacacggtc	tgggtttaaa	tcctgggtct	gcttttgact	agctgagaga	134340
cttgggagtt	tcttaacttc	tctaagcctc	tgttctctca	aatgggaaat	catcacatat	134400
gatcagtcga	gggtgaccac	taagcgtgat	ctcagtcctc	ggctaaaaag	gcagaggcag	134460
gctcataccc	ctgccctaac	agtggactca	ctgcactgtg	gccggcgccct	gcagtgtgct	134520
gggcagctca	acatgtggac	tctggaggca	gactgcctgg	gttaaagtcc	tgctgctacc	134580
acttttgagt	tgtaggacct	tgggcagggt	aagtgcctcc	attttcccac	ctggataatg	134640
ggacattatc	agtacctacc	caatgtatag	tttattttac	tgtgcttaga	acagcacttg	134700
ggacatagtt	tatgttacga	gttcttttat	atttcatgaa	taatattatt	acaatatcat	134760
tatttttagc	actctcactt	cttcccact	atgtggactt	ttaaaatgca	agaatcatgc	134820
atgaggaatt	gtatccactc	tcactcctca	gtatttagcag	agtccttggc	acatgctaag	134880
ttctcgacag	tgtagtcca	ttgactgaag	gcacccctgaa	gtgggtgggt	tttaggctgg	134940
gtttctgcagg	gtggatagga	tttggggatg	cagaggcata	aggaggcatt	tgaggaagag	135000
acaccatcac	aggcacgtgt	gcttctcgag	acaatcattc	atgcacagag	aagtttactt	135060
caccaagaga	tagttaactg	agatgaagct	gagatacaag	ggctgcccc	tgggtacgct	135120
gagtgcatga	atagtctagg	cttgagggtg	atgggagtg	cctcccgaag	aggacatcct	135180
tagcctttgc	tatgcccattg	atgatgttct	cagcatcaag	agcctttcgg	ggaggaggca	135240
ctggaggctg	ggtagaaagg	aaggacagc	cagggtatgt	gcagtagggg	ggtggcttgg	135300
gtcccagttg	ggagaattat	gcaggagaga	gattgccttt	tgcaaagtgt	ctgggagctg	135360
gtgaactttg	gatagcatcc	tccttcagtt	gtaaccaaca	ggtaggtcac	caaacaagac	135420
atcttctgag	tgtccctgg	ctctgtgtcc	tgtaaactgt	atgttgcttc	ctctctgccc	135480
agggtgatgg	tgggatccac	ggaggggggc	tgtgggtggg	tgccggcatca	acctatgatg	135540
ggctggccct	tgtgcccatt	gaaaacgtgg	tgggtgtgac	cattcaatat	cgccctgggca	135600
tctggggatt	cttcaggtaa	gaaatcggac	tctctcact	gcactttggc	ccccagaacg	135660
aggatgctag	gacccagctc	tggctcatgcc	agccctcagg	ggagcttagc	taggttccac	135720
agtaaggcat	ccaagccct	tcgtaattgg	acactaccta	ccctctcact	accagccac	135780
tcacccactt	gctctgagc	ttttgcatgt	gctgttccct	ctgcctggaa	tgcttattct	135840
atccgaagaa	cacctcttca	tcttgcaaga	cccagccccc	agttacctec	actgaaagac	135900
tcactctctc	ttcacctatg	tttctccagc	acattgcttt	tctctgtcat	gacacttagc	135960
agtcagccca	gcagggtgaag	gttgacacat	ctgacttctc	atggaaagga	gggaaggggc	136020
agagtccacg	agggagctca	gggcatgttg	tgggtgaagg	aatgggggct	gcagatgggt	136080
gggtgtggga	gcactcgacc	ccttctgtg	ggagtgttgg	gacccactca	gctcattttc	136140
tgcttgaaat	ttggcaagtg	tgggaagcaa	ggatggagtc	ttcccatcag	gtctccatgg	136200
ggacaggagt	cagatctcct	tcaaggcgca	actgctatga	accttttcta	aggttctcct	136260
ccatccatgc	cagtcagggt	tcttcttgaa	cacgccactc	agtttgtctc	attgcgggtca	136320
tcaatgacct	ccccctgctc	tccacccaac	ctctcaggac	ctcccagcag	cagcagatgg	136380
ccactcagcc	tctgtgacat	gcttcttcc	cagcccttt	cctggctctc	cctcctcctc	136440
gtccacaggc	ctctcttgct	tccctctccc	tccttactaa	ttcccagtga	tcccagggag	136500
cagccagagc	ccctgtttcc	agccacctc	acctttgaag	cccacaggca	tcactcactc	136560
cctcctcccc	acccctggct	gtctaaaggg	tgccccactc	ttcccaggga	caagttgaat	136620
ccttgactcc	cactgcccct	ccccaacaga	gaccccccct	tctcccacc	acgcctccac	136680
tcagcttctg	ctgccacatc	ctcccttggg	ctcaggagaa	ggccttgtgg	acagcccgga	136740
ctgtctcttt	tctcacaacc	ccttggctg	cgcttccaga	atccactcag	agtcccctac	136800
tttgcaactc	ttccctggct	cctagcccag	ccaaagctct	ctgtctgtca	ccttgattat	136860
gatctttaac	actttcagat	ccctgccact	tttatataaa	gctgagttgc	acagttagcca	136920
gagtgtatcac	ttaacacatg	cattgaatca	tgcgatgcct	ctgcacaaaa	ccctgcaggg	136980
gcttcccatg	ctccttacca	tgacagccga	agttcttgcc	aggccccagg	gcccctctcta	137040
gtgcacctc	ctgactcaca	ctttctttca	ctggggccca	ggccctttgc	acttgctttt	137100
tcttctgcct	ggaattcctt	tctttggata	tttacaaggt	tcatgtgtct	attgtgcttg	137160
ttttatgaag	gtctttgcct	ccaaaacctc	aaatgtcact	gcctccaaaa	agccttccct	137220
gattgggatac	tgaatggca	ccccctgtcc	cactcctggt	ttttctctta	ctccattgta	137280
tttacctcag	tgcactttga	ctacctgaca	tcattatatt	ctctctatgt	atctgtttat	137340
ctgcttgtga	tctgtagtgg	gaattcagtg	tcatacagag	ttttgctgtg	tttgcctctc	137400
gatgtgtctc	agctcataag	acagcgtcag	gcatacagta	gatgctcagt	aaatagttgc	137460
cagttgtgtg	aatgtagaac	catacatcac	cacaatgctg	tactaatgaa	agcagggtct	137520
cagagatgct	gaagcccagc	cttattctta	agggttcact	gagaacccct	agcccatctc	137580
gtggctctga	aggctcctga	tgacatctct	gctccccacc	ctcaacctgt	tctcttctct	137640
acagcacagg	ggatgaacac	agccggggga	actgggggtca	cctggaccag	gtggctgccc	137700
tgcgctgggt	ccaggacaac	attgccagct	ttggagggaa	cccaggctct	gtgaccatct	137760



ttggagagtc	agcgggagga	gaaagtgtct	ctgttcttgt	gagttttcct	gtcaccaggc	137820
ccaacccac	gcttgatgtg	atgctgatga	gacctcttgg	acacctgtca	atccagctat	137880
ggatacctct	gattacaata	cctgaattca	ggactggccc	tactcacagc	ccagcatcag	137940
ggggtagaaa	gctaagagacc	agctctcctt	ggcccccagg	aagctcagag	ctcagcttag	138000
tgctctgggg	ccatatgaat	ctccagttgc	agcctgcaat	ggtggcattc	tcctcttcca	138060
gcttggttga	gctctctctc	tctctctctc	tttctctctc	tccttcacac	tcattttaac	138120
ataaggactc	acatcccttc	tcttgggaag	taggaatagg	cataaattat	gagtaagggc	138180
aggcagagag	aagaggtgga	cagaggtcat	tgtttggcta	aaccagacct	acatgtggag	138240
gggacatgga	cactgagcag	gctgggaatt	cctctggggg	ggtctgatgg	cttgtccatg	138300
cccaagaagg	aggcgacagt	ctttgtgact	gtggggctca	gtggggctagg	ggaggcaggc	138360
agaggaagga	gggatggagc	cgcggaatag	gagggatggg	gcagggggtg	tgggtcatag	138420
acacaacctt	gggtgtgagg	ggctctgctg	ggattgggga	ttgggttcag	gagacactgg	138480
gggatctggg	atgaaaaccc	agatgagagg	tgctgggagc	tgtaggaaga	cttccacctc	138540
cttgaggtgg	gcagaggggc	agcccactac	tggattcctc	agtcccgtgt	tggttttata	138600
gtggagttaga	tctagcctgg	aatagcgagt	gagtcactga	ccccactcct	gagcatgaac	138660
tctctctccc	tcactcttgc	tgtcaggttt	tgtctccatt	ggccaagaac	ctcttccacc	138720
gggccatttc	tgagagtggc	gtggccctca	cttctgttct	ggtgaagaaa	ggtgatgtca	138780
agcccttggc	tgaggtaggt	ctccggctgg	tacgtctccg	gctggagacc	cccacctcct	138840
tggctctatg	ctcctgaatc	ctcagggatc	tctcttgggg	tcggtttag	ctaattgttct	138900
cctagaatca	ctgaggcacc	aatggctgag	caggaagggc	gaggagacac	cttgatcagc	138960
gtcccagttt	cacagccagg	caaaccgaca	cagggcttgg	aagggatttg	ccaagggcag	139020
caggtgatca	gggcagagct	gggactccag	ctcatggccc	tagcagccag	tacagtggcc	139080
tatctgtgac	cacactcctc	ctatgtgcca	gggcctgggtg	ccatgttggg	cagtgtatgg	139140
gtcttgtgtc	tctctgggtc	tgccaatagg	ctggtaagtg	gaacaaccag	gatttgaag	139200
cagacaagga	aattcaggat	tccatgtctc	ctatcccagc	tccacctcac	atttcttgac	139260
acattcacct	tgagatgatt	atgtccattt	caatggagat	aaggtagcag	agatgagaga	139320
ttacataaatt	gaccatggtt	acaattgaga	ttagtaacag	aggcaacgct	ccgtgggacc	139380
tggaaccac	accacgggtg	ctacagtatc	tctctgtgct	ccctgccact	agtacaagtt	139440
gggcttggga	tagaatgcca	ctttcctctt	tgatggaggg	aagggatgtc	gctcttgaac	139500
tctgttgttg	cctgtgatct	ttgcagcaaa	ttgctatcac	tgctgggtgc	aaaaccacca	139560
cctctgtgtg	catggttcac	tgccctgcgac	agaagacgga	agaggagctc	tgggagacga	139620
cattgaaaa	ggtaggttgc	ctgttcccgt	agcccaaac	ctgtaaactt	ggtcccagac	139680
ttcttcattt	cagctgtcct	cttgcccagg	gacagtttcc	tgggacaatt	tctcaactct	139740
cagtatctga	atggggaatc	tgatttgtcc	ttttttattg	taaaatgcca	caaattgtaa	139800
aaaagaaagt	caaaaaataa	catgataaaa	aattgtgtaa	caatccccag	tcctgaccac	139860
aatttaatat	tttgccattc	ttgttttcag	atgtattttt	aagaaattaa	atgttacata	139920
ttcccagggg	acaccatcat	cctgaatttg	ggggatggag	atattaagct	caaagatttt	139980
cagaaaagatg	tcacaattta	tcttggttga	cttagaaact	gtctgtatta	gacctagtgg	140040
tggtccagtt	ttctagattt	tctgagactg	actcagttgt	catcctagga	tagtcatcca	140100
tccacccatt	cgttaatccg	tctatctatg	attgtcttat	ccatctatct	gttactaat	140160
tcatccaatt	cactcatatc	tttttatcaa	tctaattgca	acctattcat	aactttgtat	140220
ttatctattt	tcaatccatt	caccattcat	ggatcatcca	gccaccttat	atctcaactc	140280
catcacccat	tcctccaaaa	tcaacaatcc	aattatcgcc	tgtctgctag	ttttcaccca	140340
tctattcatg	tactcattca	attcaactgt	actccatgta	ttgaccaact	ccatccatcc	140400
ctccattgat	ccatccatcc	atccatgcta	aatatgtagg	ggtgggtgtt	agaggtagca	140460
aaacagacat	gaagtggaca	tagtccctgc	tctcaaggaa	ctatccaaag	agaaatacat	140520
tcatatactt	cgcaggttga	gtatgggtgc	agcacagagg	ggaagcattc	attgtagtaa	140580
tcagggatgc	ttcacagaga	aggcggagga	gccagatttg	agaccagaca	gtggaattca	140640
ggagttcatg	cccttaatcc	tgactccacc	ttatctttcc	tgagaaattc	agctttcaga	140700
tcattgtgcc	cattttaaca	gaggtaacaa	agacagataa	attttgtaat	tgccccatgt	140760
cacagttcaa	attagtcaca	gaggcaacac	tgtaggaccc	agaaccgaca	cctgcgggtc	140820
tagagtatct	tctgccttcc	ctgctccctg	ccatcctcac	atattaggac	ttggggacct	140880
ttaggattgt	tggatggcca	tggcagttct	tcattcacagg	gaagaccagg	aggacaaaca	140940
cccagatgac	acagacccca	gggcatttgg	gaactattcc	ctttgagggg	gaagagtgtg	141000
aattccaagc	tcaggagtag	cctggactct	ctccttggac	ctgaggctac	tcctggatcc	141060
cagggctggc	ctctaccact	ggactctgct	tgtgtttcca	tgagttgagt	ccaatgtggt	141120
attgggtgctt	aggtcttggc	tcaggctcta	agtgaccaaa	gtgttcaagg	aatgaaaaca	141180
caactgtttt	ctaaccgccc	gaaggaggca	aatattccag	caattctgca	tgtggcatca	141240
gaggacccag	cttaaaaggg	aagagttgag	tctttgggaa	aacccatccc	taagatccta	141300
gaacattctt	ttgagttttt	ctgagatctt	gtggaagcac	ctccatgatt	acgcgtgccc	141360
tccagtacac	acacatgcag	acacacagac	acacacacac	acacacagac	acacacacag	141420
agaaacacat	acagacacac	acacacagag	acacacacag	acacccacac	acaaagagcc	141480
acacacagac	acactcatat	acacacacac	acacactcct	ggctagtggg	acttcaatcc	141540



ttaatggagg	gacctgcact	ggttacatcc	tgagcacagg	tcagatctgg	gaactacagt	141600
gcaacactac	agtcactgca	atccttggtga	acacacacca	aagagaagca	tggggtagga	141660
tgagactcag	tgagcttgcg	tgagttaggg	ctttctaatg	ggagatgagg	aaactctccc	141720
aagtaccttg	aacagaaaaa	gaaatgtgtt	gcaatagcat	cgctgtgtaa	actgaaaatc	141780
tcaggagttg	atggcttcag	gcatggctgg	gtccagatga	tcataggata	ttattgagaa	141840
tctaccattc	tctgtccttc	agctttgcac	atctctgtgt	tggcttcact	cttaggcaga	141900
tatatctcct	gggaaggtta	aagacaacag	cactctagac	ttatgtccta	tctgtctaaa	141960
aacctctctt	ctaaacaatt	cctgcaaaag	ttttggggta	aactctattg	gattgacatg	142020
agtgtatgcc	catccctgaa	ctaattattca	tgttcaggga	gatggagcac	cgagggtcac	142080
atatagatat	acgaattcac	ggagtgtatg	gggaagaacc	tgacacctct	gttgccccac	142140
tcacccagct	cagtgttctc	ctggtaaagg	tctcaccac	atcctctgcc	tttgtcttca	142200
cagaaattct	tatctctgga	cttacaggga	gacccagag	aggtaaggac	cttttgtttc	142260
tggattacgg	gttttgagtc	ttagcacctt	taagctccaa	ttactgtga	gtgaaagaat	142320
catctcttgg	gtaattatag	taactctcgc	gtgtttgttt	ctgaggccca	gagaggggta	142380
gtgactcacc	tgggtaaacac	agccaggaag	actagtggct	ggcctgggaa	ccattttcct	142440
gactccagct	ccagtgtctc	caggcatcac	ctctgtgtgc	cctgggctct	gcccactccc	142500
cttctttttt	acattttctg	ctcccaaaaa	tggcactgta	ggaggaggct	gaaacagaa	142560
cttcacaaat	caggaggcag	agataaacag	gatgattagc	caaggagagg	ggaagcctaa	142620
atctcagctc	aaggacactc	gtctctctcc	agcacacagg	aaactccaac	agtattctcc	142680
caatctcttc	atccccactc	ccacccccac	ctccagtggt	gttgacagtt	tctgggtgaca	142740
tcacctctga	cgaatcttac	aatcctgtcc	tctctgtctc	ctccctggag	atcacagcac	142800
tctcctaaat	ggtcatgggc	ggagtacatg	agattcatct	agcaaagact	taataaacac	142860
ttcctatgtg	ccaggacttg	tttaggagct	ggggatataa	cagtgaaaaa	agaaagactc	142920
cctaccctct	tgggaccttc	cattacagtg	ccaggacagt	gcaataaaaa	agcaaatcaa	142980
gtatgtattc	cgatttgatt	tgtgcagcat	taggggatag	agtttgtggg	tggcttcaat	143040
ttaagtagca	ggatcaggga	atggttcaat	gagaagggtg	catttgagcc	aagctctgga	143100
ggaggcagga	agccagctgt	caggaaacct	ggagaagcct	attccaggca	gagggaaacag	143160
tcactgcaaa	gacctgaca	gaaggggcca	gtctggctgg	agaggaccga	gtgtggggac	143220
agactggctt	gaggctaaag	aggtaatggg	cagtgggaga	gagatcaatt	aaagtacttg	143280
gatttggatt	cagagcaaga	tgggaagcct	ttggagggtt	tgaacagagg	agtcacatga	143340
tcttagatct	cacaaaggct	tctgtctctg	gtgttcaaat	agactgtagg	aaaggggcaa	143400
agtggatgca	gttgaccagc	tgggcagcca	ctgcattgcc	ataatccagg	caagggtctc	143460
tggctgctta	gacagggtcg	tggcagtggt	gatgggagga	gtagtgggag	tctggatatc	143520
tttgaaggaa	tagctgacag	gatttgctga	tggacaggat	gcaaggggta	agaaacgggg	143580
aggagtggag	gacgacctga	gttttctgac	acaacaaggt	tgtgcccaac	cagggcagct	143640
acttgcaaac	tctaagtggg	gaacaatcac	ttgtcattgt	tgtgatgggc	agtcttccag	143700
catggctgtc	acccaactga	ggtgctcccc	tctcttgctc	caacttttag	cctcttctac	143760
ttcaccttct	ctccccattt	ccatgtctca	tgggtgcagc	agactggcct	tccttaacag	143820
aattagagca	cgtcaccccc	acttcttaaa	agcctgacct	tccttatgag	acaaatcccc	143880
ttccctccat	ggagttagtc	cttcaaaaac	cacctgctgt	cacactgtgt	gccagactgt	143940
gcagaaggta	ggctctgcac	ctgtccctcc	ctctagacct	tgccccacag	catttctcca	144000
agccaagaac	tcttggttgt	ttctggaatt	tacctgcac	agtgcacct	atgtcctttt	144060
gctcatgcgg	ttccactgt	ttagaaatcc	tcactccttt	cctcacctgg	caataccatt	144120
cactgcccag	agccacccgc	aggcaggcgg	cgtctcttcc	acgtagtctg	ccctgcatct	144180
tccttccaga	ggggctgctc	ctcttgctgg	cctccacag	cagccctgcc	tgaactgcac	144240
agcctcttaa	ggaggctgga	cttgacccc	aatcctgttc	ttcattgtca	gccatattgg	144300
attaggatct	gatcttgtcc	agctaggctc	ggctccactt	tcagaacatc	tccccaggc	144360
agtccgaact	agctcgtcat	tcattggctt	ttgtagagca	gaccaaagg	cccagaagcc	144420
atagggtctc	aaaggctagg	aattgtccag	ttccatctga	tatccagaag	ggaaatacag	144480
cccatggggc	gtggaactgg	gaagattcca	cagaggactg	gtgtctatga	gagggaccga	144540
cagcaacctt	gctaacaagt	aatacctaac	agttattcag	cctttccaga	caccagggtg	144600
tgtgtctaagt	attttcatag	tgttcagcca	tttaactctc	acaataactc	acctcttaga	144660
tgagaaaact	gaggcccaaa	cagggtgaaac	tcccagccag	taagtagcag	agccaggctt	144720
cagatgcagt	taatctggtt	tcaaagtcca	tgtcttatct	tagcaacatc	cacgctctat	144780
cgtagcaact	acaccattgt	gactaaatat	gaaatataac	tgtaccaga	accagctgcc	144840
ctgatggcaa	cacatgagtt	gggctctctc	taatctgtga	ccatataaaa	attattctac	144900
aaagggtgaaa	ccataaatta	agacatggat	caatatactg	tgagttaact	actgattctt	144960
ttactcatga	ttttctctct	agtagggaa	catgtcctag	tctaggctcc	ttgagtgcac	145020
aggggttcgg	acctcctcaa	agccaccctg	ggatcaataa	cagctcttgt	ttaaatacag	145080
atagatagca	taatctcttc	ctcatctaate	atggattctg	tgtttataaa	ttcacctgct	145140
tgctaaaatg	tccttataac	ccccaaatca	atactgggtg	cactttcatg	gtcacacaca	145200
ggcagggtaca	gagcagggga	agctggattt	gcattgatgg	catgttccat	ctgagatccg	145260
gcgagggaac	ctctctcttc	ttgtttcctc	tctgatgttt	acaagtgtcc	tcttcgctgg	145320

ctattttagtg	ccgtgtgttc	tgcattttttg	tgttttttgt	agtgatgtca	ctgttttagag	145380
cgaacccaag	agtagcgctg	ctgtctggcg	tctctgagct	aaacaggctg	tgtgtgtcct	145440
tacgggggaa	gtgctgtgtg	gagacaagct	tggatgaggg	aggagctgca	gtgctgtctg	145500
ccgtgcattt	gggtgtgaaa	aatccacata	atagcacatt	cagaaaaagg	agaaggaaat	145560
tggccgattc	atacatgagg	ctgtgataga	aagggtctaa	gtaacacctt	ttgtgtggga	145620
tggagccgtg	gaagtctctt	tcaacagaaa	cccacacata	aaagaagggt	gatgaaaatg	145680
ttgtggccag	aggtttgcaa	aaacctaacc	cagtatttcc	cccttgagt	atgacctgt	145740
attctctaat	tcagtactca	cgggggcttt	atcagaagca	actgccagga	ctaccgaaaa	145800
tcaattgtgg	acacacagag	gaaaatgcat	gcacttcaaa	ttgaaatata	tagacatgta	145860
attttacata	gataatacat	gtatttcaat	atgagtgaag	atttcttctt	ctcctcatca	145920
cctgagcagt	gtcagcctct	gcctgaagtt	ctgcccctga	gtcatggaga	cctaccccc	145980
taagtttaga	tcctgagcat	gtgcagccat	ggcgcatggc	catgccggct	tatggtagct	146040
gtctcaccct	cagacaggca	gagttgggga	ctgggtgtg	actaggagg	gaatcacagg	146100
tgtgtgactg	ctctctcccc	agagtcaacc	ccttctgggc	actgtgattg	atgggtagct	146160
gctgctgaaa	acacctgaag	agcttcaagc	tgaagggaat	ttccacactg	tccccacat	146220
ggctcggaatt	aacaagcagg	agtttggtg	gttgattcca	atggtgagaa	ggcacatgtc	146280
tgttgagggg	actcaaccac	ccccatcagc	cctcctgtct	ctggtcccg	gaatgcttcc	146340
ctctccgagc	tgcactctga	gtcctgggca	gtcttccct	tcagcaggag	ttaacatttc	146400
cacggaaatc	ttctccagga	gggcacagtt	tccaccggg	tatcagggcc	ctgggatttc	146460
ctctccccag	actctcttat	tgtcttccct	ttgaagaatc	ctgaagtgtc	tgtgctggga	146520
gggcccagtag	agaaaaatac	tctgcagatg	ggaaaacgga	gggggcctag	aagggggaag	146580
gagtggagga	gtcccgagaa	gcagtgggg	gcttccctgg	ttcccacctc	gggctgggtg	146640
tgcgtaattc	ccctgaaaa	cactcatgct	cttcatcacc	tcattgaaaa	tatccaaaga	146700
aagtggcttc	ttcttgagtt	accattgact	tctagggaac	agcagacatc	agcgtctact	146760
aagagagtgg	atggtcagag	gaagatgagg	atggaaaagc	tacctaatcg	ggtgctatgc	146820
tcaatacctg	gtaacaaaat	aatctataca	gcaaactcca	gagacccaaa	ttacccatga	146880
tcaaacctgc	acagttaccc	ccaaacctaa	aataaaaagt	ggaacaaaat	aaatggaaaa	146940
agtaattgag	ttctaaaagt	aaagaagtgt	tctccttcca	ggtgaagata	aacaaaactg	147000
accctgggta	aagcagtagg	acagatttat	tcagtaatat	gattgcaata	ggggaaatag	147060
tccagcgtgg	agtgagactca	catccctgaa	acaaaagcct	gatgacgttt	cataggccag	147120
gtgtgcccaag	ggaaacactg	tggctctatg	ggagaggctt	ggttcatgtg	actagaccac	147180
ctggatgtct	tcactctggc	tcacctgggg	cagaaacaaa	ctcctcttat	ctttaggaca	147240
ggaagccatg	cattagaccg	caggaagaac	ccactgaagt	caggctctac	tctttcgaca	147300
gggactggga	agatcaggag	tgagctccct	gaatgtttgc	attgcaaaga	gaaggctctc	147360
aggctcctca	ggaaaatggg	ttgggtggta	gattcacatc	ccaaagggca	gagaaagtgt	147420
ttatcattgc	aggcttctaa	agtaactgct	ctagttgggt	tcgggggacct	ggctgcttgt	147480
ctccaggttt	tggctggagc	agagtaaatt	gtcctggcag	ggttgagcct	tcccaggcag	147540
ttatgttaag	gatactgggg	tcattctagg	gacacagcct	taagtgtgta	gaagcaatgc	147600
tagagattgg	tcgagtccct	gagtgcagag	gtttggggag	agttgttatg	tgcgtagaga	147660
tgtgcagttc	gcccctcaga	aggatttcag	aggttatacc	aaagacccaa	gccacgaaga	147720
caggatttaa	ggatttcagt	gtcatctgtg	acagggtggg	gtactaggga	ggtctacatc	147780
ctcttcccca	gagccctcta	ttccacactg	gcctggcaga	caccttgcat	ctccatgtca	147840
ctgaccactg	tagggatccc	agccacagac	acacacacac	acacgcgcgc	acacacacac	147900
actgcaaaac	actgccacag	cttctctgaa	attttgtttt	ttgttttttt	tttttgtaaa	147960
ctttgcaatg	cttgagtttc	tggatataag	cccatttgat	tcattgattt	caccttcttc	148020
agtaaaagact	catgccctta	aaagccccc	taattagagg	actttcagac	tgcattgggt	148080
tgggtgggtg	gtcagtttgt	ttcttatcat	taattcccaa	tgattcataa	atgctgaact	148140
tttttttttt	tttttagcag	tgatgagcta	tccactctcc	gaagggaac	tggaccagaa	148200
gacagccatg	tcactcctgt	ggaagtccct	tccccttggt	gtaagagtct	aggaatcatg	148260
ggaattgggt	gagaccagga	gagggacaag	gacttgccca	aatcatagag	caattaaatg	148320
gcagaatgaa	gactggggcc	tcagggtttc	ccccatcttt	ccaccttttc	cacttcatct	148380
tccaccctag	cggggagttg	cacagggtct	atgggggtca	ccattgaggc	aggactttct	148440
ggtgggctgg	agaagctgca	tcgctcacc	ggggctgggt	gtcacttttt	gatctatttc	148500
agtgcattgc	taaggaaact	attccagaag	ccactgagaa	atacttagga	ggaacagacg	148560
acactgtcaa	aaagaaagac	ctgttccctg	acttgatagc	agatgtgatg	tttgggtgtc	148620
catctgtgat	tgtggccggg	aaccacagag	gtgagtcaca	gaggtcgaac	gggagggaca	148680
caaaccacac	gagcttctgt	atctgaccca	ctcactctcc	agcatagaca	gacatggaaa	148740
cagctgaggg	tcaggccctca	aaggctgatt	ccatatggca	tgggatgagg	tgtgtgtcta	148800
ttttggttta	tgccagcaga	agactgtgag	aaaaaaaaat	ccagaggcaa	gtgggttttt	148860
taaggtgatg	atcccagata	acagcagtag	ggaggtgggg	aagtgagaga	ggaaagagat	148920
ggaatccaat	ccaagatgcg	ttgtcaaggg	agtatccact	gtggacaact	ggagcgggga	148980
aactcaaggaa	aacaccaaga	atacagggct	caggggcac	ccatctgagt	ggcaaggagg	149040
ccgggtattt	attcaccagc	ttctacttgt	cattggttga	aggctcttgc	aaggaaatgt	149100

ttattcctcg	tgacttcgac	ctgctgcaca	caagggcaga	gtagtctctt	gtgaccagac	149160
aaaggcctca	ggcctggagc	tgacagatgct	ggaggtggaa	gtcaggctgg	catgcccagg	149220
aagaggggat	ataggtgaga	ccctggcagc	atctgctgca	agggctccat	gcctggagtt	149280
attgtgggac	atagggctgc	tgtaggacaa	atattgaaag	atgagtcgtg	gaagggtttt	149340
aaggtctgag	ccagctgcaa	acaagtttgt	taagcattgg	agctggataa	aaagtgggag	149400
ccctgcatgg	gatccagagg	attgtccagg	accaagaagg	ccagagagag	gagccagggc	149460
gggtgtggga	gaggtggtct	gtagaatggc	agtgtctgag	ggtggttttt	atgcatctca	149520
gtgctgagc	tagcatgcaa	gcacagggca	agggcagggg	ctatgcagga	cctgctacca	149580
ctgacccaag	gctgtgtggg	tggggcatga	cgttagggat	gtgtgtgtct	acctagagag	149640
gagtgctctg	tcctgcgtgc	cagctagagg	agattcacag	gattcctttt	cttcagctc	149700
tcattcgct	agtctgcaag	ctaggaaatg	tcctctctct	aaccatgctg	gaagggtttt	149760
taaatttaga	acttcataag	catgataaaa	actagctaac	gcttaactag	caggtgccct	149820
gacacacctt	tgacagggaa	ggggcaggtg	ctcataaccc	tcatttcttc	acagggctct	149880
gataaaaacc	tttaaccaag	accactggag	ttgaatctgt	tccttcttaa	acttgcctct	149940
gccctatgct	ctgcgtctga	actatatata	gagttcccat	ctccattttc	tgatggtttg	150000
agcaatctg	aaacttatgt	tttcatctgg	tttcccatga	ctttaagttc	agggcttttt	150060
tttttttttt	tttttttgcc	aggactacac	agattttatc	tactttcact	tattgtgtgc	150120
tcactctttt	tgataaaata	acattttctga	atataaaatt	aatatgttaa	attatagaaa	150180
ctttcaaaaa	tatggaaaca	caaaaagag	aaactatgta	tcactcatth	ccactacctg	150240
gaggcaagtg	ctataaattt	tttgtgtttt	cgtctaaaga	ttttccatgt	cctatatact	150300
ttaaaaatca	attttatatt	ttacttttgt	ctatagaaca	ctatgtgtg	aggattttct	150360
caatgttgat	acaaactcat	caaagcattc	cttattccat	gaaatggctg	tggttaaatag	150420
actttaatat	tcatactcta	ttagatgttt	agcctggcta	ctcacattct	gatgctacaa	150480
taacattgag	ctcagcctaa	tgttcataag	tctctaaaca	catgtctaat	aattttctta	150540
ggattattht	tagaagtaaa	taactaggtt	ggacaatgca	aatgttttag	aactttgggc	150600
aaatctgta	aaattgcatt	ccactgcata	agaatgtgga	tttcttaatt	ctctttctca	150660
tttgggatgc	taagattaaa	aattagcata	acacttccag	tttcataagc	cttccccacc	150720
aacaagaagc	acatcagcct	gttttaatct	gcattgcctc	catgactagc	cctctcattg	150780
tctctgcttc	tcttattatg	tctaattgtc	attacccaaa	tctgtgcgct	actttcctct	150840
gaagacttgt	gttgtgattg	taagaattgt	ataaatatca	atggcttttag	ccaaaagagtt	150900
ttacaaagta	cgttttgggc	agcatgctgc	ctataataag	ttctatcatt	cacaaaagct	150960
ctttcttcta	tgtttggctc	tgagtttctt	tggaataatgt	tcgaggggca	aaggcaaggt	151020
caaaccctcc	ttttagcaag	ttttgtttga	ccttgaagca	gccatttaac	aggtggatta	151080
cagagccaca	gaaggatggc	atcttcccag	gtgcgcttcc	tgctgagccg	aggggtgcagt	151140
gcaggaggct	gacaaagatg	agtgaataga	ttattcttca	ttctcacatt	gaaatgacat	151200
gtgcgggtgg	ggcatgaggt	tagggatgcg	tgagctccca	ttgttaaatc	cttttgtgaa	151260
cgaattttta	atgatgttaa	gaaatgatgg	ctggaggcgg	tggtctctgc	caacactctc	151320
agcatttttg	gaggctgagg	tgaggagcct	atgagagcct	aggatttcaa	gatcagcctg	151380
ggcagcatag	tgagaccctg	tctctacaaa	acaatttaaa	agggaaagtga	ttacagtgtg	151440
ctacaaaata	ccatatataa	tatcatcccc	agttaaatac	ataaaaagaga	gatatgctaa	151500
aataaaaaag	aagcattctc	tgagtggtag	agttatgagt	gatactttaa	atttgattgt	151560
taaaattgat	tttttaatta	tatagatat	ggaaaaattt	tagaaggaaa	tacaaaaaatt	151620
gcattggcct	tgcttcaggt	agtggaaatta	tgagtgatat	ctagttttgc	tttatgcgct	151680
tccatatttt	tgtttcttct	aattattcct	aattgttttt	attttccaaa	tttcttactg	151740
taccctaaag	ggaggacatt	gtaaattttc	tccaccagcc	tggtattgcc	ctgactcttt	151800
ccgtcttagt	gtcacttctc	agtgggtatc	atgaccagtg	caaagtgtctg	aggcacaggg	151860
ccaggcgcc	cacgaggtag	ccctgaaggg	gcagcgatct	gtggctccaa	tgagccaatc	151920
attgggaaac	tggcatcttc	ctggggctgg	gacaggagag	ctttgttggg	gggagaggag	151980
ggcagagccg	aaggagagag	ggcaggggag	aggcaaggct	acccttgctc	agcgcttctc	152040
tttctctgcc	agggttttac	tgcttaaca	ccctaact	cccaggccag	gcaggcagca	152100
agacacatgg	ggacagttag	ctataaaagca	gtgagtgcctg	cagggttctg	agacacaaga	152160
ggcagattgt	tccctctctg	catatgtttg	tatttaaaata	gcctcatgtt	cagacaagca	152220
acttggaatt	gcttcagctc	tctcaggatg	ggtgagaaaa	acactggaaa	tgctcaaaac	152280
gaggcagaac	agaagacacc	tgctatgggtg	gagatggcat	ccaagtgaat	gaacgcgagt	152340
ctgttatcaa	tgaattatat	cgggtgtaac	cagatgtaga	gagattgtct	tgtgtgagaa	152400
tgaccagca	ggcaaggggg	tttacgaggc	agagtcaggg	tcctgcacc	ggcagctgtt	152460
ttaaatgaat	tgacccaggg	tttccacatt	cattcattaa	acatttgttc	attgaacaaa	152520
tatttggtc	taattccgct	tccacctcag	acagctatgc	agcccgaggc	acatcactga	152580
gctttctcta	gactctgttt	ctctactgtg	ctcagagcca	gaggtttggc	gcagagctgg	152640
agaccttgg	agcctccagg	tggtgtgtctg	gcaacatgaa	ctgtgcatga	atccttgtct	152700
tctcagatgc	tgagacaccc	acctacatgt	atgagtttca	gtaccgtcca	agcttctcat	152760
cagacatgaa	acccaagacg	gtgataggag	accacgggga	tgagctcttc	tccgtctttg	152820
gggccccatt	tttaaaaggt	aatgctcctt	cctgtctgtg	agctaggagt	tagagacttg	152880

gggtccagtc	ttggtgtggt	ggccttcagc	aattttgtcc	tctcctggtc	ttagtttccct	152940
gattctgtat	aacaggggttg	aatgtcactg	gggtgtccgc	cggttctctc	ccactctaac	153000
acatgtgagg	agggatgtgt	attcatgtgc	cctctgcaca	gacgtcaga	atcctgtgtg	153060
gtgacatcaa	gacaggtggt	gggtgggggtc	tcctgcagga	ttcactatga	cagggttgaa	153120
tgctactggg	ttgttccccg	gcttctctcc	gctctaacac	acctgaggga	ggatgtgtat	153180
catgtaccct	ctgccacaga	cactcagaat	cctgggctgt	gtcatcaaca	agataggcgg	153240
tgggacacat	gcggggccct	gctctaggtt	gagaagccac	caatcaattt	ccctctccca	153300
ggagcgctga	gacagttagt	gaggggtgaga	ttagaattgg	tgtaaaccct	aagtcaggtc	153360
taatgtgtgc	ctgtttgtct	ttctgtctgt	ctctaacaaa	aactcataaa	cctttacatt	153420
tagtacattt	aataattggt	gatttagaat	tcacaggatg	tatgaatttg	gaacaggaga	153480
agagaatatt	ttttatatgg	tttatagtca	gcaagggtggc	catcccacag	gctgggaagg	153540
tgctcttggc	caagcccaga	aacgggctca	ttggaggagg	gggtgggtag	gagctttatg	153600
tgaacggatt	ggctaacaat	acatgttcaa	caggttacag	ggggagcaat	ggatattcat	153660
gaagacagtc	ctgacacatg	tgtattaaac	aaacatgtat	gtaacatggc	ccatgttcac	153720
ctgggtgggtg	agacctaata	tttaaatgta	ttacaattag	ggcctgtaag	tccaaaggtc	153780
ttctcaggac	acgaagctca	gcaagtggag	agcttctgta	caccggccag	gtccagtcga	153840
tggtgtgtga	tgttcttctc	tggagaaagt	tactgaaatc	agtctcttat	gcaatcaaag	153900
cagtagttaa	gtctggcaag	tcagggttct	gtttgtctgc	gtatcccagc	tcagccggtt	153960
gttattgttt	tccttttgct	tagctccagg	cagtgctggg	tttagctgct	agagaaaggag	154020
aagcacctcg	tggcagttag	aacaaagtgg	attctttttt	ttttttatta	ttataacttta	154080
agttttaggg	tacatgtgca	cattgtgcag	gttagttaca	tatgtataca	tgtgccgtgc	154140
tggtgcgctg	cacccactaa	ctcgtcatct	agcattaggt	atatctccca	gtgctatccc	154200
tccccctcc	ccccacccca	ccacagtccc	cagagtgtga	tattccccct	cctgtgtcca	154260
tgtgatctca	ttgttcaatt	cccacctatg	agtgagaata	tgccgtgttt	gggtttttgt	154320
tcttgcgata	gtttactgag	aatgatgggt	tccaatttca	tccatgtccc	tacaaaggac	154380
atgaactcat	cattttttat	ggctgcatag	tattccacgg	tgtatatgtg	ccacattttc	154440
ttaatccagt	ctatcattgt	tggacatttg	gggtgggtcc	aagtctttgc	tatttgtaat	154500
aatgccgcaa	taaacatacg	tgtgcatgtg	tctttatagc	agcatgattt	atagtcattt	154560
gggtatatac	ccagtaatgg	gatggctggg	tcaaatggta	tttctagttc	tagatccctg	154620
aggaatcgcc	acactgactt	ccacaatggg	tgaactagtt	tacagtccca	ccaacagtgt	154680
aaaagtgttc	ctattttctc	acatcctctc	cagcacctgt	tgtttctctg	cttttttagg	154740
atgcaggcct	gaacccttgc	ccgacgtggc	cttaggtctc	gtttttaatt	tggtgtctta	154800
ttgccacaaa	gagtgtgttc	tgtcagaatg	atgaccttca	ttttattgct	gatgctgggc	154860
cgggtgggtc	taaatcacaa	aagggaggga	gtattatgag	gcgtgtctga	cctcctgtcc	154920
gttcccgagg	aggaacagag	ttgaagggtt	ttcgaggctc	cccttagccc	agagagggtc	154980
tgttcagtc	gttgggggtg	tcaggatttt	atttttagtt	tacattatac	aatagtttaa	155040
aaaatccttt	cacgggtgtct	tctaagtctt	aactctcagc	agttacagat	cagatgggac	155100
tcaccccatg	gctgctcaga	acgcaccagc	gcctctgggc	atctcactgt	gcatgcttag	155160
gcgccttgcg	gctctgttgt	ttttcagaat	gtgaattgtg	gggtgtgtgt	ggggaggagg	155220
aaaagaccca	agagagagca	accctggaaa	gtgggggtgc	tgtagaggaa	accctggggg	155280
ggggcatttc	ctgtgaccct	gagcgaggag	agggtcacag	agggtcacag	gagacaaagg	155340
cagccagcca	atggaatgac	gcatgcccac	tgctgagccc	taggtcagat	atgctgaaag	155400
gtaaagtaca	cacaaatcca	ccacgatctt	ctaaaagtgc	agacctcagc	tcagtgggtg	155460
tggggcatgt	gccaagacta	tgtttccagc	agactcgcat	gtgatgttga	cgctgcagtc	155520
cacggaccac	actttgagta	acaaaggctt	tttttcttct	tccccacaga	gggtgcctca	155580
gaagaggaga	tcagacttag	caagatgggt	atgaaattct	gggccaactt	tgctcgcaat	155640
gggtgaggct	ggtggcaaaag	acagagcacg	gctggtgagg	gtggggggcg	gggcatgcct	155700
attgggaagg	ggcagcttct	aaggttctag	tgatcaaact	tctgacctg	tgaccatagc	155760
actctgataa	tgagagctct	ctgcaaacgg	agaggccgcc	cctggagata	gtgagctctc	155820
catctctgga	ggtatacaag	cctcttgaca	gagataaact	gggcatcctc	acacatctct	155880
gaagattggt	gggaacacac	agcagctttg	gggcaattct	aattgattct	gtttccagaa	155940
accccaatgg	ggaagggtcg	cccactggc	cagagtacaa	ccagaaggaa	gggtatctgc	156000
agattgggtg	caacacccag	gcggcccgga	agctgaagga	caaagaagta	gctttctgga	156060
ccaacctctt	tgccaagaag	gcagtggaga	agccacccca	gacagaacac	atagagctgt	156120
gaatgaagat	ccagccggcc	ttgggagcct	ggaggagcaa	agactggggt	cttttgcgaa	156180
agggattgca	ggttcagaag	gcattctacc	atggctgggg	aattgtctgg	tggtgggggg	156240
caggggagag	agggcatgaa	ggagcaagtt	tgtatttgt	gacctagct	ttgggaataa	156300
aggatctttt	gaaggccaaa	ttggtgcttg	tgtctgttac	tggagattaa	tactttgtcc	156360
tcagagacag	aacgggtgatg	aaagaggcga	tgtgagaagg	aagggtggctt	tgtgggggat	156420
ggcctgggtct	caggatgagc	agagtccaga	gggctgggtc	atggacgggtg	ctcaggggag	156480
ctctgggctc	gatgcacctt	tctgggcccc	caacaatttc	caacaatacg	agttgggggtg	156540
gccagagtcg	aggatcccta	ccctctattt	ggagtggccc	atggaaatgg	aagtggccca	156600
ggctgagaat	gagtcctggat	cagggaagag	ggagcgtgct	tgagggtatc	ccgtggcact	156660

gttgcatggc	acttactgac	cattgcacag	gcctgcaaca	cctttctgag	tatgtacact	156720
agcctcccat	acccctccat	gaggttgtct	cttcaccaa	ctggctcgaa	ctccttctgt	156780
agcctggacc	acttctgtg	tgggcagtga	ccaccttgga	ggtggtccat	tcttctccag	156840
agggtcatcc	taaactgtgt	ctttcagaat	cccatgggtg	atcttctggat	tctgttagta	156900
cgtagaaaagc	tctaaagcat	gtcattcccg	ccttatcagc	aagaggaagc	cggattgtcc	156960
tcaaaatcat	aacttttct	gcaccaaaga	gctgaagtgt	caaggcacat	ggttccctcg	157020
aaatcgaagg	gaagacaagc	acctggggga	gtggtgggat	gtgaacactg	gcttacttct	157080
cacctgcagg	caggagacgg	cgtgaccata	atgagcagaa	atactctatg	aattttattc	157140
agtgtggaag	gccaagggtg	ggccactgtg	agagtataaa	acctctggga	accatggacc	157200
catggggagt	tgaactccat	cacagactct	actccatggg	tatttatcag	ggcccatgag	157260
aaagattggg	gtagacagt	agactggaga	aagtctgcct	tcaggaatgc	aggcatgagc	157320
cctgctgaca	cccttcaccc	ctaaagaaca	aaatccttca	atcattgcgg	aatggccagg	157380
aaatcttgtc	ctcctcaagg	tactggtaga	gacatattga	ggttgaagat	aaggaacctt	157440
ttaaaactct	atacccttg	gagagggaca	gggagtcac	ttgggcccag	attatcggct	157500
ttttactgct	ggggatggtc	agtatctctg	gcaaacctcc	atctccaaca	gcaagaaatg	157560
aaggctctgc	ctaaggttga	ggctggacca	cgacaagagc	aggcactcct	ggctgctacc	157620
atggagttag	ccagtcccg	gtaacagaaa	tctgctgctg	ggagagagag	caaagcatgc	157680
agatcaaccc	tcttgtaaaa	gcaggtgcac	aggacaggcc	taaagctgag	agtggaacaa	157740
gagattagga	aaatcgttca	gaaaaaccggc	ctttacacaa	gcacaccaga	accagcacia	157800
ggtagcactg	gaagcatttg	aagcagatgg	tgcattgatg	atagccatag	caacaacaaa	157860
actattcccc	gatcaccaca	ctcgaataac	acacgcacac	acacacacac	acgcatgcat	157920
gtacacacaa	aatcagtcct	gcagcagaag	aaaagatatg	tccacttct	gtcacggata	157980
ctacttactt	cagtttcaac	tactttaccc	atgatgtcaa	gtattgaatt	caaaattgca	158040
aaccttataa	aggaagcaac	acctatgaac	aagagacaaa	gcagttgggc	acagtggtgc	158100
atgcctgtag	tcccagctac	ttaggaggct	gatgcaggag	gattgcttga	acctgtgagt	158160
tcaaggctgt	agtgcactgt	aattgcacct	atgaataacc	acctgcactc	tagtcatggt	158220
attatggtga	aatagcatcg	cttagagtga	gagagagaga	gagagacaga	cagacaaatc	158280
aatcaacaga	accagattca	gagataacct	agggtgttaga	ctaacagact	gggaatttaa	158340
aataactata	tgggaatactt	ccatgaacag	atggctagt	tcagcagaga	ggtagaaaat	158400
atgagaaaaga	agcaaataga	aatgttagaa	atgaaaaaaa	atagtaacag	aaattagaaa	158460
tgctctaat	ggattcatca	gtagatctga	cacagctgac	gaatgaatga	gtgtagcaga	158520
agacaggcca	atataaatta	cccaacttaa	aatgaagaaa	atcagtgaat	aaaaaacaaa	158580
acaggggaatc	aaagaactgt	cagataatat	ccaatggtcc	aacatagtca	taactggaat	158640
cccagaaaaga	gaagacaaag	caggcagaag	aaaatatttg	aagagataat	ggctgagaat	158700
tttccaaaag	ttaatgaaaa	catcaaggca	tacgtccaag	agcctggaaa	accccaagca	158760
ggattcaaca	acaacagcaa	caacagcaac	aaaaacatac	acatttagac	acacactgag	158820
aaaatattga	aggcagccag	aggaaaaaga	cattgcatac	aaagaaagg	attagagcag	158880
atttttcact	ggaaactatg	caagccaaaa	aataatggag	tgacaccttt	aaagtattca	158940
aacgaaaaaa	atctttgcag	aattctatat	ccagaaaaaa	cactgttcaa	aaaatacagg	159000
gaaaaatgtt	ttcagatgaa	caatagagag	aattttatact	tacatacttg	tgctaccaa	159060
aatgtaaaag	gaaattctct	acgcataaag	tatatgatag	aggataaaaa	ctttgatatt	159120
tatcaaagaa	gtgaagctct	acatatagct	ttaaaaataa	ggtaatgtag	gctatttttc	159180
ctatatttaa	ttactgttta	aaacaaaaat	agcaccaatg	aactgtggat	ttagagcata	159240
cgtaagaata	aaatatacaa	caaaaataat	atgaaagatg	agagacagg	atttgaagca	159300
cacttttcta	agattcttac	actctgtgta	attggtattg	tctgaaggta	taaggtgatt	159360
aatgtatat	gtatgtatat	tgtataccca	ggaaaaacaa	taaaataatt	taaaaggaga	159420
catgaataat	aacacaatag	aggagataac	atgaaatcat	aaatactcgc	tacacgagca	159480
agcagacaga	agaagaacaa	agacacagga	acaaatgaaa	aagtactgca	gaagtgcag	159540
attttaatcc	aaccgtatca	ataactatac	tacacaaaaa	tgatgtaaac	acaccaatta	159600
aaaatgattt	tcagattgga	ttaaagaaaa	cacaaaaacgc	aacctaacgc	tgctgctgag	159660
ttagtccaaa	ttcacgttct	agtgtttgac	tcctggtggc	ttttaagcct	cagccttccc	159720
ttgtcccctc	ttgtgcacac	ctggaaagct	gataagaaaag	cctgggtgct	tcctcctttg	159780
ttgtctggag	aaaattcaaa	gcttaccgtg	agaaagctga	ccacggcccc	agtgcggaat	159840
cctcatacca	cacctggtcg	tcctgtccaa	gacagcgtcc	cagagctcct	tgagcctcag	159900
cgggggggaag	aaacagcata	ttttttcctc	ctggtccaga	gagaggggag	acgctacaga	159960
gcaggggtcg	gtaagctgca	gcccacaggc	caaacctgtc	agaccgtggg	atccttgggt	160020
caggaccaag	gtcaaaactcg	ttttggggct	ccccaagaag	tgctggggcaa	tgcaacctgg	160080
tggatggact	gagagctgcc	cagcagatgg	atctgtaccc	agggaaagtc	acattggcct	160140
ttggtgaaca	gtccatggta	cccttgaact	ctataataat	agcagtaata	ggccggggcgc	160200
ggtgactcgc	acctgtaatc	ccagcacttt	gggaggccga	ggtgggaggga	tcacctgagg	160260
ttaggagtgc	gagaccagcc	tgcccaaacac	ggtgaaatct	catgtctaca	aaaaatacaa	160320
aaattagctg	gacgtggtgg	cgggtgcctg	taatcccagc	tagtcggggg	gctgaggcag	160380
gagaatcgct	tgaacccggg	aggcggagg	ggcagtgagc	caagatcatg	ctactgcact	160440

ccagcctggg	caacaagagt	gaaacaccgt	cataaaagaa	agaagaaaga	aagaaggaaa	160500
gaaggaaaga	aagaaagaaa	gagaaagaaa	gaaagaagga	aagaaggaga	gataaagaaa	160560
gaaggaaaga	aggaagggaag	gaaggaaaga	aagaaagaaa	gaaagaaaga	aagaaagaaa	160620
gaaagaataa	tagcagtaat	agaaataact	aaaactcact	gcatagttat	tatgtgttta	160680
attataaaat	actcttcata	ttaactcaga	gagtcttcac	agaaactcta	tgagcagttc	160740
atttggtatc	aacca					160755